3 November 2023

COVID-19 Genomics Insights Dashboard (CGID) #43

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:

650*

genomes from cases since the last report (5 October)

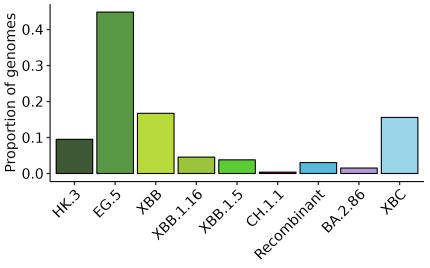
~10,500

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:

In Aotearoa, the most common variant is EG.5, a descendant of XBB. This increase is partly due to HK.3, a variant found in 9% of the cases we sequenced in the last two weeks. Additionally, other variants of EG.5 made up 44% of the cases



Hospital surveillance:

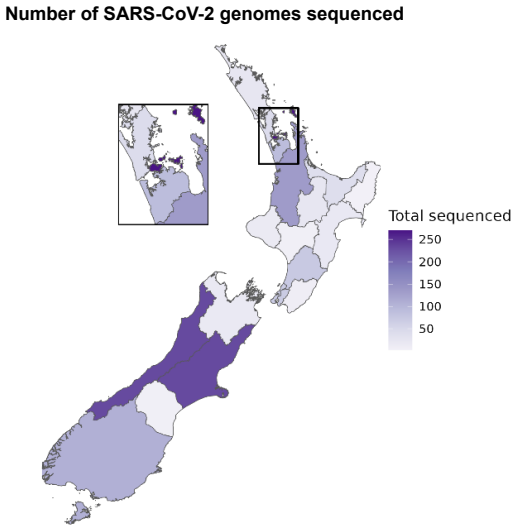
31% (100 of 318*) of PCR-positive cases with a hospital admission date from 13 to 27 Oct successfully produced a genome (to date)

The approximate composition of hospital cases:

- EG.5: 45%
- HK.3: 7%
- XBB: 17%
- XBB.1.16: 7%
- XBC: 17%

*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:

- The EG.5 variant is the most common in Aotearoa, causing 53% of cases sequenced. Within EG.5, there's a descendant called HK.3, which makes up 9% of all cases.
- The XBC variant has remained strong despite the more contagious EG.5 and HK.3 variants. All XBC variants are now grouped together for reporting.
- While EG.5.1.8 and FL.20 variants have shown growth advantages over EG.5, these are not expected to impact caseloads and hospitalisations significantly. We continue to monitor emerging lineages.
- The BA.2.86 variant remains at a low frequency. This variant has been detected in a small number of clinical staples from Canterbury, Auckland, and Counties Manukau District Health Boards. There is currently no indication it has a substantial growth advantage over established lineages.
- Wastewater analysis aligns with clinical samples, reflecting the dominance of EG.5, the rise of HK.3, XBC's stability, and the presence of BA.2.86 at low frequency (demonstrating consistency in results between different data sources).

