August 2024

COVID-19 Genomics Insights Dashboard (CGID) #51

CGID provides a public and high-level overview of SARS-CoV-2 genomic surveillance across Aotearoa New Zealand. It aims to explore and explain how whole genome sequencing (WGS) complements other epidemiological data to support public health decision-making.

Summary Infographic & Insights:

genomes analysed

243

genomes* from cases reported since the last CGI report (12 July 2024)

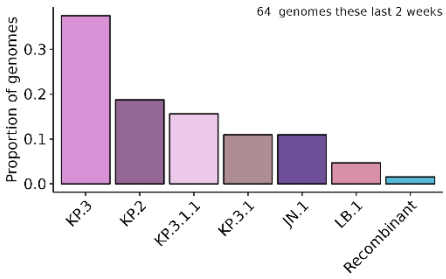
~7100

genomes* reported in 2024

*Number of genomes successfully sequenced. Number processed is higher due to failed WGS attempts & cases sequenced multiple times

variant & lineage

KP.3 lineages dominate (64% overall) with KP.3.1.1 emerging (16%) among KP.3.1 sublineages (11%) with KP.2 increasing (19%) and LB.1 stable (4.7%), while JN.1 lineages continue to decline (11%)



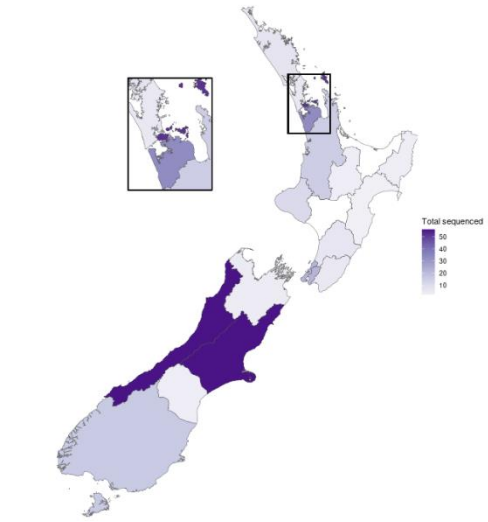
hospital cases

22% (122 of 554*) of PCR-positive cases with a hospital admission date from 27 July to 9 August have been sequenced to date.
The approximate composition of hospital cases:

- **KP.3** **43%**
- **KP.3.1** **13%**
- **KP.3.1.1** **9%**
- **KP.2** **11%**
- **JN.1** **11%**
- **LB.1** **5%**
- **KP.2** **5%**

*The total number of PCR positive admitted cases includes high Ct samples not suitable for sequencing, samples that fail to produce genomes and cases reported late in the reporting period.

Origin of sequenced samples



Number of SARS-CoV-2 genomes sequenced

Key trends and insights

- The rise of KP.3 lineages is led by KP.3.1 and especially KP.3.1.1. All KP.3 lineages make up 64% of sequenced cases and are expected to continue to dominate over the coming weeks.
- KP.3.1.1 displays a 5% growth advantage compared to the dominant KP.3. This result is consistent with international results and the designation of KP.3.1.1 as a Variant under Monitoring by the WHO.
- The sampling for WGS-based surveillance of COVID-19 has changed. From July 2024 onwards, ESR will sequence approximately 95 samples per week.
- We explore the effects of the decreased sampling for SARS-CoV-2 surveillance by calculating the power to detect a variant of interest while it is still uncommon in the community.

WGS sampling

The sampling strategy for Covid-19 Genomic Surveillance recently changed. Prior to 1 July 2024 ESR requested all PCR positive samples with PCR Ct values less than 30 (and samples with no recorded Ct) from cases not recently sequenced. From July 2024 ESR has been performing one sequencing run (sufficient to attempt sequencing on 95 swabs) per week. The sample selection criteria have been altered to prioritise samples expected to produce the best genomic data and provide appropriate geographical sampling. From 1 July 2024 ESR has performed incidence-weighted sampling by health district (i.e. requested samples from each health district to reflect the number of reported cases in that region) and prioritised samples with Ct less than 25.

