July 2024

COVID-19 Genomics Insights Dashboard (CGID) #50

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

585

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

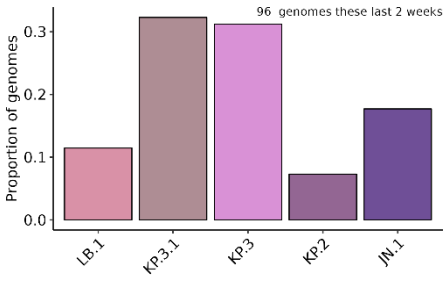
~7,000

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.3.1 (32%) is emerging among other KP.3 sublineages (31%) while JN.1 lineages continue to decline (18%), with LB.1 (11%) and KP.2 (7%) stable



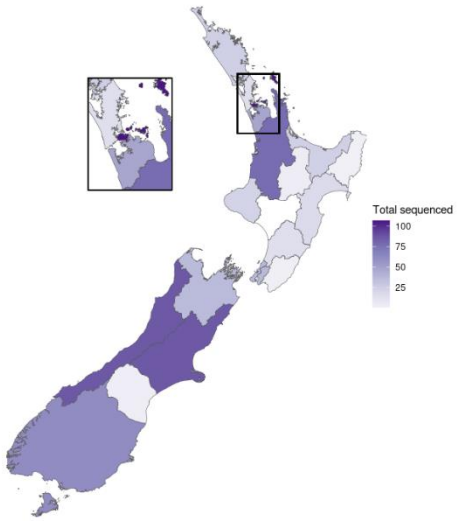
hospital cases

15% (48 of 312*) of PCR-positive cases with a hospital admission date from 29 June to 14 July have been sequenced to date.
The approximate composition of hospital cases:

- **KP.3** **38%**
- **KP.3.1** **27%**
- **JN.1** **16%**
- **LB.1** **14%**
- **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, that is currently the most common variant in Aotearoa. Together KP.3 lineages make up 63% of sequenced cases and are expected to continue to dominate over the coming weeks.
- Although KP.3 and other lineages continue to acquire new mutations, none of these emerging lineages are displaying a substantial growth advantage compared to the dominant KP.3
- The sampling for WGS-based surveillance of COVID-19 has changed. From July 2024 onwards ESR will sequence approximately 95 samples per week

WGS sampling

The sampling strategy for Covid-19 Genomic Surveillance changed during this reporting period. 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 will perform one sequencing run (sufficient to report approximately 95 genomes) 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 DHB (i.e. requested samples from each DHB to reflect the number of reported cases in that region) and prioritised samples with Ct less than 25.

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 substantially older than reported cases (**Figure 1**, **Figure 2**). The bias apparent from a younger age group (70 to 79) noted in the previous report is also present this month.