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

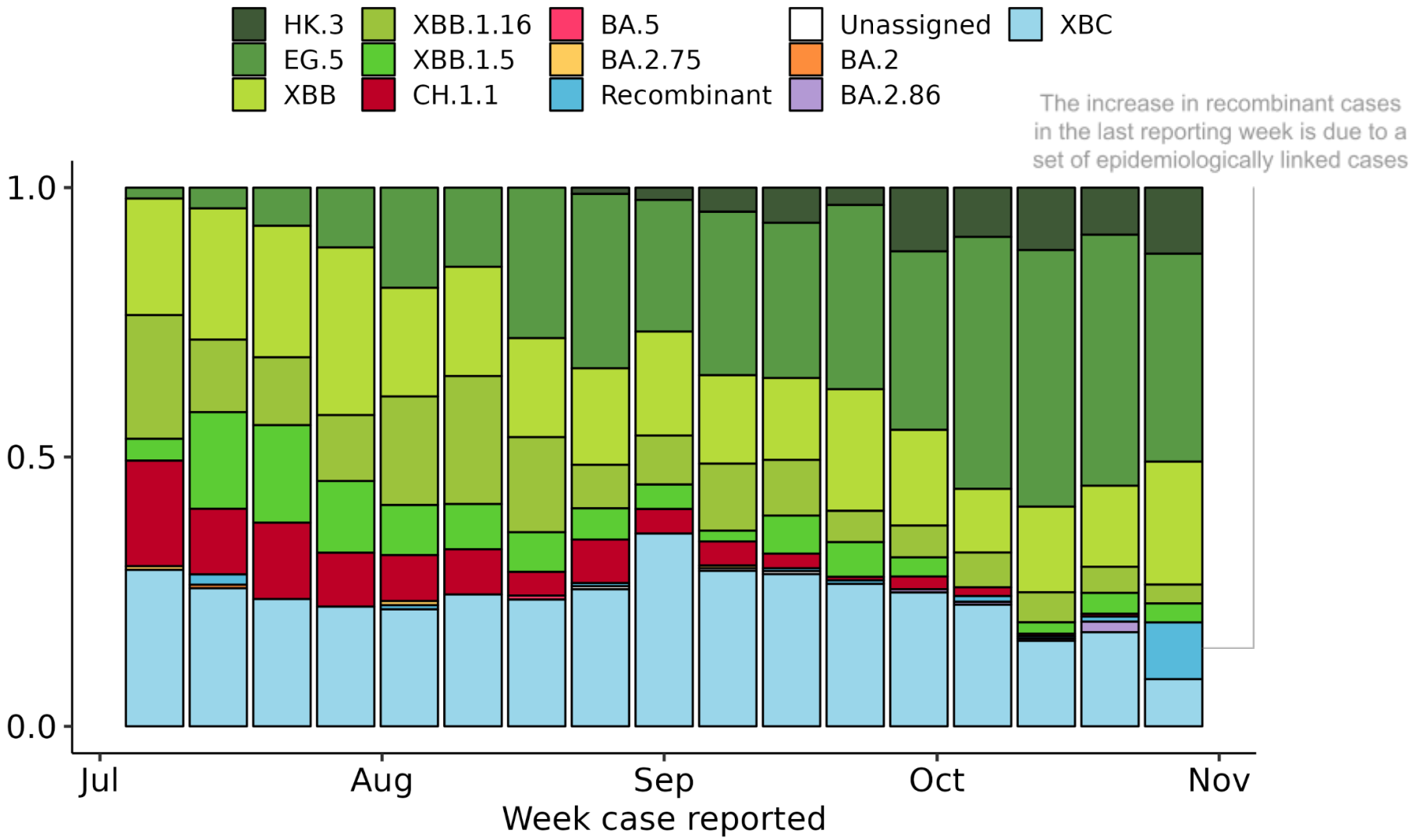


Figure 1: Frequency of SARS-CoV-2 variants in the New Zealand community each week (for the past 16 weeks) as determined by whole-genome sequencing*. Only variants with a frequency above 1% are shown. Data is subject to change as samples will still be added to the most recent two-week period.* In this case d*ata from the last reporting week is based on a limited number of genomes (57) 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].*

