8th September 2023

COVID-19 Genomics Insights Dashboard (CGID) #41

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 in Aotearoa New Zealand, and abroad.

Summary Infographics & Insights:

Genomes analysed:

687*

genomes from cases since the last report (4th August)

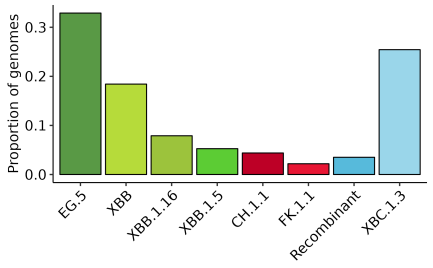
~9,500

genomes reported so far in 2023

* number of successful genomes. Sample no. processed is higher due to failed WGS attempts & cases sequenced multiple times

Variant surveillance:

The number of EG.5 (and its related XBB derivative) cases has been steadily rising, and now makes up 32% of all cases sequenced in the last two weeks. Meanwhile, XBC.1.3 cases have stayed at a consistent 21% throughout this fortnight



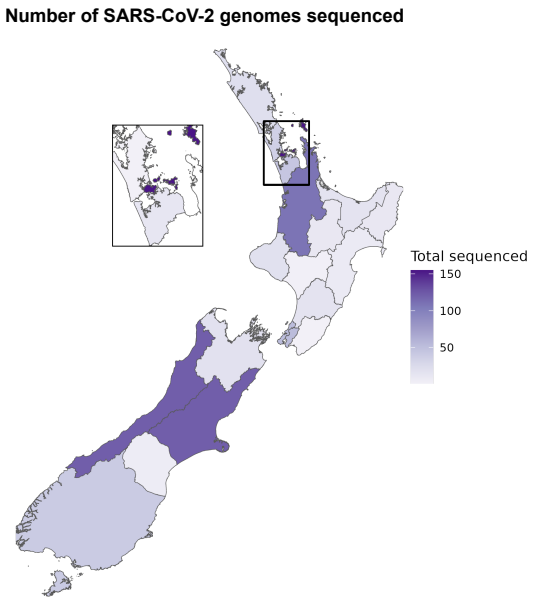
Hospital surveillance:

36% (85 of 239*) of PCR-positive cases with a hospital admission date from 18th Aug to 1st Sept successfully produced a genome to date. The approximate composition of hospital cases:

- EG.5: 31%
- XBB: 23%
- XBB.1.16: 13%
- XBC.1.3: 21%

*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.

Graphical overview showing sample origins



Key Trends & Insights:

- In Aotearoa, there hasn't been any detection of the BA.2.86 lineage so far
- The EG.5 lineage is spreading quickly. It's responsible for 32% of the recently analysed cases in the past two weeks, and it's growing by 4-6% each day, which is higher than other variants
- WGS relies on PCR samples, and COVID-19 testing prioritises PCR for hospital and care cases. This means the cases sequenced aren't random, and they mostly involve older individuals
- In August, we noticed a steady increase in a pair of mutations called "FLip". Right now, ~6% of genomes have both "FLip" mutations, and they can be found in different variants of the SARS-CoV-2 virus
- In Aotearoa, no specific EG.5 sub-lineages show a clear growth advantage over the wider group
- The results from wastewater testing match what is found in clinical samples, showing that EG.5 is consistently increasing. However, we can't distinguish XBC.1.3 in the wastewater data, but its parent XBC lineage remains stable

