

This page shows the frequency of the top 6 "L2" lineages, across recent months.

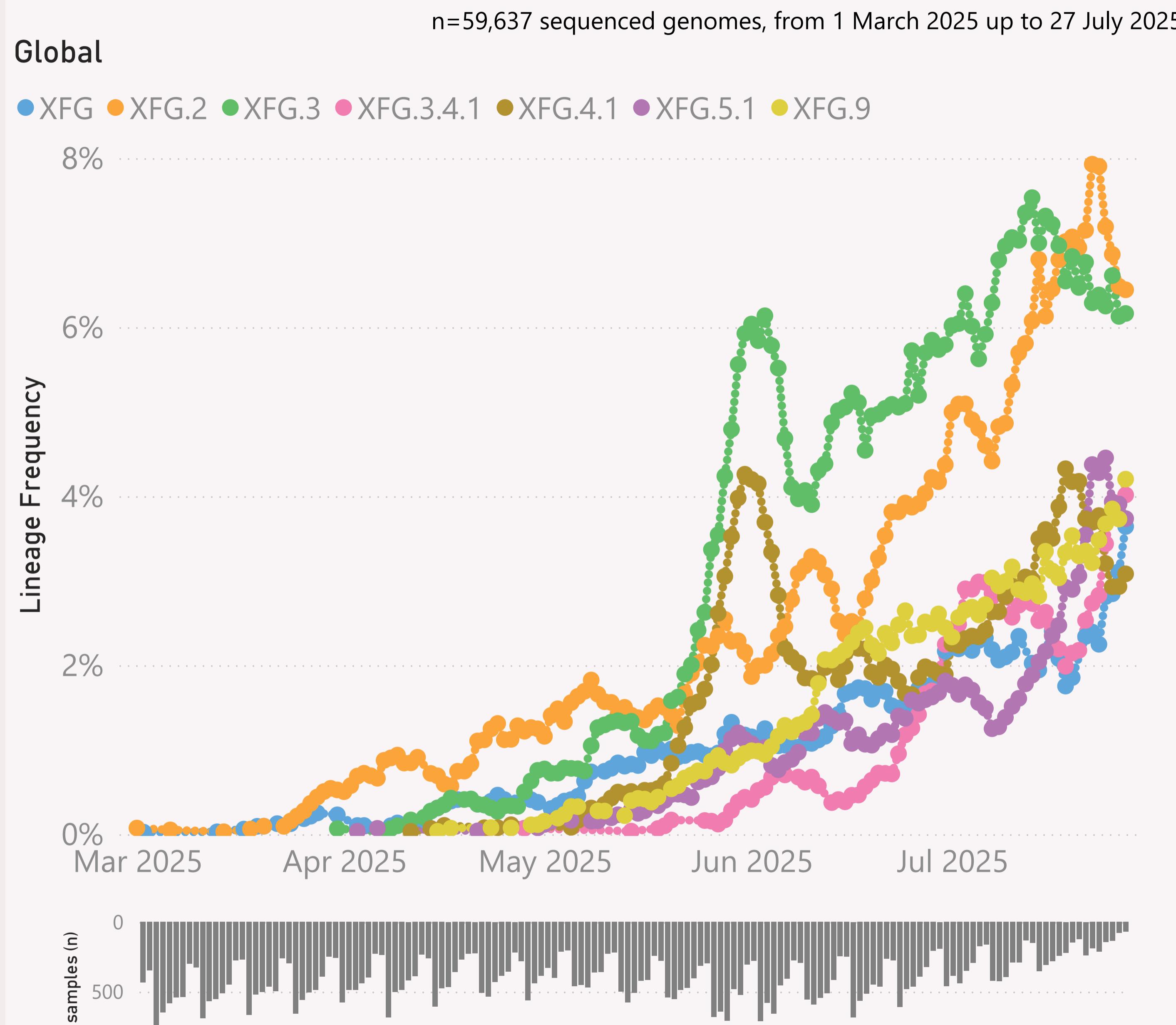
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.\*" group includes BA.2.86 and all its descendants, e.g. the JN.\* lineages.