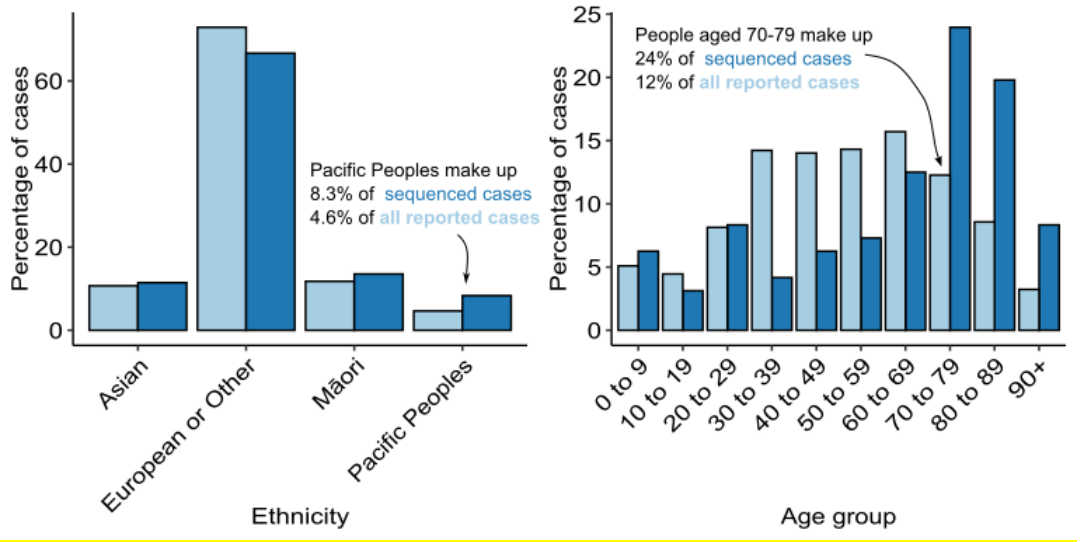


Figure 1. Left: *Distribution of sequenced cases (dark blue) and all reported cases (light blue) by ethnicity. Each case is assigned to a single ethnicity for this analysis, with priority order Māori, Pacific Peoples, Asian, European or Other.* ***Right****: Distribution of reported and sequenced cases by age.*

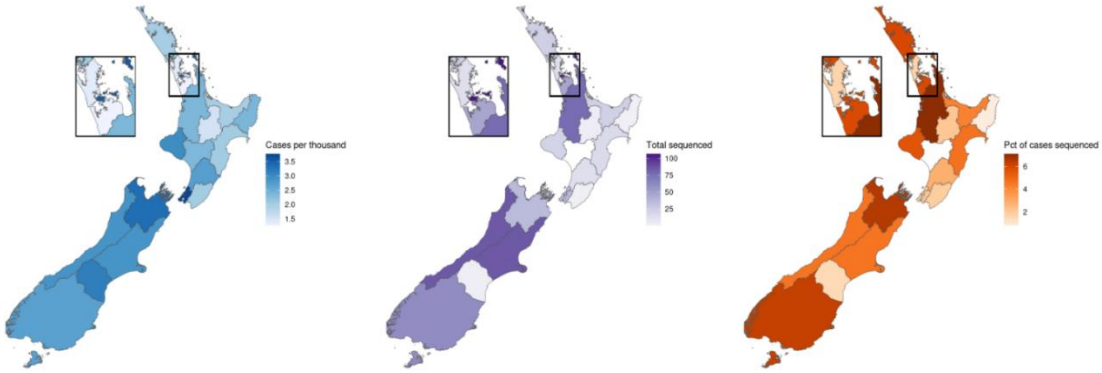


Figure 2. *Geographic sampling of COVID-19 cases and genomes since the last CGI. From left to right, each Health District is shaded by the number of reported COVID-19 cases per thousand, the number of sequences obtained, and the percentage of all reported cases sequenced.*

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 3** 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.

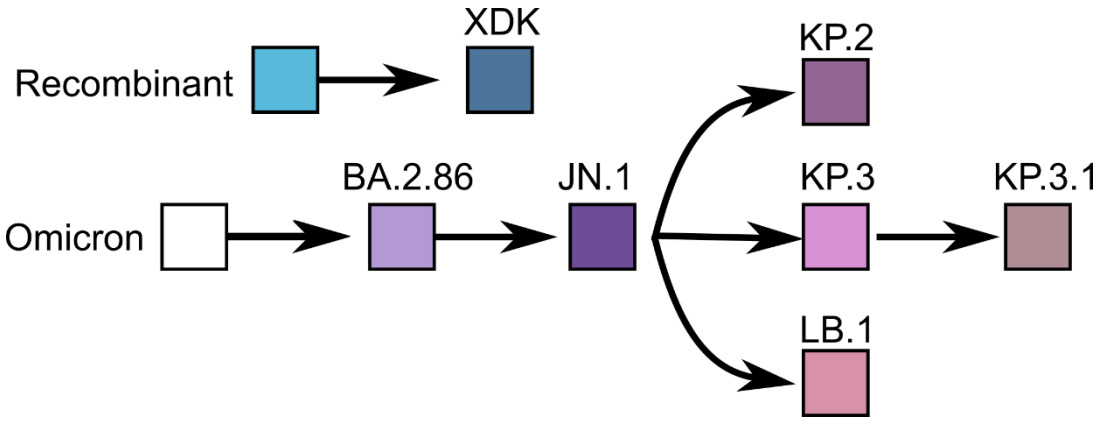


***Figure** 3. Relationships between the variants tracked in this report.*

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 has been added to the list of tracked variants.
- Several lineages circulating at very low levels are no longer being tracked separately: XBB, EG.5 and HK.3 are now reported in the "Recombinant" category, and, similarly, JN.1.4 and JN.1.16 are now reported under their parent lineage JN.1.

