COVID-19 Genomics Insights Dashboard (CGID) #15

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 in the past week*:

1009

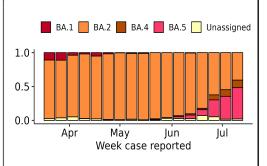
new genomes since the last report on 29/6/22

~12,500

genomes reported so far in 2022

Variant surveillance:

BA.5 (pink) is now the most prevalent Omicron lineage across NZ community samples, making up ~47% of cases in the last week. See next page for annotated figure.



Hospital surveillance:

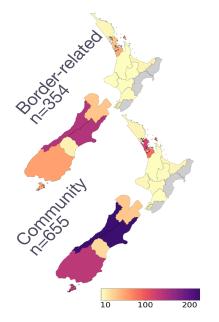
~22% (122 of 554)

of PCR positive cases with a hospital admission date in the past fortnight have been genome sequenced.

Composition of hospital cases:

- 57% BA.2
- 8% BA.4
- 35% BA.5

Graphical overview of where new border and community genomes originated from*.



Number of genomes sequenced [*border/community metadata is sometimes missing]

Key Trends & Insights

- This past week Omicron BA.5 has overtaken BA.2 as the most prevalent variant circulating within Aotearoa. Models predict BA.5 will reach 90% of all community cases in early August.
- Given the relative growth of BA.5, there is very high certainty that BA.5 is driving up case numbers around the country (and internationally).
- Border surveillance reveals that ~63% of border-related cases arriving into NZ are BA.4 or BA.5.
- Two additional BA.2.75 cases are reported at the border this week. As yet there is no indication of community spread of BA.2.75.
- BA.4/5, was detected at all (~21) wastewater sentinel sites tested this week. Tracking variants over the past 5 weeks had BA.4/5 at: 2.8%, 6%, 10.5%, 33% and now 53%.
- Cases of reinfection are being detected across the country, but remain a relatively low proportion of total cases. ESR continues to monitor genomes of reported reinfection.

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.

^{*}new genomes are typically collected over the preceding fortnight

Frequency of SARS-CoV-2 variants in the New Zealand community each week (March 2022 - 11th July) throughout 2022 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 'Omicron unassigned' is typically where a partial genome has been recovered and a definitive assignment to a variant is not possible.]