The detailed Lineage classifications are quite numerous and dynamic, so the "Lineage L2" groups give a simpler and more stable basis for analysis and comparison.

The frequency shown at each point is based on the 7-day rolling average across all lineages.

The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

The frequency results calculated for the most recent dates might not be representative, due to those lower sample sizes.



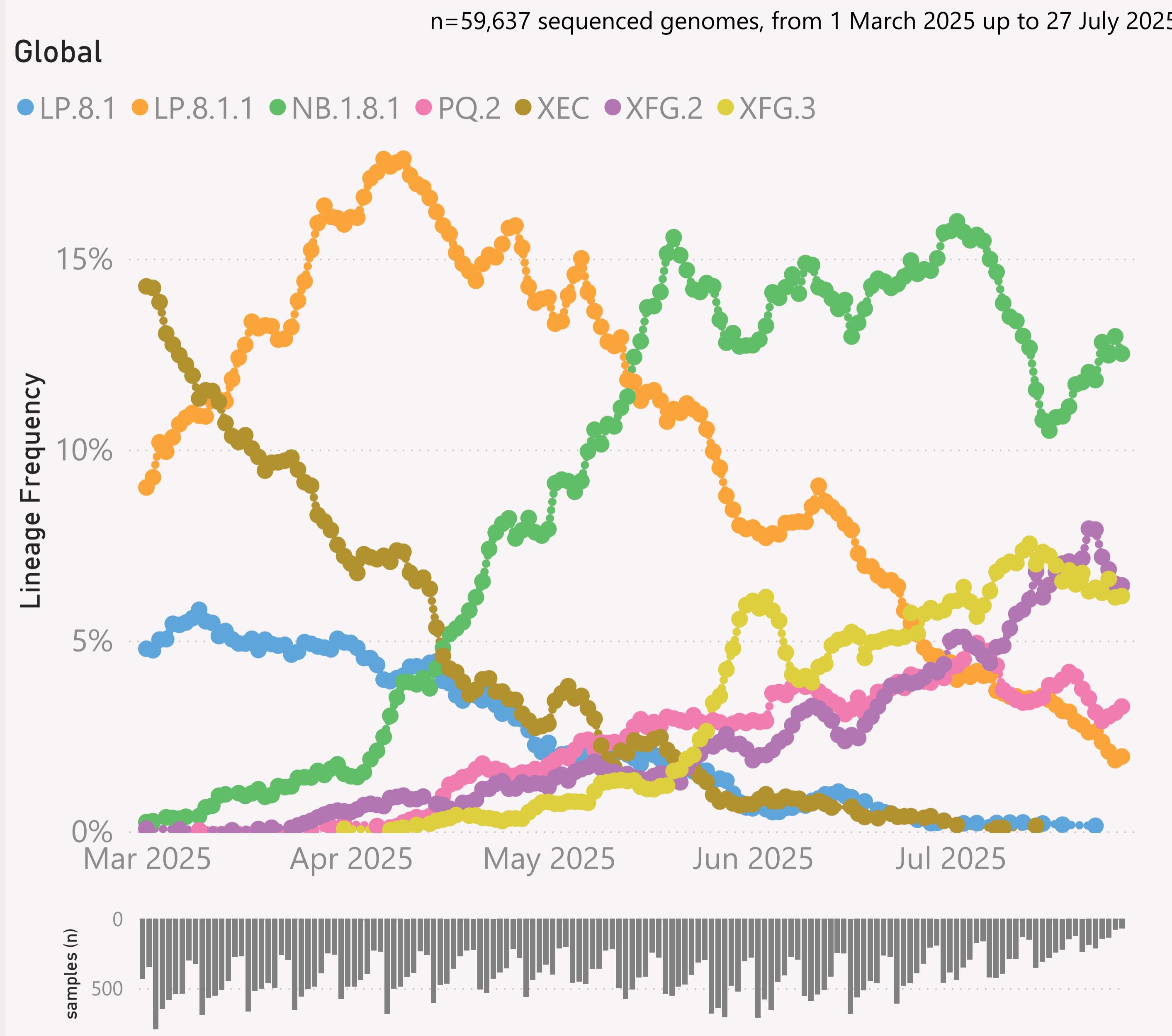
This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently XFG.\* Stratus.