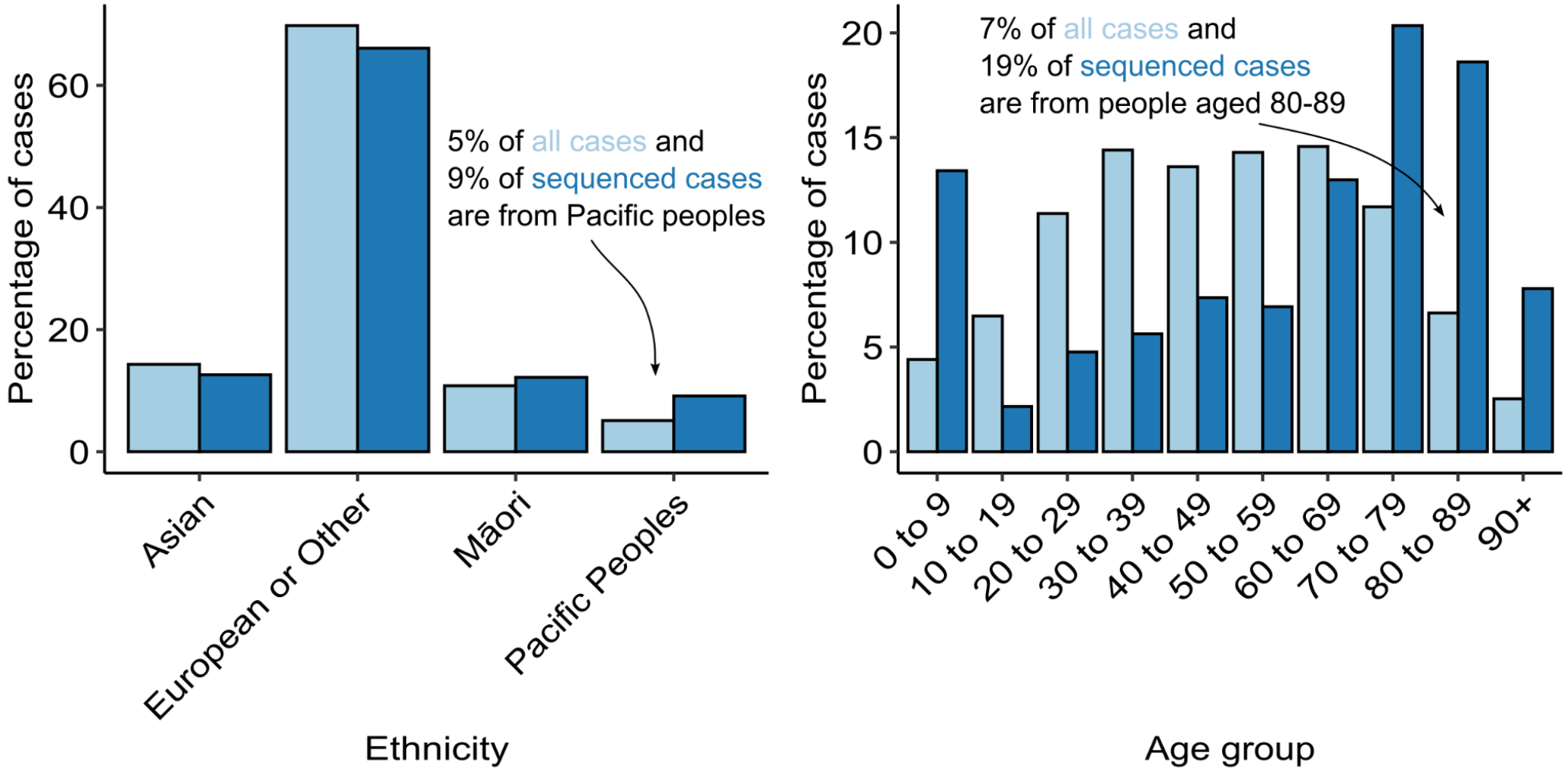


Figure 2: *(**Left**) Composition of sequenced and reported cases by ethnicity. Each case is assigned to a single ethnicity for this analysis, with priority order Māori, Pacific Peoples, Asian, European or Other. (**Right**) Comparison of age distribution across all reported cases (light blue) and sequenced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