One of the major goals of the genomic surveillance of SARS-CoV-2 is the early detection of fast-growing variants that may have an impact on caseloads. We used a mathematical approach[1] to measure the effect of the recent decrease in sampling on this goal. Assuming an unbiased sample of 95 swabs and a sequencing success rate of 85%, we would expect to detect a variant with a 10% per day growth advantage before it reached 1% of community cases 71% of the time (**Figure 1**).

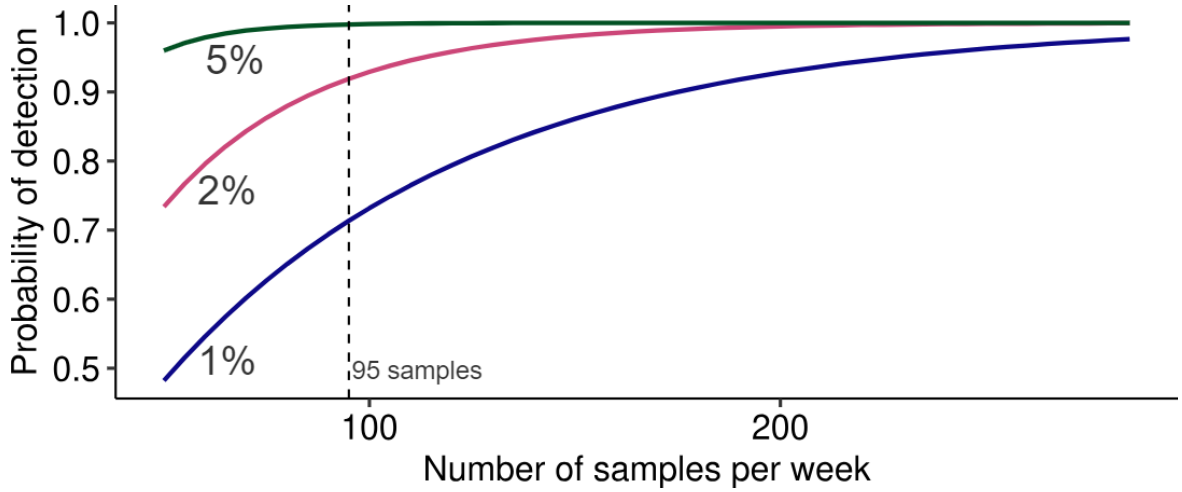


Figure 1**.** Probability of detecting a fast-growing variant (y-axis) before it reaches 1% (blue line), 2% (red line), or 5% (green line) of community cases with respect to the number of samples sequenced each week (x-axis).

The current sampling approach retains relatively good power to detect a variant of interest while it is still rare in the community, however it should be noted that the uncertainty of estimated growth rates or regional differences in the frequency of variants will be increased compared to the previous approach.

Only PCR samples are suitable for WGS, and the COVID-19 Testing Plan prioritises PCR testing for cases in hospital and residential care. For this reason, sequenced cases are not a random or representative sample. As previously reported, the most notable bias is in the age of sequenced cases, which is either substantially younger or older than reported cases (**Figure 2**, **Figure 3**).

[1] Wohl S, Lee EC, DiPrete BL, Lessler J. 2023. Sample size calculations for pathogen variant surveillance in the presence of biological and systematic biases. *Cell Reports Medicine*. 4:101022. doi: https://doi.org/10.1016/j.xcrm.2023.101022