The Lineage classifications are provided by Nextclade. The colour assignments are random.

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This page shows the frequency of the top 7 lineages, across recent months.

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**NB.1.8.1.\* Nimbus**

• Australia • Canada • China • New Zealand • Singapore • Spain • United States

100%

80%

60%

40%

20%

0%

Lineage Frequency

0

samples (n)  
500

Mar 2025

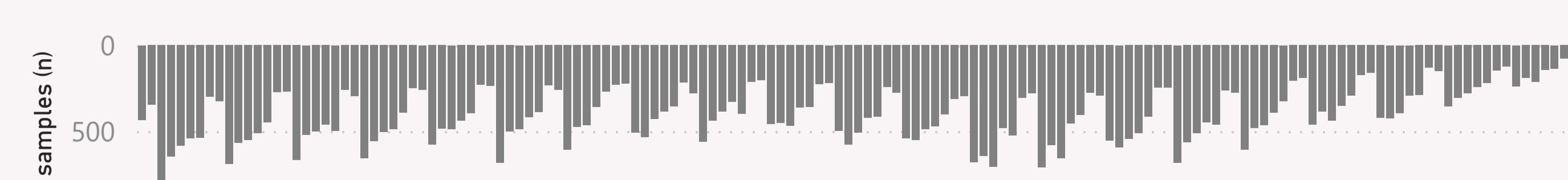
Apr 2025

May 2025

Jun 2025

Jul 2025

n=59,637 sequenced genomes, from 1 March 2025 up to 27 July 2025



This page shows the frequency of a selected "Lineage L2" group of interest, for the 7 countries reporting the most samples over recent months.