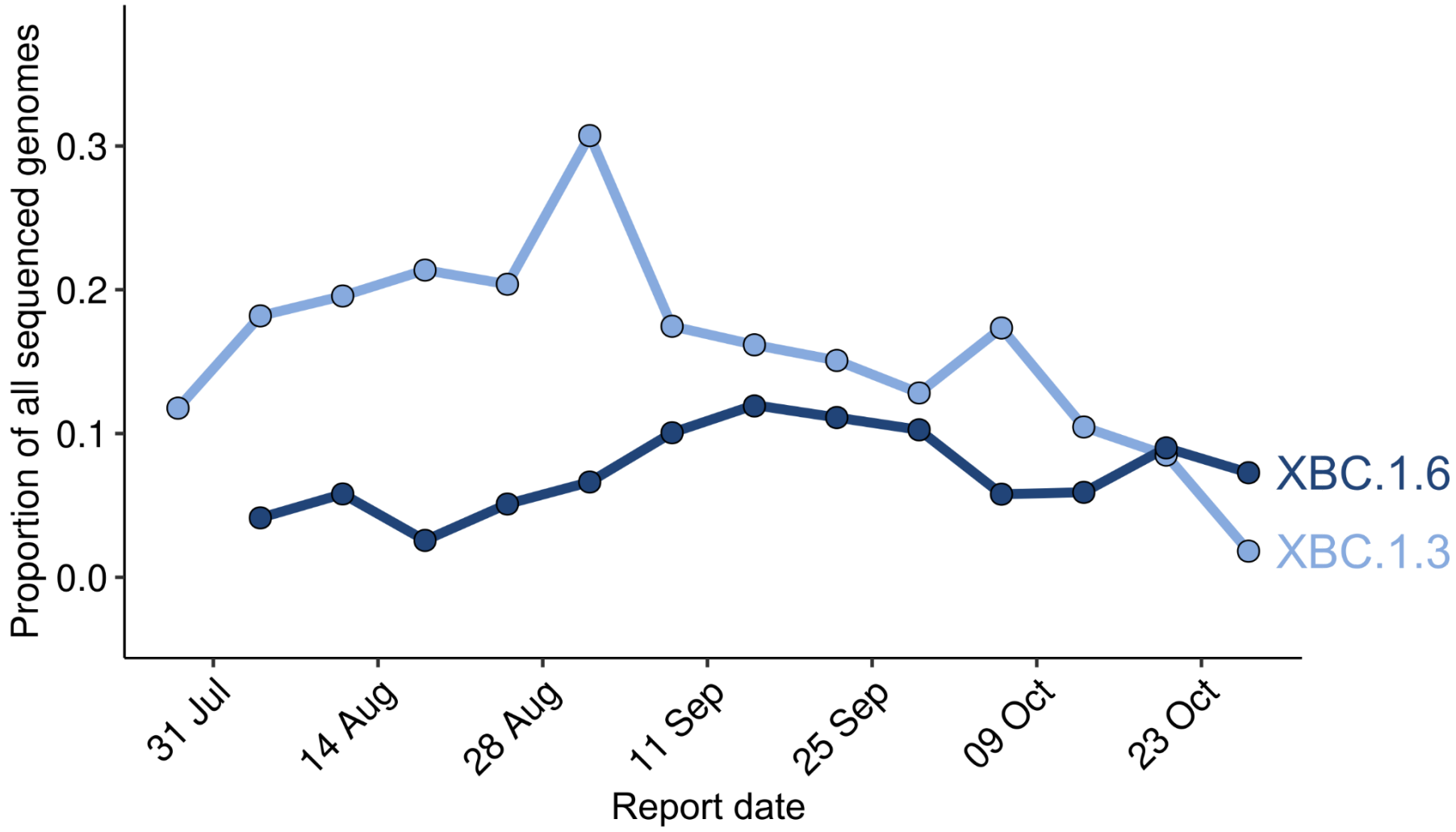


***Figure 3: Frequency of XBC lineages in recent weeks**. Each line represents data from a single XBC lineage and all of its descendant lineages.*