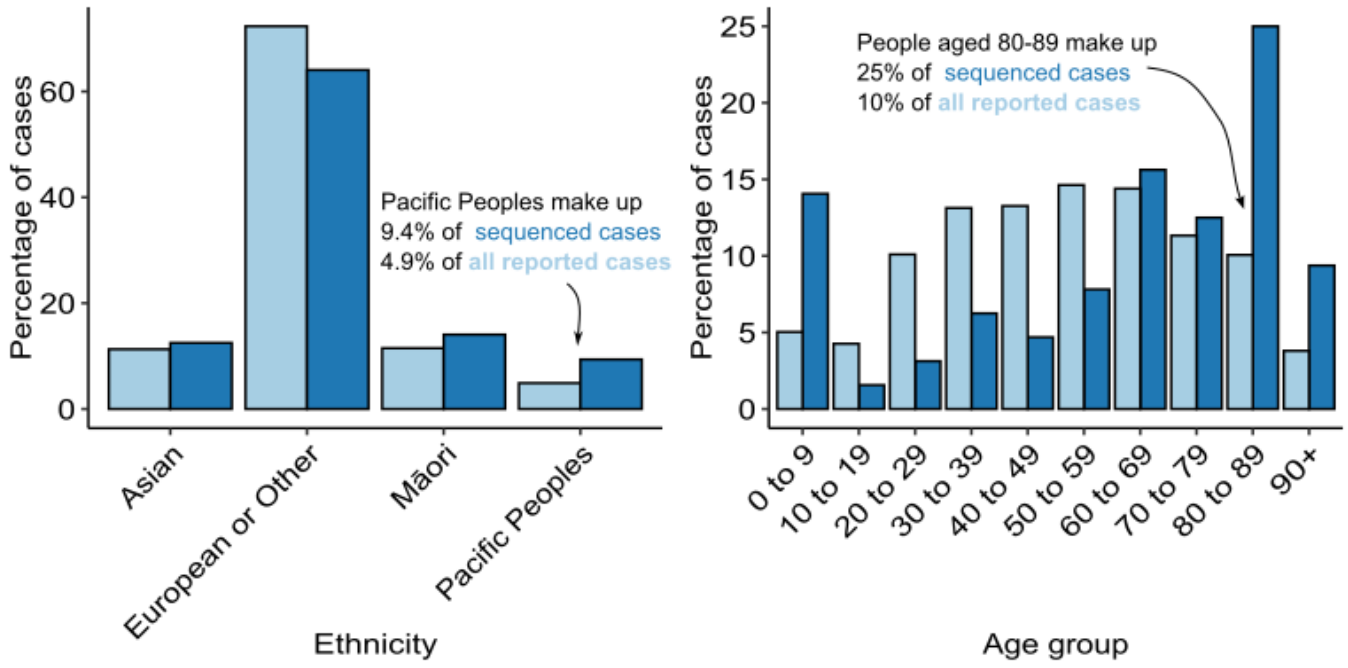


Figure 2. Left: *Distribution of sequenced cases (dark blue) and all reported cases (light blue) by ethnicity. Each case is assigned to a single ethnicity for this analysis, with priority order Māori, Pacific Peoples, Asian, European or Other.* ***Right****: Distribution of reported and sequenced cases by age.*

