

# COVID-19 Genomics Insights Dashboard (CGID) #26

The COVID-19 genomics insights dashboard (CGID) provides a public and high-level overview of viral genomic surveillance across Aotearoa, New Zealand. 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:

<p><b>Genomes analysed:</b></p> <p style="font-size: 2em; color: orange; text-align: center;"><b>728</b></p> <p style="text-align: center;">genomes from cases reported within the past two weeks (15<sup>th</sup>-28<sup>th</sup> Oct)</p> <p style="font-size: 2em; color: green; text-align: center;"><b>~23,500</b></p> <p style="text-align: center;">genomes reported so far in 2022</p>	<p><b>Variant surveillance:</b></p> <p>BA.5 (pink) continues to be the dominant Omicron lineage across Aotearoa, making up 80% of cases in the last reporting week. BQ.1.1 has been added to regularly tracked lineages (~8% in the most recent week)</p> <p style="text-align: center;"><i>See the next page for the annotated figure.</i></p> <div style="text-align: center;"> </div>	<p><b>Hospital surveillance:</b></p> <p style="font-size: 1.5em; color: blue; text-align: center;"><b>43%</b> (133 of 308) of PCR-positive cases with a hospital admission date from 15<sup>th</sup>-28<sup>th</sup> Oct have successfully produced a genome. Composition of hospital cases:</p> <ul style="list-style-type: none"> <li>- &lt;1% BA.2</li> <li>- 11% BA.2.75*</li> <li>- 6% BA.4.6</li> <li>- 80% BA.5</li> <li>- 3% BQ.1.1</li> </ul>
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Graphical overview showing sample origins (15<sup>th</sup>-28<sup>th</sup> Oct)

Num genomes from cases reported  
October 15 - October 28

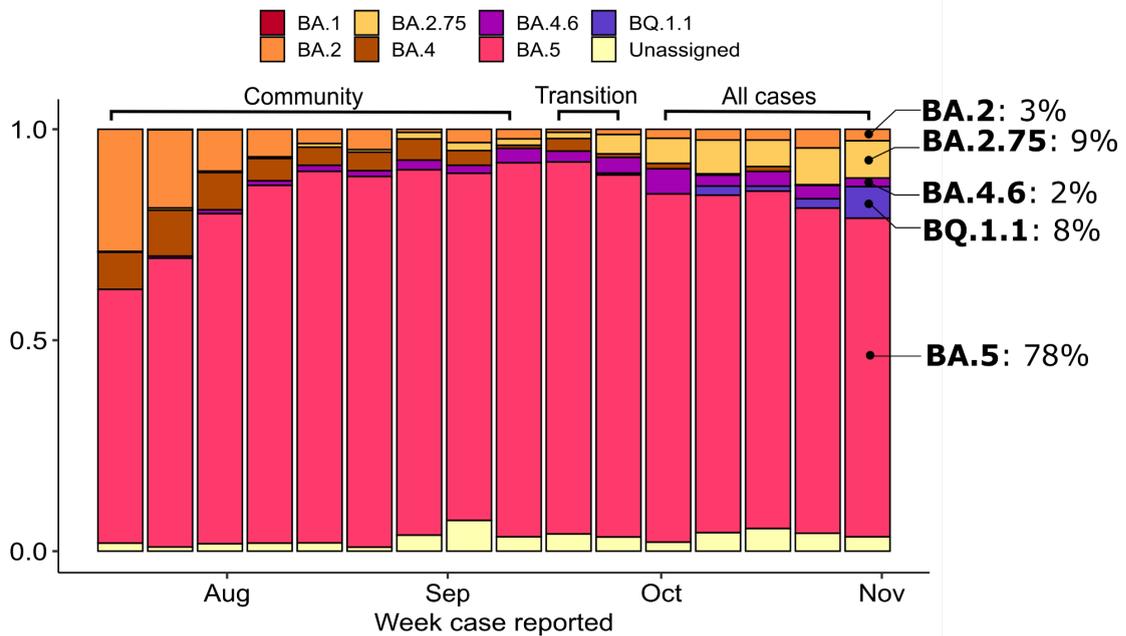
0    50    100    150

**Key Trends & Insights:**

- BA.5 remains the dominant variant, accounting for ~80% of cases in the two-week reporting window. BA.2.75 and BQ.1.1 have grown relative to BA.5 in recent weeks.
- In the past fortnight, ~2.1% of all New Zealand COVID-19 cases were sequenced.
- We continue to watch variants that are trending up overseas. We identified 26 cases of BQ.1.1 and 15 XBB cases in the past fortnight - these are spread around the country. Consistent with overseas data, there is preliminary evidence that new variants (such as BQ.1.1) are over-represented in reinfections.
- BA.4/5 remains the dominant variant in wastewater (~87%). However, detections of BA.2.75 and BQ.1.1 are trending upward. BQ.1.1 was detected in 6/20 sentinel sites. The XBB variant was detected for the first time in wastewater in a single wastewater catchment.
- There remain challenges tracking the growth and locations of new Omicron variants such as BQ.1.1 and XBB due to the relatively low number of samples currently available for genomic surveillance.

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.

**Figure:** Frequency of SARS-CoV-2 variants in the New Zealand community each week (for the past 16 weeks) as determined by whole-genome sequencing. Only variants with a frequency above 1% are shown. 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]. For weeks before the end of the COVID-19 Protection Framework, only data from community cases were used. In the period marked as “transition”, cases known to be associated with the border are removed, but not all such cases can be reliably identified. Data from all New Zealand cases are used since October.



**Figure:** The Omicron variant ‘Infection history’ of community cases across Aotearoa, New Zealand in 2022. Estimates are calculated by projecting Omicron variant frequencies (as determined by WGS) onto the 7-day rolling average of cases (y-axis). Note; Biases in samples referred for sequencing and case underreporting will be reflected in these projections, accordingly they should be regarded as indicative.