Overview of sequenced cases

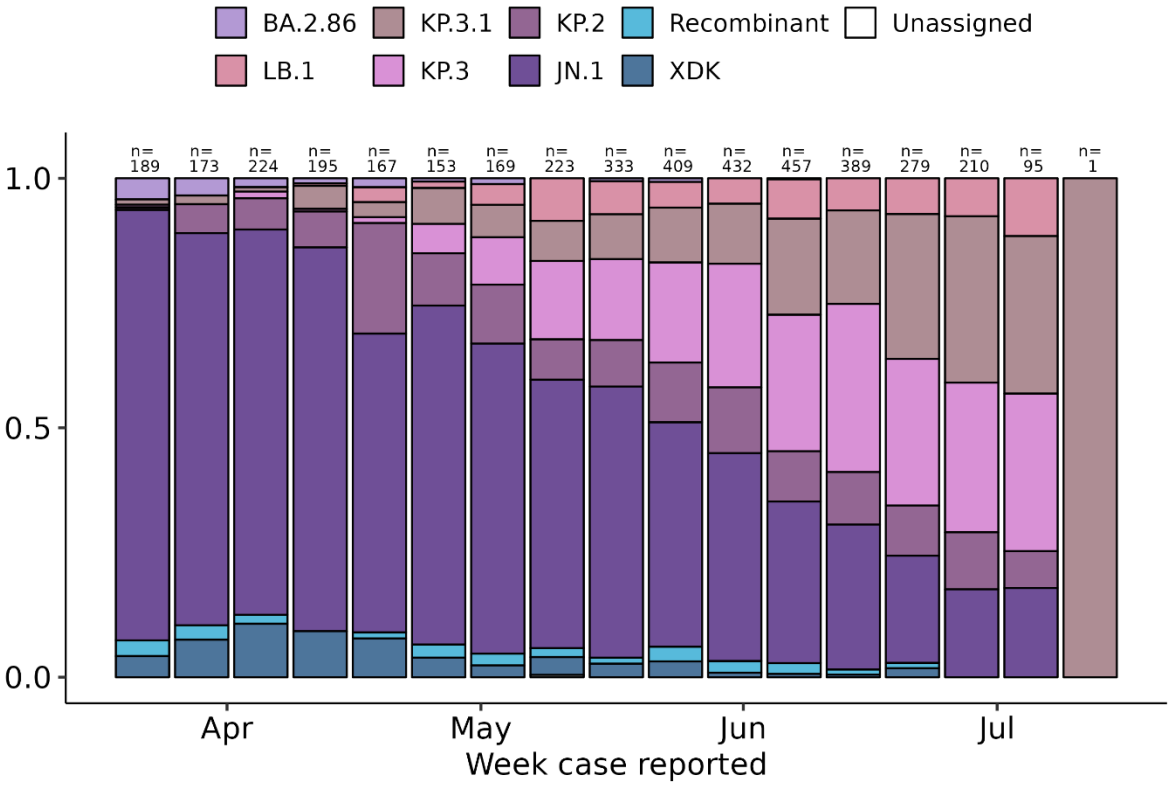


***Figure** 4. Frequency of variants/lineages in the past 17 weeks. Note, data for the most recent two weeks is preliminary. It will be updated as additional cases reported within these weeks are referred to ESR and sequenced. Data from each reporting week is based on the number of genomes indicated above each bar. Tracked lineages are defined in **Figure 3**.*

KP.3 continues to replace other JN.1 lineages

The KP.3 lineage (sometimes referred to as a 'FLuQE' variant due to specific mutations it contains) has continued to out-compete all other linages tracked in this report (**Figure 4**). Overall, the KP.3 lineage was responsible for 63% of sequenced cases from the last two weeks. A specific KP.3 lineage, KP.3.1, accounts for approximately half of these genomes (32% of all sequenced cases in the last two weeks). Given the large number of KP.3.1 cases, this lineage has been singled out as a tracked variant for this report. Both KP.3 and KP.3.1 demonstrate moderate growth advantages over the previously dominant JN.1 lineage (1% and 3% per day respectively).

Among other tracked lineages only LB.1, a JN.1 lineage containing several mutations known the be associated with increased transmission, appears to be able to compete with KP.3. This lineage made up 11% 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 5**). These "emerging lineages" may give an early indication of the arrival or establishment of more transmissible variants in Aotearoa.

