

COVID-19 Genomics Insights Dashboard (CGID) #16

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:

1101

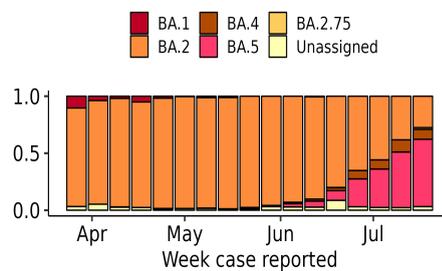
genomes from cases reported within the past two weeks (2nd-15th July)

~13,500

genomes reported so far in 2022

Variant surveillance:

BA.5 (pink) is firmly established as the dominant Omicron lineage across NZ community samples, (~61%) of cases in the last week. BA.2.75 appears for the first time. See next page for annotated figure.



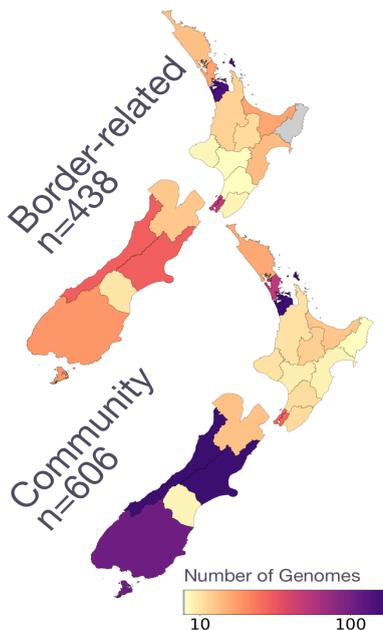
Hospital surveillance:

~21% (140 of 665)

of PCR positive cases with a hospital admission date in the past fortnight (2nd-15th July) have been genome sequenced. Composition of hospital cases:

- **37% BA.2**
- **11% BA.4**
- **52% BA.5**

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

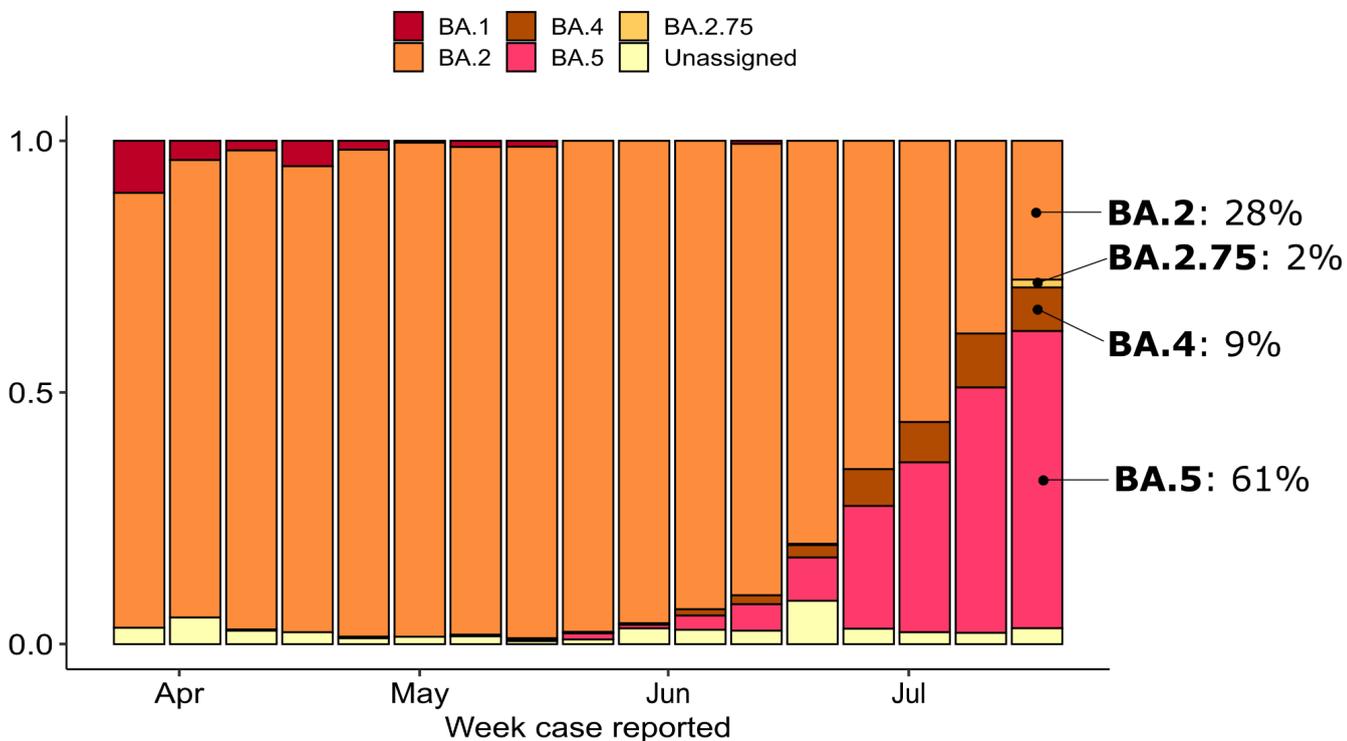


[*border/community metadata is sometimes missing]

Key Trends & Insights

- Omicron BA.5 is firmly established as the most prevalent variant within NZ, models predict it will reach ~90% of all community cases in the next fortnight.
- Six new cases of the Omicron BA.2.75 variant have been detected. Two of these cases are from the community and have no clear epidemiological link to the border (there are genomic links). It is probable that small numbers of BA.2.75 are transmitting within the NZ community - it remains highly uncertain what impact, if any, this will have on case numbers, reinfection and spread relative to BA.5.
- Variants detected at the border (dominated by BA.5) are consistent with international surveillance and trends.
- BA.4/5, was detected at all 21 wastewater sentinel sites (see next page). Aggregated data over the past 6 weeks detected the proportion of BA.4/5 at: 2.8%, 6%, 10.5%, 33%, 53% and now 73%. No BA.2.75 was detected at any of the sentinel sites.

Top: Frequency of SARS-CoV-2 variants in the New Zealand community each week (for the past 17 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 28: ending 17th July. Note: The level of precision and sensitivity in the percentage estimates can be uncertain.



Wastewater Variant Data Week 28 (ending 17th July)