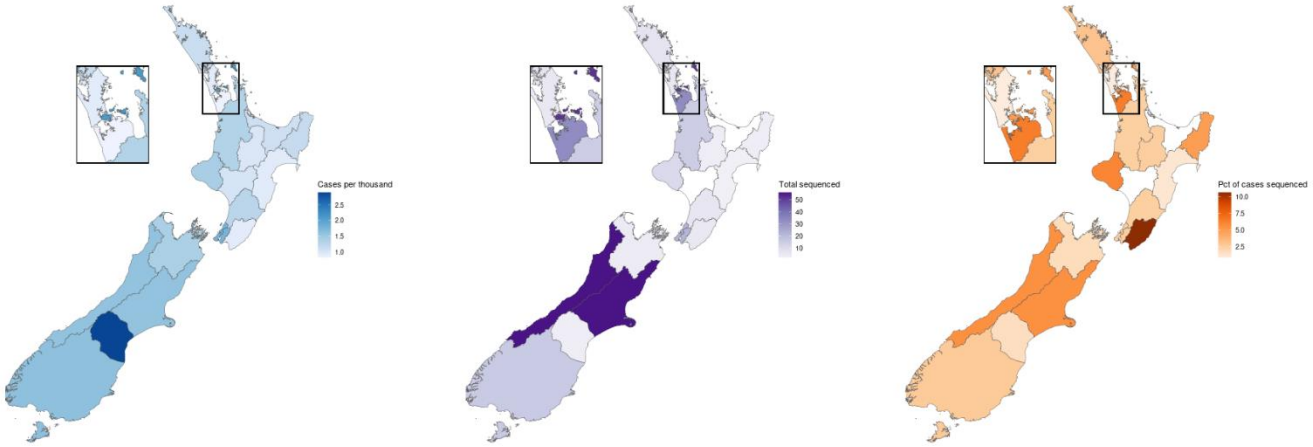


Figure 3. *Geographic sampling of COVID-19 cases and genomes since the last CGI. From left to right, each Health District is shaded by the number of reported COVID-19 cases per thousand, the number of sequences obtained, and the percentage of all reported cases sequenced.*

Tracked Variants

Tracking the frequency and epidemiological properties of SARS-CoV-2 variants is a key goal of the CGI report. These reports follow the Pango nomenclature to classify sequences (https://cov-lineages.org/). The specific lineages of the sequenced genomes are then grouped into higher-level classifications representing the evolutionary relationships between lineages and potential increases in transmissibility or immune evasiveness. **Figure 4** describes the set of tracked variants used for this report and how they relate to each other. A fuller description of these variants is provided in the Appendix to this report.

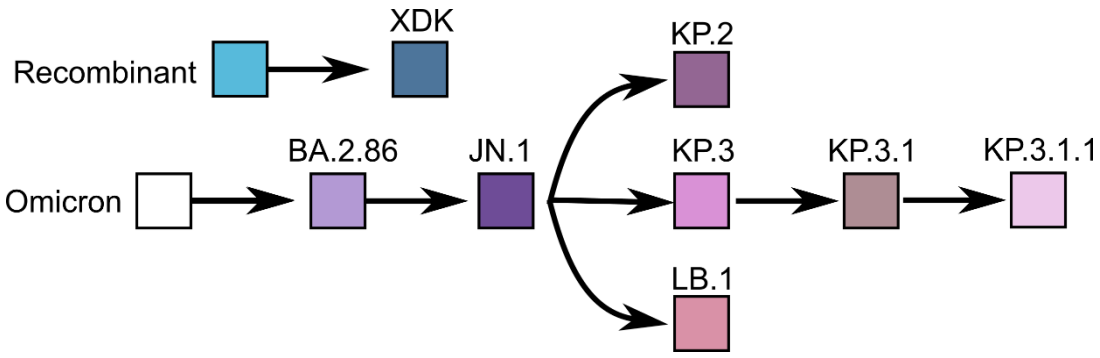


***Figure** 4. Relationships between the variants tracked in this report.*

Changes made since last report

The variants tracked in the CGI reports are frequently updated to reflect trends in SARS-CoV-2 evolution and epidemiology. This month the following changes have been made:

- KP.3.1.1 has been added to the list of tracked variants.