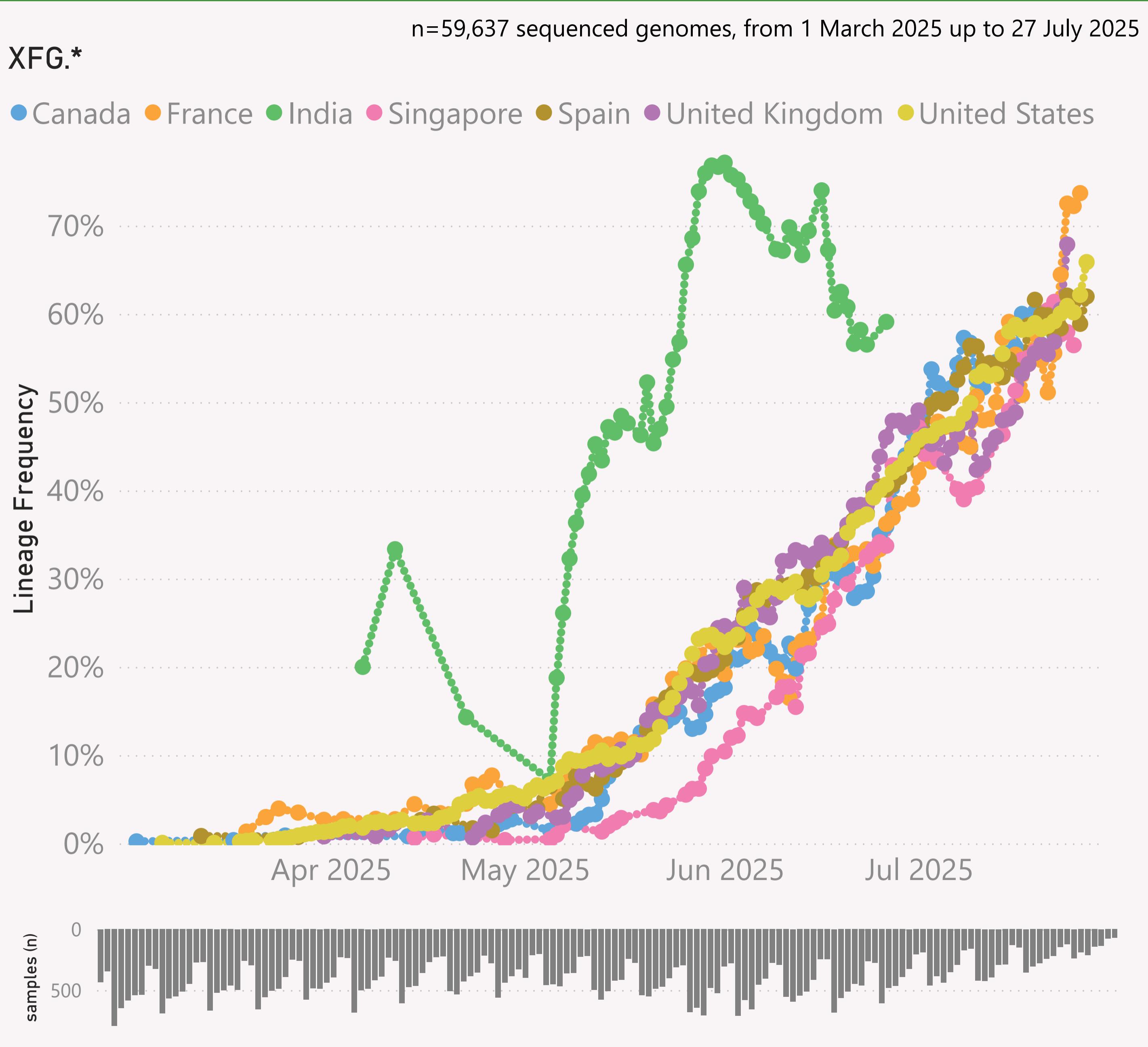
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.\* +FLiRT" group includes the descendants of JN.1.\* with the mutations: F456L & R346T.

The detailed Lineage classifications are quite numerous and dynamic, so the "Lineage L2" groups give a simpler and more stable basis for analysis and comparison.

The frequency shown at each point is based on the 7-day rolling average across all lineages, for that country.

