

# COVID-19 Genomics Insights Dashboard (CGID) #20

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:

**1,394**

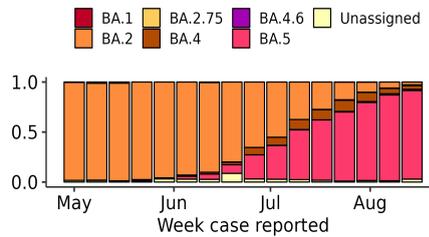
genomes from cases reported within the past two weeks (30<sup>th</sup> Jul-12<sup>th</sup> Aug)

**~18,000**

genomes reported so far in 2022

### Variant surveillance:

BA.5 (pink) continues to be the dominant Omicron variant across NZ, making up 91% 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:

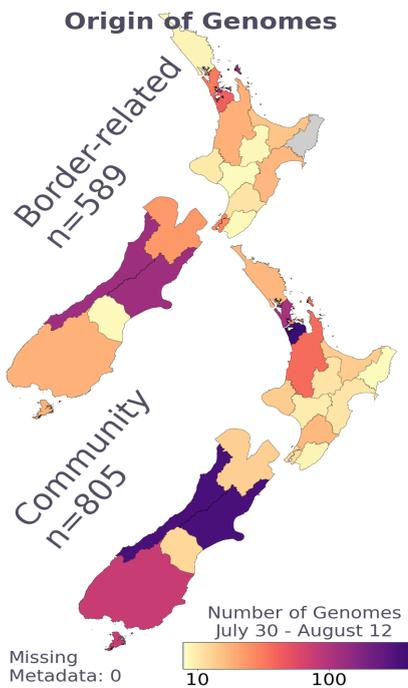
**~27%** (177 of 664)

of PCR positive cases with a hospital admission date in the past fortnight (30<sup>th</sup> Jul-12<sup>th</sup> Aug) have been genome sequenced.

Composition of hospital cases:

- 7% BA.2
- 8% BA.4
- 85% BA.5

### Graphical overview of sample acquisition (30<sup>th</sup> Jul-12<sup>th</sup> Aug)

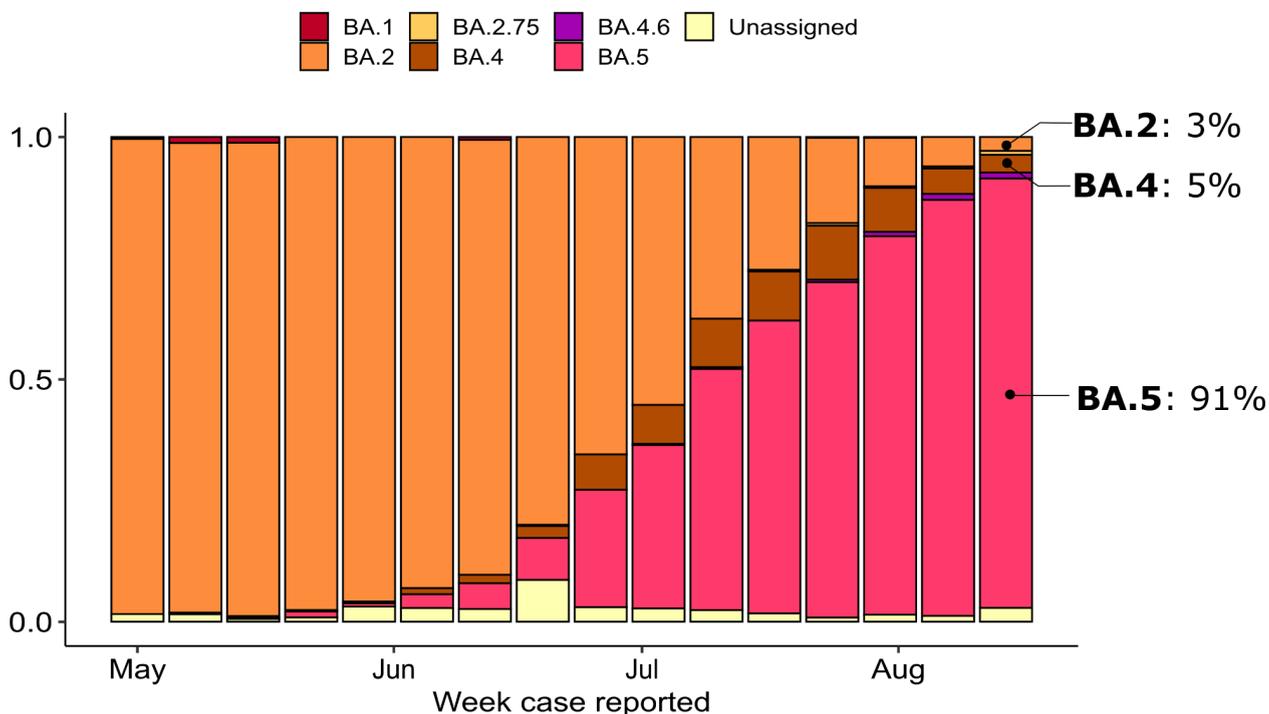


### Key Trends & Insights

- Omicron BA.5 remains the dominant variant and continues to increase in prevalence week-on-week. In the last reporting week it was 91% of all sequenced community cases.
- We continue to monitor and report upon a relatively small number of Omicron BA.2.75 (4 cases) and BA.4.6 (9 cases) that are detected within the community.
- BA.4/5 was detected at all wastewater sentinel sites. Estimated BA.4/5 levels are at 98% (up from 93% last week). 13 of the 20 sentinel sites were 100% BA.4/5.
- 21% of all reported border cases had their genome sequenced. Variants detected at the border (dominated by BA.5.2) are consistent with international surveillance and trends.
- In this reporting window ~3.4% of BA.5 cases detected in the community were suspected 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 32: ending 14th 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.



### Wastewater Variant Data Week 32 (ending 14th August)