Overview of sequenced cases

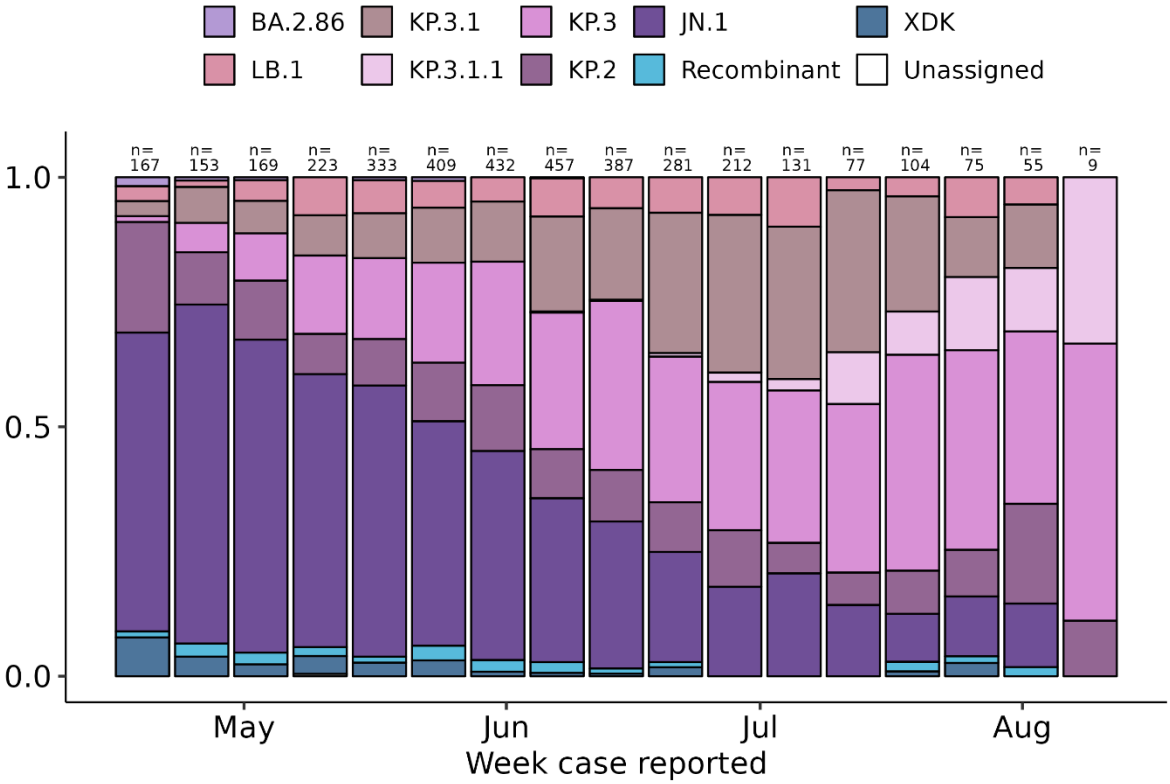


***Figure** 5. Frequency of variants/lineages in the past 17 weeks. Note, data for the most recent two weeks is preliminary. It will be updated as additional cases reported within these weeks are referred to ESR and sequenced. Data from each reporting week is based on the number of genomes indicated above each bar. Tracked lineages are defined in **Figure 4** and Appendix Table 1 Error! Reference source not found..*

KP.3.1.1 emerges among KP.3 lineages

The KP.3 lineage has continued to grow in frequency (**Figure 5**). Overall, the KP.3 lineage was responsible for 64% of sequenced cases from the last two weeks. A specific KP.3 lineage, KP.3.1.1, has steadily increased in frequency during July. This lineage first detected on 7 June 2024 now accounts for a quarter of KP.3 genomes (15.6% of all sequenced cases in the last two weeks). The rise of KP.3.1.1 in Aotearoa is consistent with international trends. This lineage has consistently increased in frequency in North America and Europe and has been identified as a Variant Under Monitoring by the WHO

Among other tracked lineages only LB.1, a JN.1 lineage containing several mutations known to be associated with increased transmission, appears to be able to compete with KP.3. This lineage made up 5% of sequenced cases reported in the last two weeks and has been stable at approximately this frequency since May 2024.