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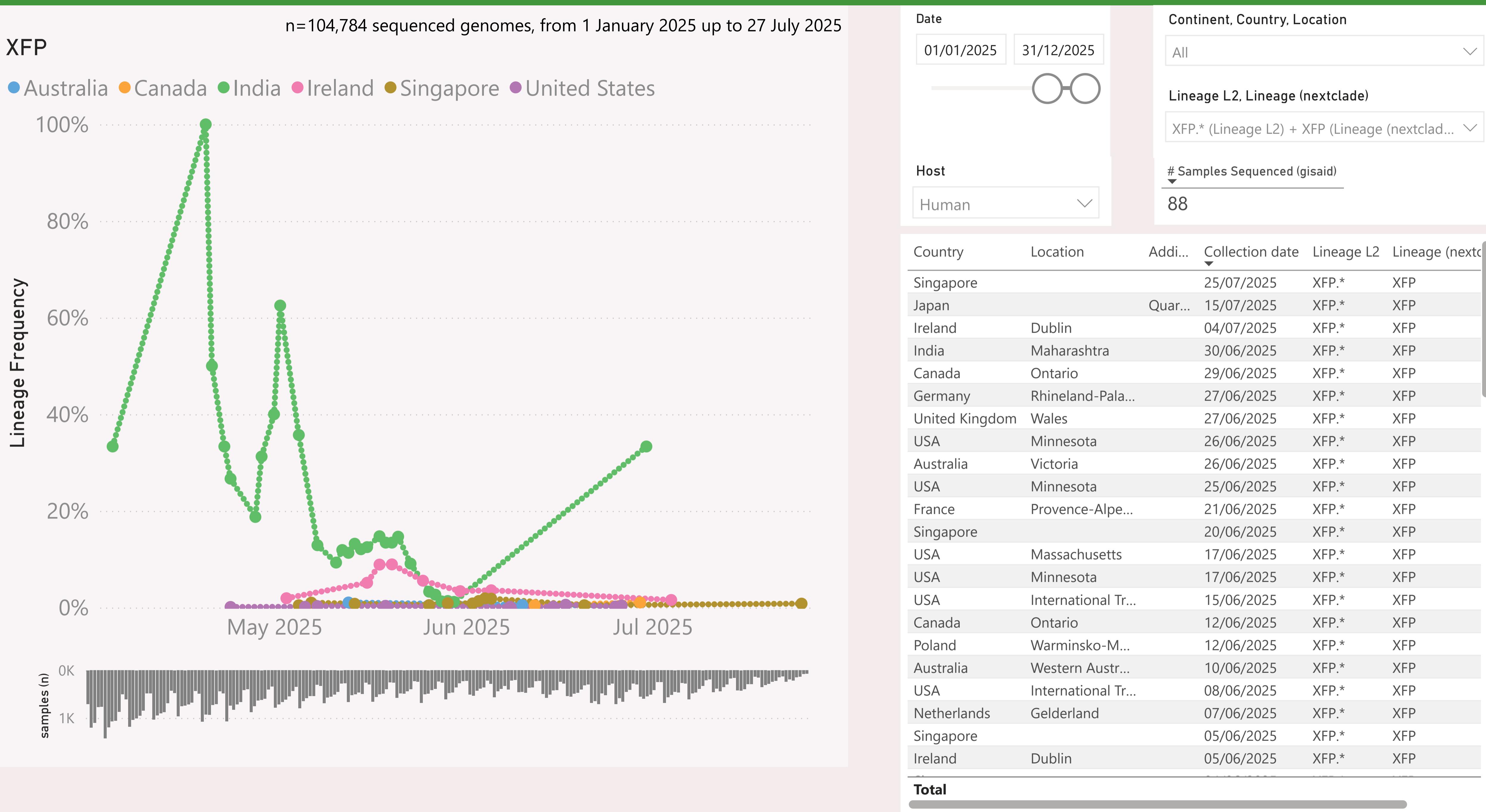