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

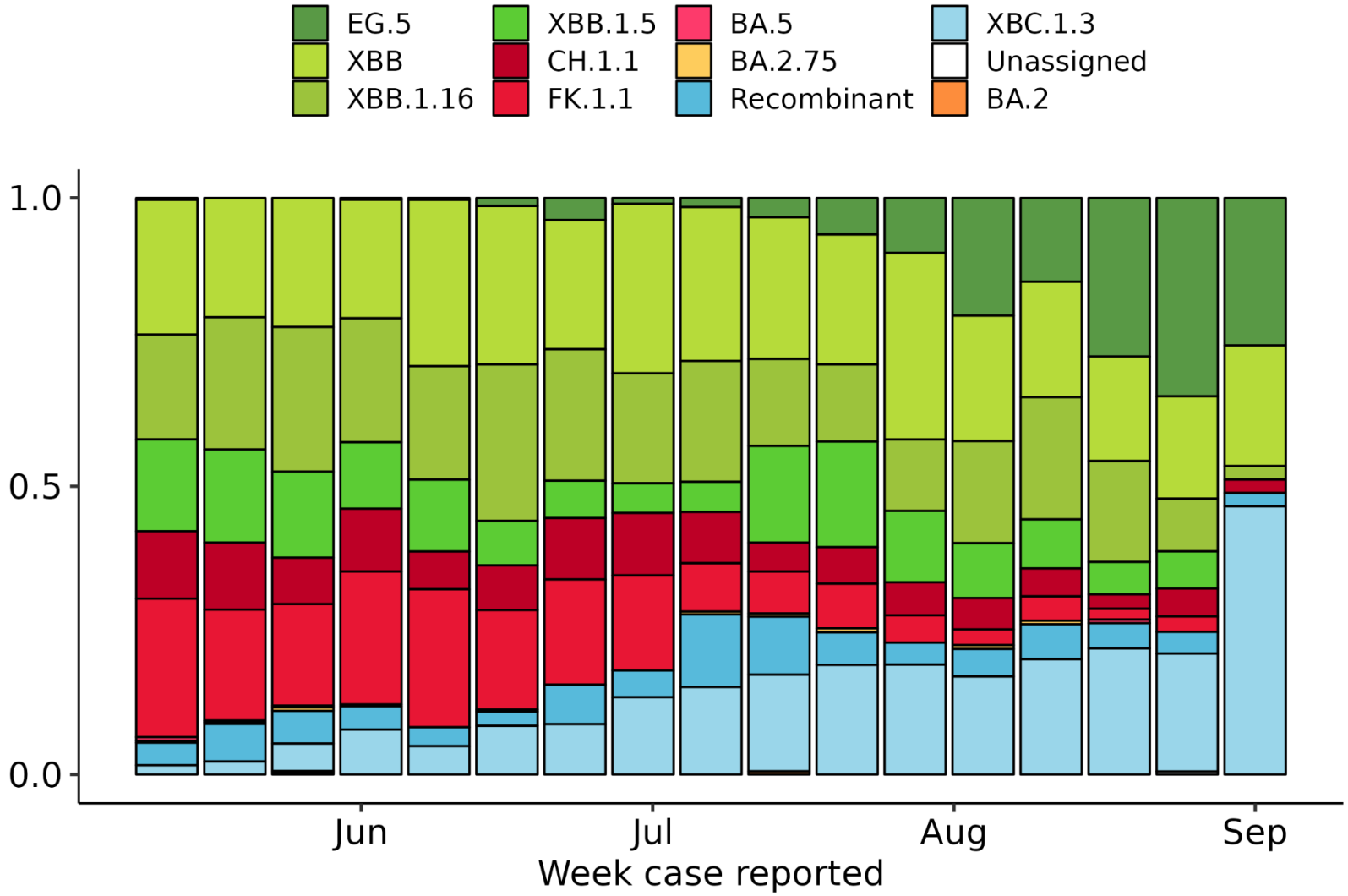


Figure 1: Frequency of SARS-CoV-2 variants in the New Zealand community each week (for the past 16 weeks) as determined by whole-genome sequencing*. Only variants with a frequency above 1% are shown. Data is subject to change as samples will still be added to the most recent two-week period.* In this case d*ata from the last reporting week is based on a limited number of genomes (42) as data is still being generated for this week. [The category 'unassigned' is typically where a partial genome has been recovered, and a definitive assignment to a variant was not possible].*