Emerging Lineages

Most of the tracked variants defined for this report contain several distinct named sublineages, each of which descend from the named variant. ESR analyses SARS-CoV-2 genomic surveillance data closely to identify any sublineage that may display a growth advantage over the currently tracked lineage (**Figure 6**). These “emerging lineages” may give an early indication of the arrival or establishment of more transmissible variants in Aotearoa.

At present no emerging lineage has a growth rate comparable to KP.3.1.1. Among KP.2 lineages, KP.2.3 has been circulating at low levels for several months (first detected in NZ in March 2024) and appears to increase in frequency in recent weeks (**Figure 6**), with a 3.9% daily growth advantage over KP.3. KP.2.3 has one of the key mutations associated with increased transmissibility in JN.1 (S31-) and an additional spike mutation, and has been growing in frequency internationally and will continue to be monitored closely.

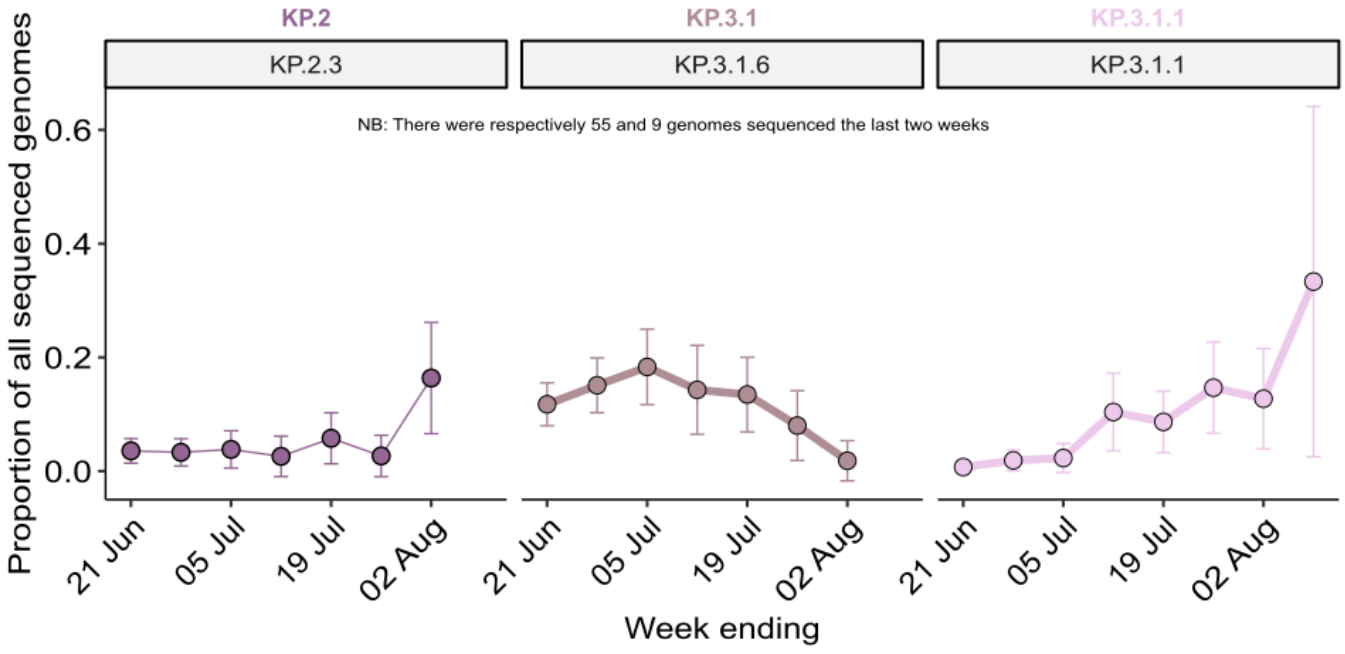


Figure 6. *Frequency of specific lineages in recent weeks. Each sub-plot represents data from a single lineage and all its descendant lineages not included elsewhere in this graph. The label above each subplot describes the tracked variant this lineage is reported under for the rest of this report*