

COVID-19 Genomics Insights Dashboard (CGID) #25

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:

Genomes analysed:

359

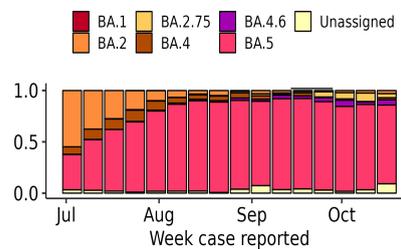
genomes from cases reported within the past two weeks (1st-14th Oct)

~22,500

genomes reported so far in 2022

Variant surveillance:

BA.5 (pink) remains the dominant Omicron variant across Aotearoa, making up 85% of community cases in the last reporting week. Other variants continue to be detected at low levels. *See the next page for the annotated figure.*

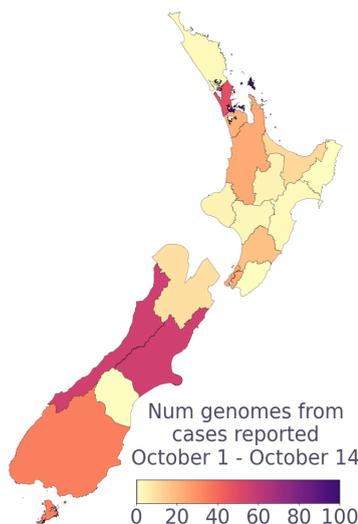


Hospital surveillance:

During the current report period, a Ministry of Health review identified a coding issue that affected the identification and reporting of COVID-19 hospitalisation data.

As a result, we cannot determine the WGS composition of hospitalised cases in this reporting period.

Graphical overview showing sample origins (1st-14th Oct)



Key Trends & Insights:

- BA.5 remains the dominant variant among sequenced cases, accounting for ~85% of cases in the two-week reporting window. BA.2.75 (8%) and BA.4.6 (3%) levels remain fairly constant.
- We identify three cases of BQ.1.1 and one XBB case - we continue to watch these variants closely based on overseas trends.
- The relatively low number of cases is reflected in fewer samples available for genomic surveillance (ESR is currently requesting all positive samples). In the past fortnight, ~1.5% of all New Zealand cases were sequenced.
- BA.4/5 remains the dominant variant in wastewater (aggregate ~91%). Detections of BA.2.75* are trending upwards. BQ.1.1 was detected in wastewater from Western Auckland, Rotorua and Porirua. No XBB has been detected in wastewater.
- There are 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 and the lack of ability to distinguish cases associated with the border from those actively spreading in the community.

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 in the most recent weeks.