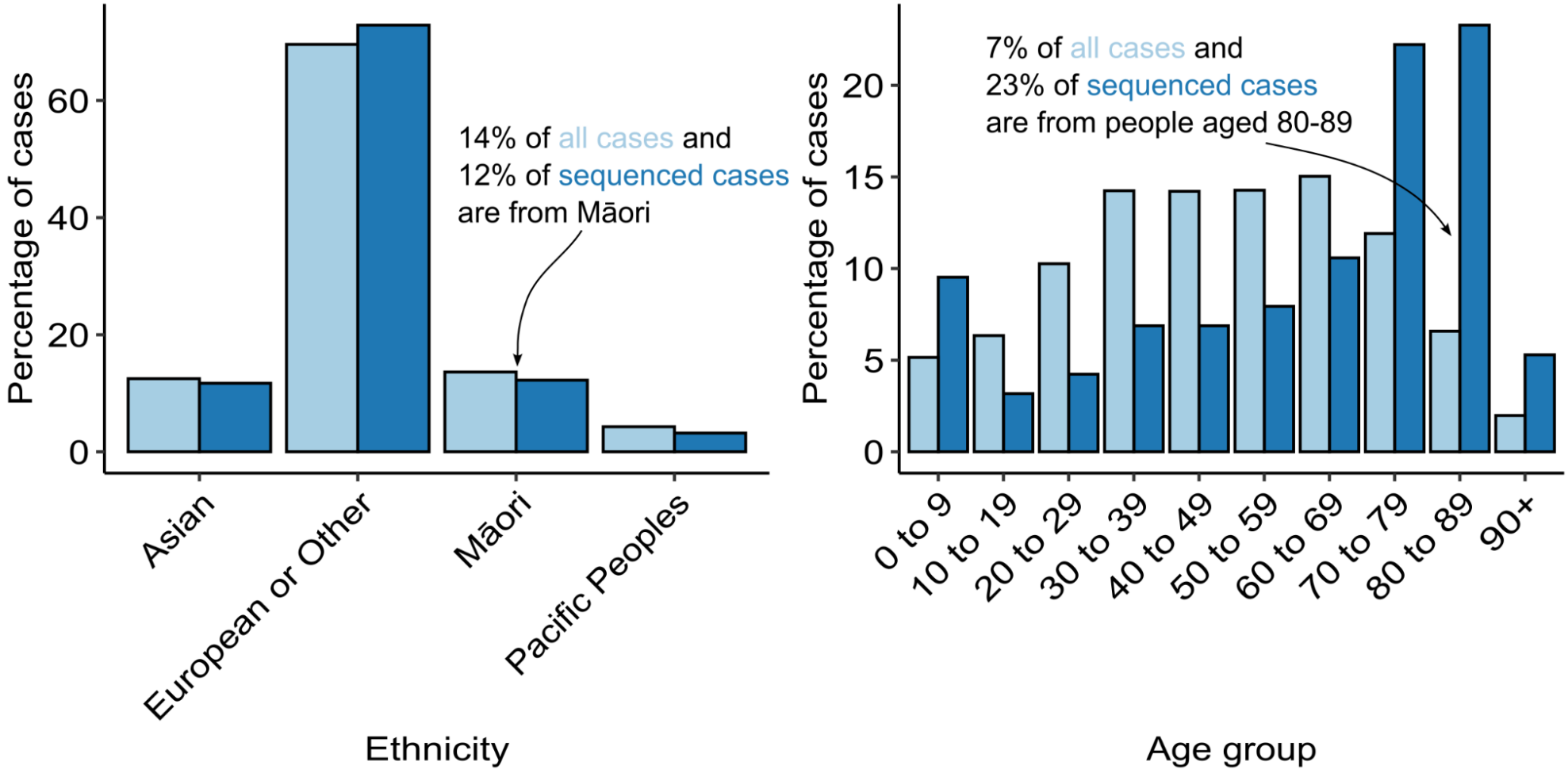


Figure 2: *(**Left**) Composition of sequenced and reported cases by ethnicity. Each case is assigned to a single ethnicity for this analysis, with priority order Māori, Pacific Peoples, Asian, European or Other. (**Right**) Comparison of age distribution across all reported cases (light blue) and sequenced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