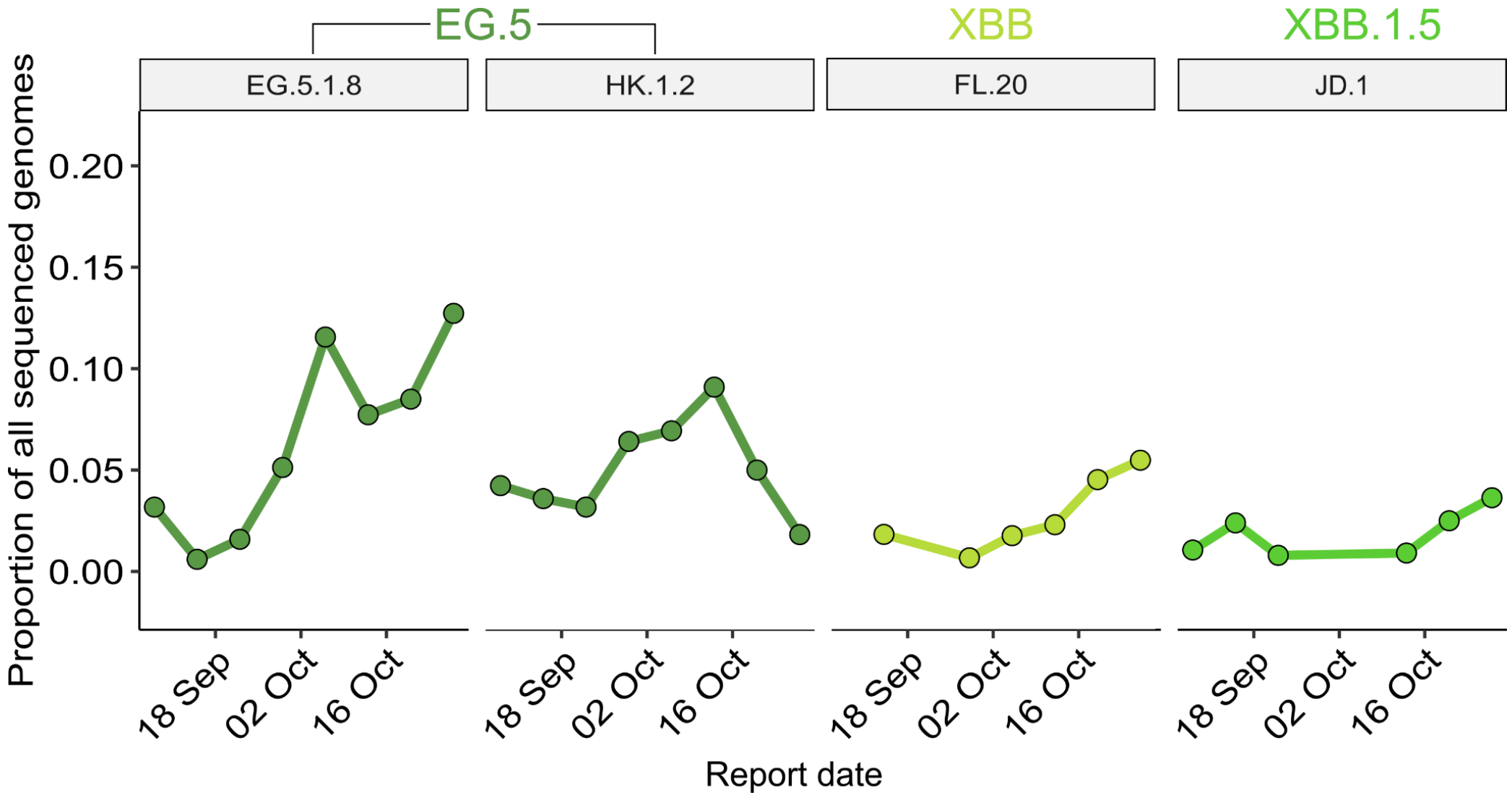


Figure 4: The trajectory of specific sub-lineages in recent weeks*. Each subplot represents a single-tracked lineage (and all of its descendants not covered by another category), with points representing the proportion of all sequenced cases falling to that lineage in a given reporting week.* The labels above the subplot describe which variant each lineage is reported under in Figure 1.