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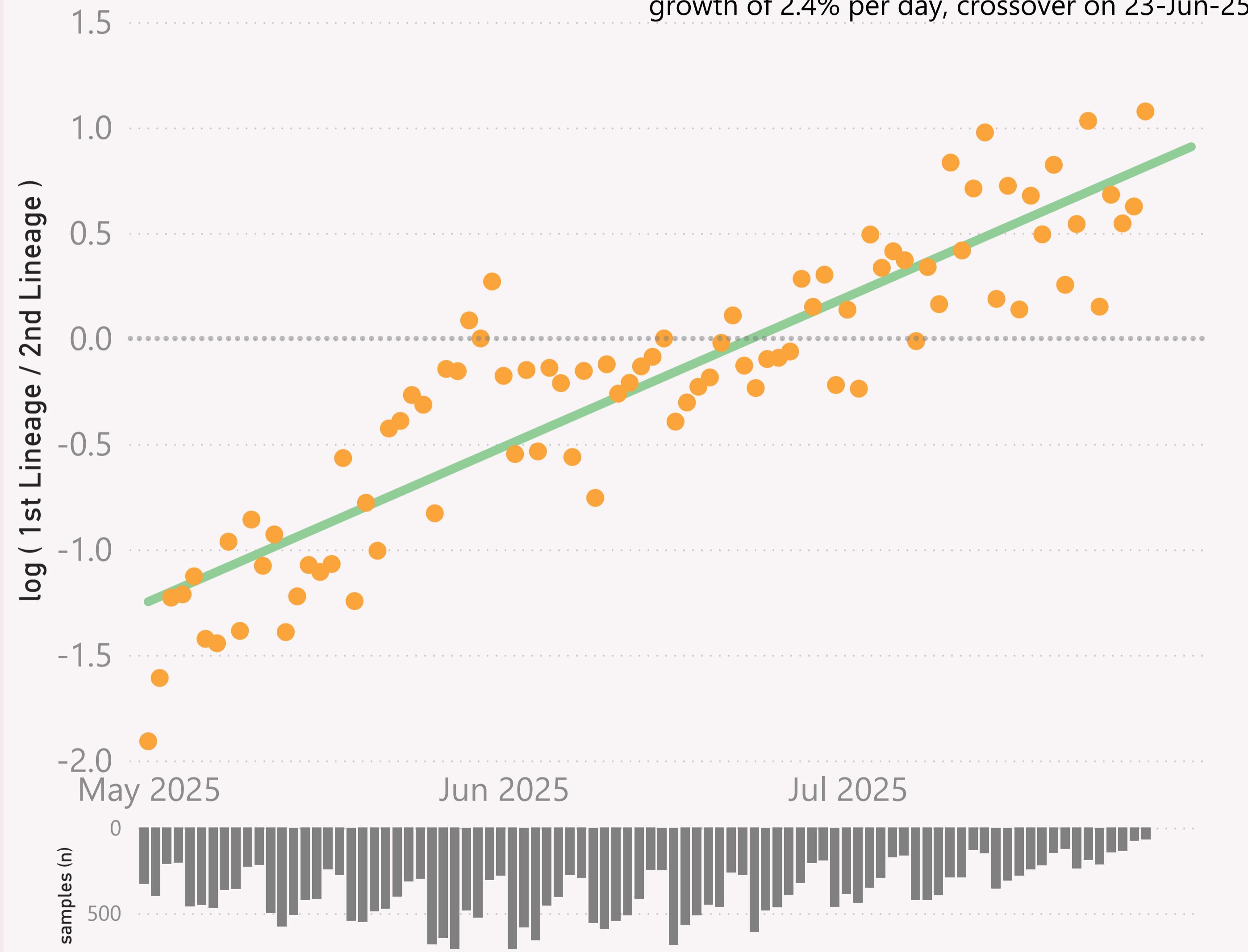