Having firmly established as the dominant lineage, KP.3 is now generating new lineages with unique mutations. Two of these linages, **KP.3.2 and KP.3.3 are growing,** albeit at a rate similar to KP.3.1 or the parental KP.3 lineage. Neither of these lineages contain mutations known to be associated with increased transmission. Internationally, the KP.3.1.1 lineage has been a focus of attention. This lineage contains the S31- Spike deletion also present in LB.1, and has been growing in North America, Europe and other parts of the world. While it has been detected across different DHBs in New Zealand, it remains at very low levels currently, with only 8 genomes of this variant detected in the reporting window.

Among JN.1 lineages KP.1 (with one FLiRT mutation) and KW.1 (which includes KW.1.1, carrying one of the “FLiRT” mutations) represent the majority of genomes reported within the JN.1 lineage but neither are showing a growth advantage at present.

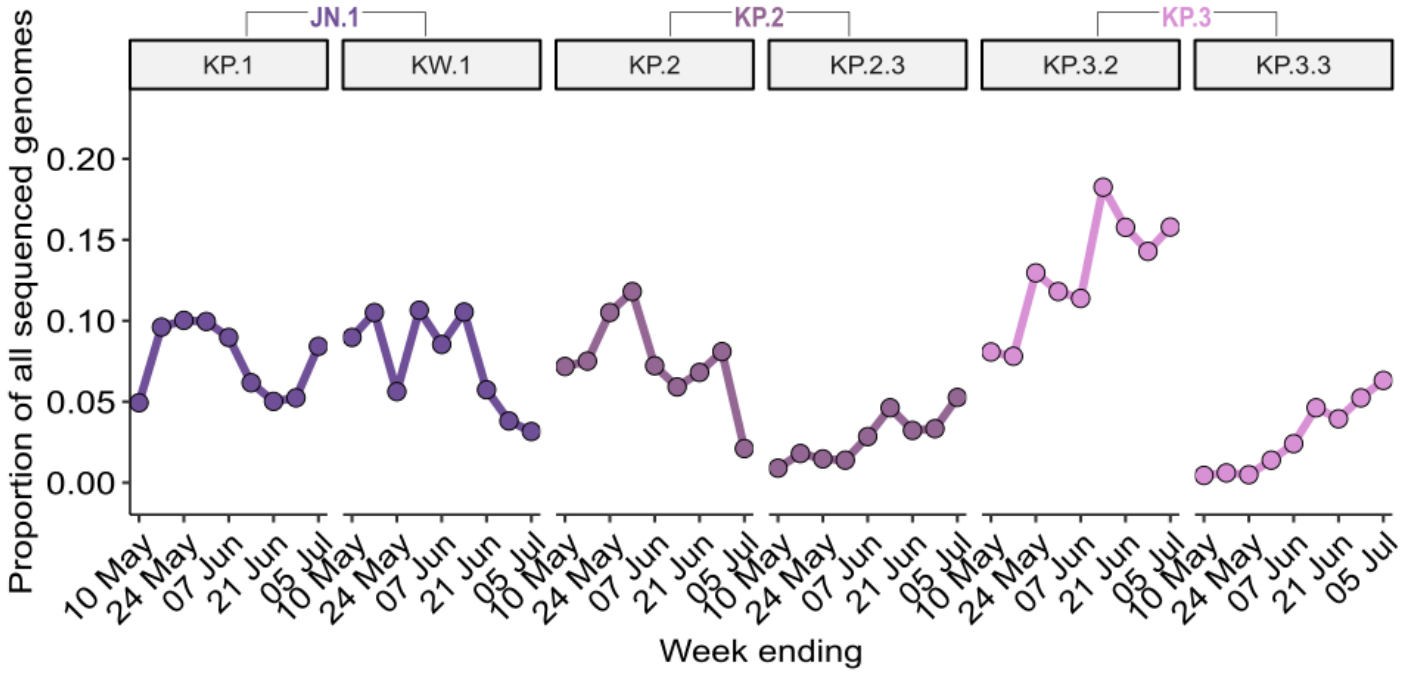


Figure 5. *Frequency of specific lineages in recent weeks. Each sub-plot represents data from a single lineage and all its descendant lineages not included elsewhere in this graph.*