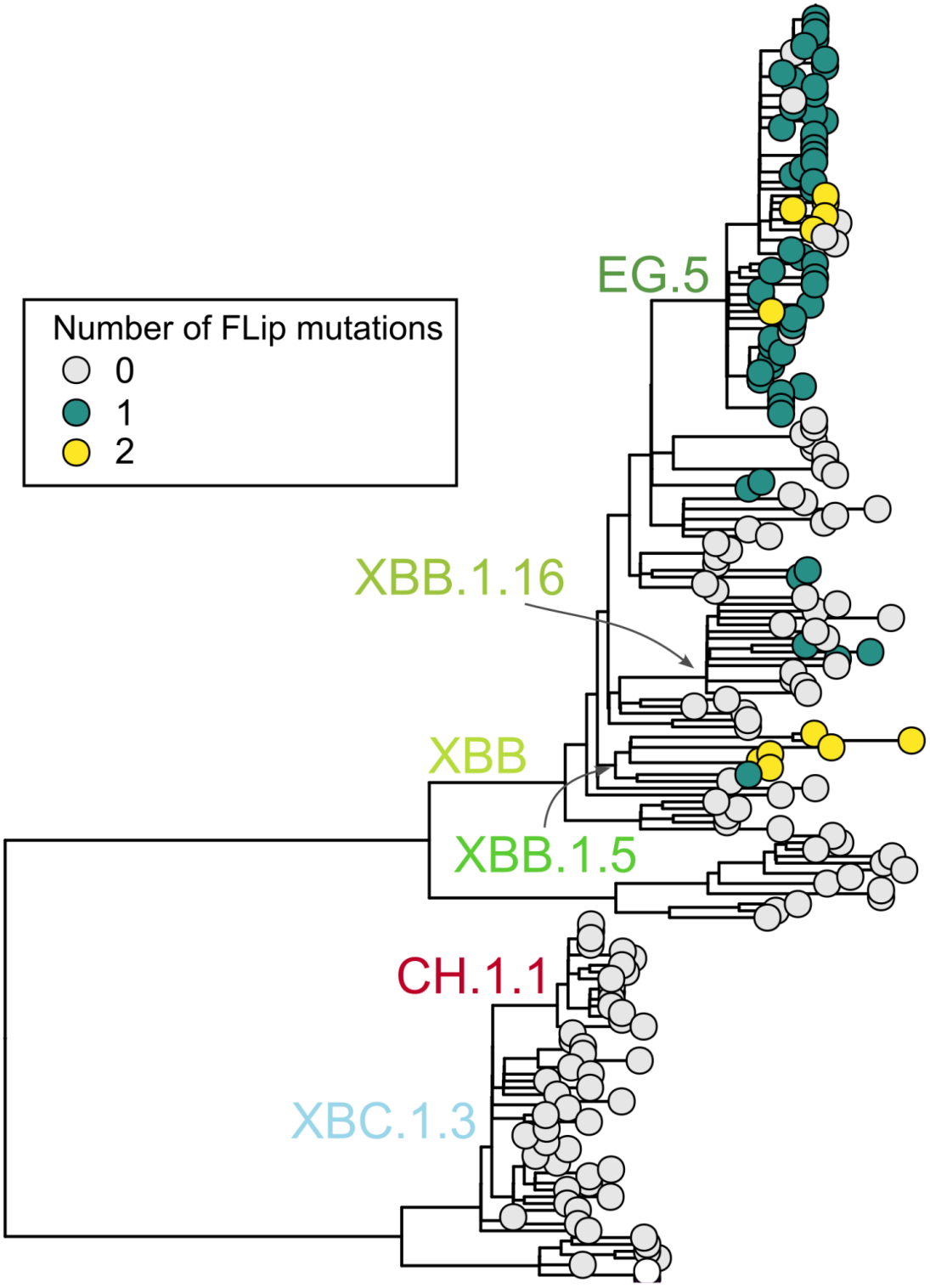


Figure 3. *Distribution of "FLip"* mutations across the diversity of SARS-CoV-2 lineages. The tree represents the evolutionary relationships of all sequenced cases in the current two-week windows Each tip represents a single genome, with the tip-point shaded to represent the number of FLip mutations present. Nodes corresponding to tracked lineages are labelled. The fact FLip mutation occur in multiple different parts of the tree demonstrates that have evolved independently multiple times.*

*International genomic surveillance efforts have identified two adjacent mutations, L455F and F456L, in the spike protein. Because these mutations represent the swapping of neighbouring "F" and "L" amino acids, they have been named the "FLip" mutations