n=32,884 sequenced genomes, from 1 May 2025 up to 27 July 2025

**Global - XFG.\* vs NB.1.8.1.\* Nimbus**

● log ( 1st Lineage / 2nd Lineage ) ● trend

growth of 2.4% per day, crossover on 23-Jun-25



This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage L2 is considered to have "crossed over" or taken over dominance from the incumbent Lineage L2.

The Lineage classifications are provided by Nextclade. I add the "Lineage L2" groups, typically following common variant groupings, but occasionally being "creative".

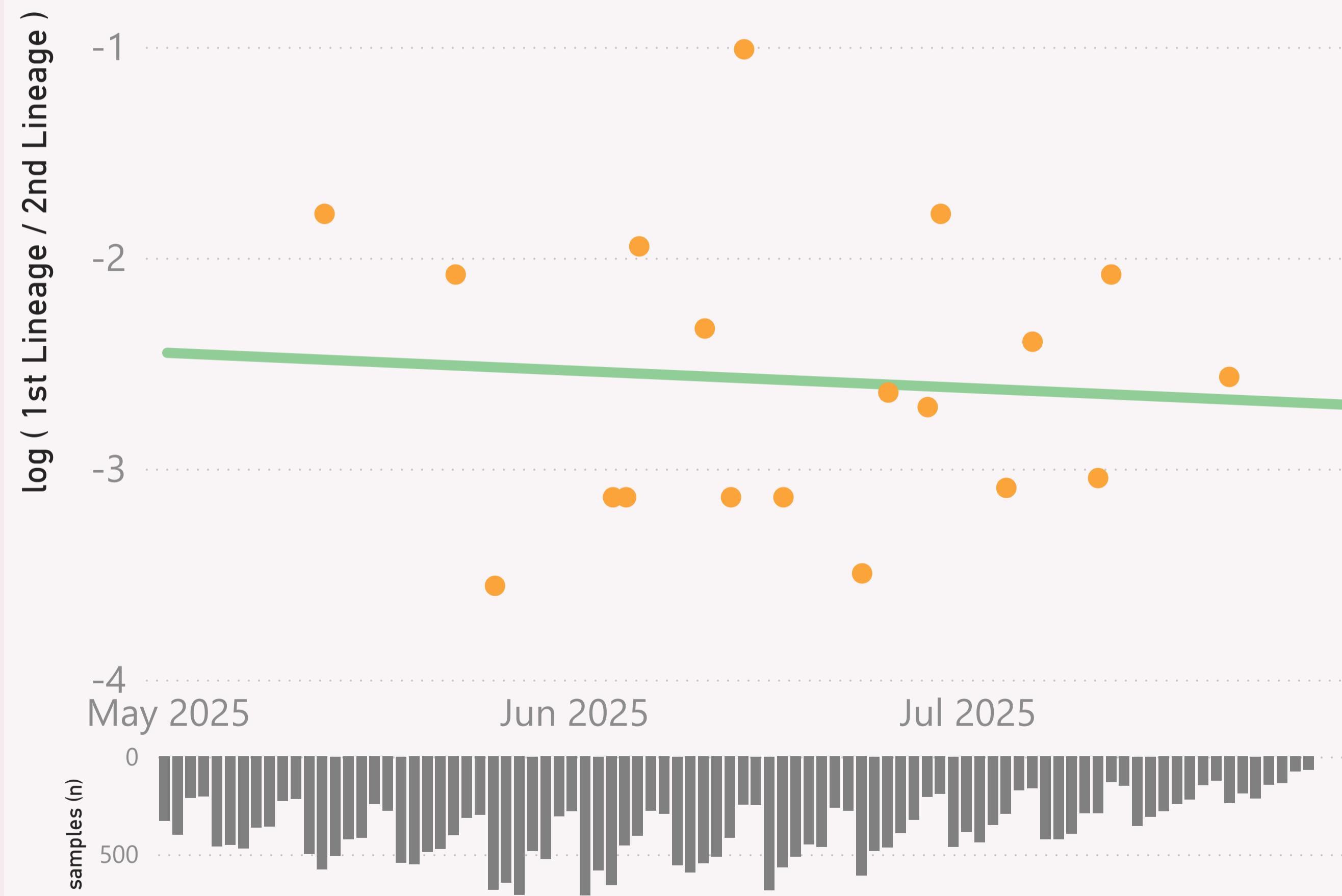
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