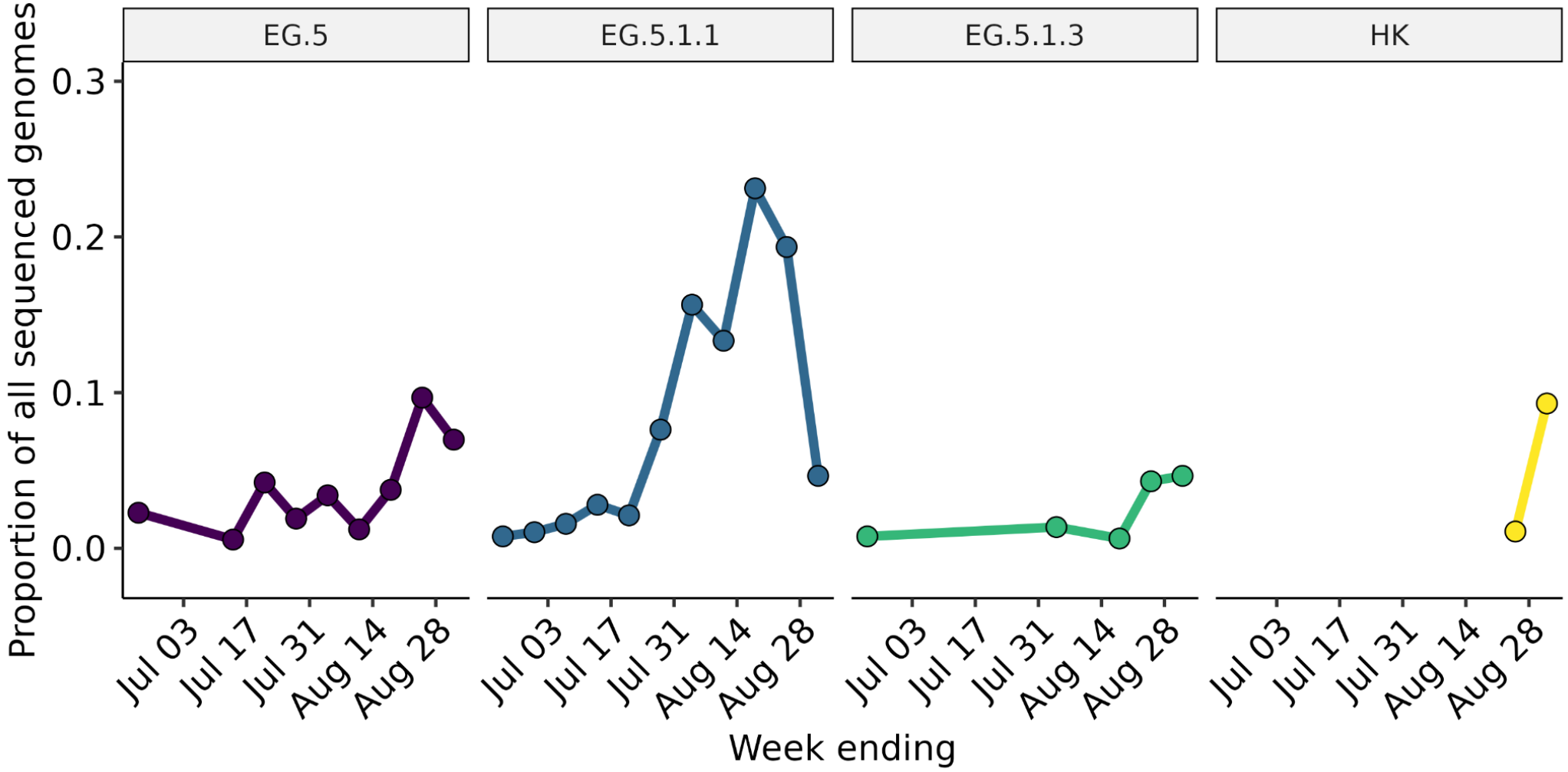


Figure 4: *The trajectory of specific sub-lineages included in the "EG" category. Each subplot represents a lineage (and all of its descendants not covered by another category), with points representing the proportion of all sequenced cases falling to that lineage in a given reporting week.*