n=32,884 sequenced genomes, from 1 May 2025 up to 27 July 2025

**Global - XFN vs XFG.3**

● log ( 1st Lineage / 2nd Lineage ) ● trend

0 ..... decline of -0.3% per day

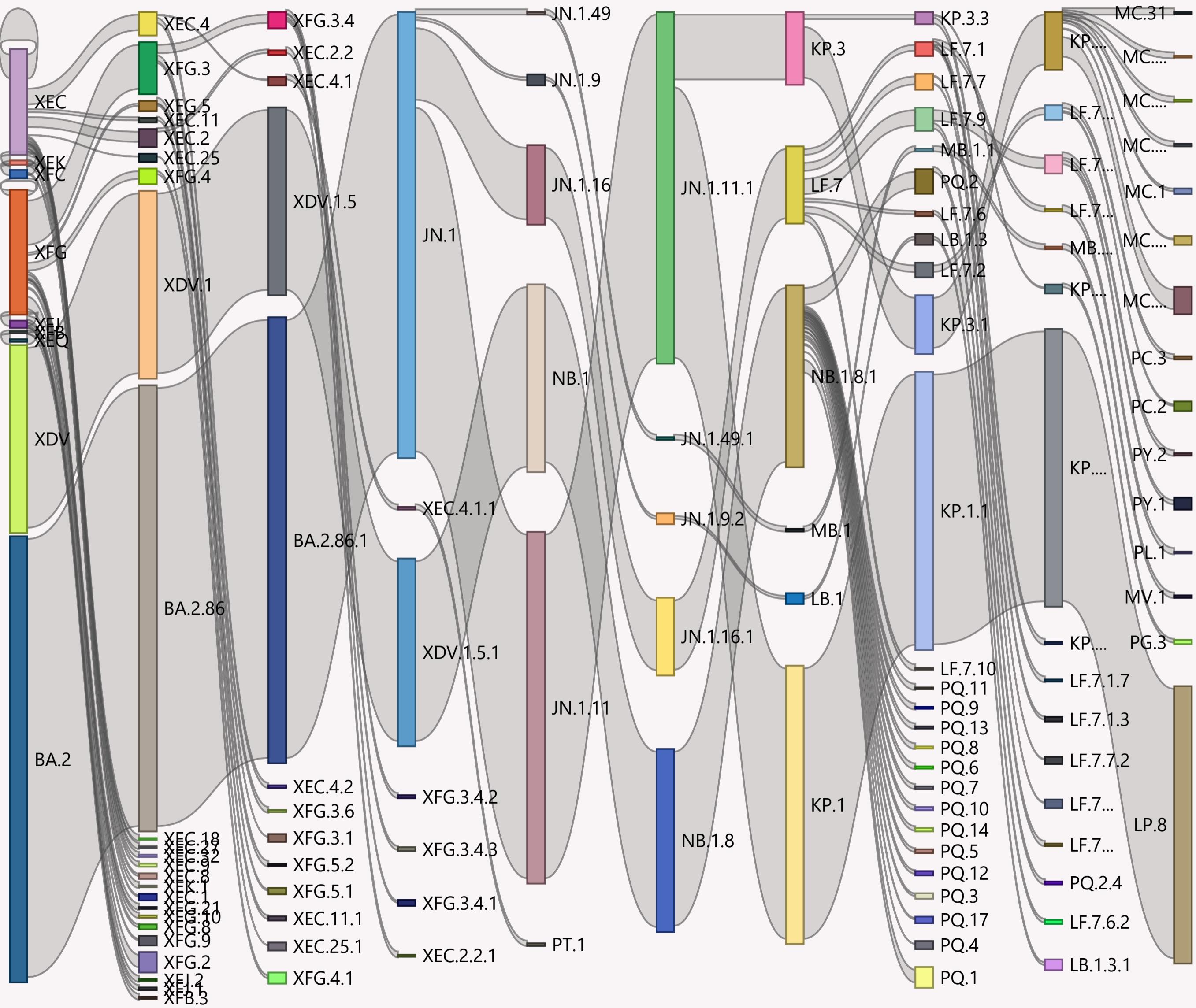


This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage is considered to have "crossed over" or taken over dominance from the incumbent Lineage

The Lineage classifications are provided by Nextclade.

The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

**Global**

This page shows the hierarchy of the significant Lineages, over recent months.

The hierarchy can be read from left to right, starting with the earliest/highest Lineages being broken down into more detailed child Lineages.

The vertical height of each bar segment represents the relative volume of all the samples of that specific Lineage, as well as all its descendants.

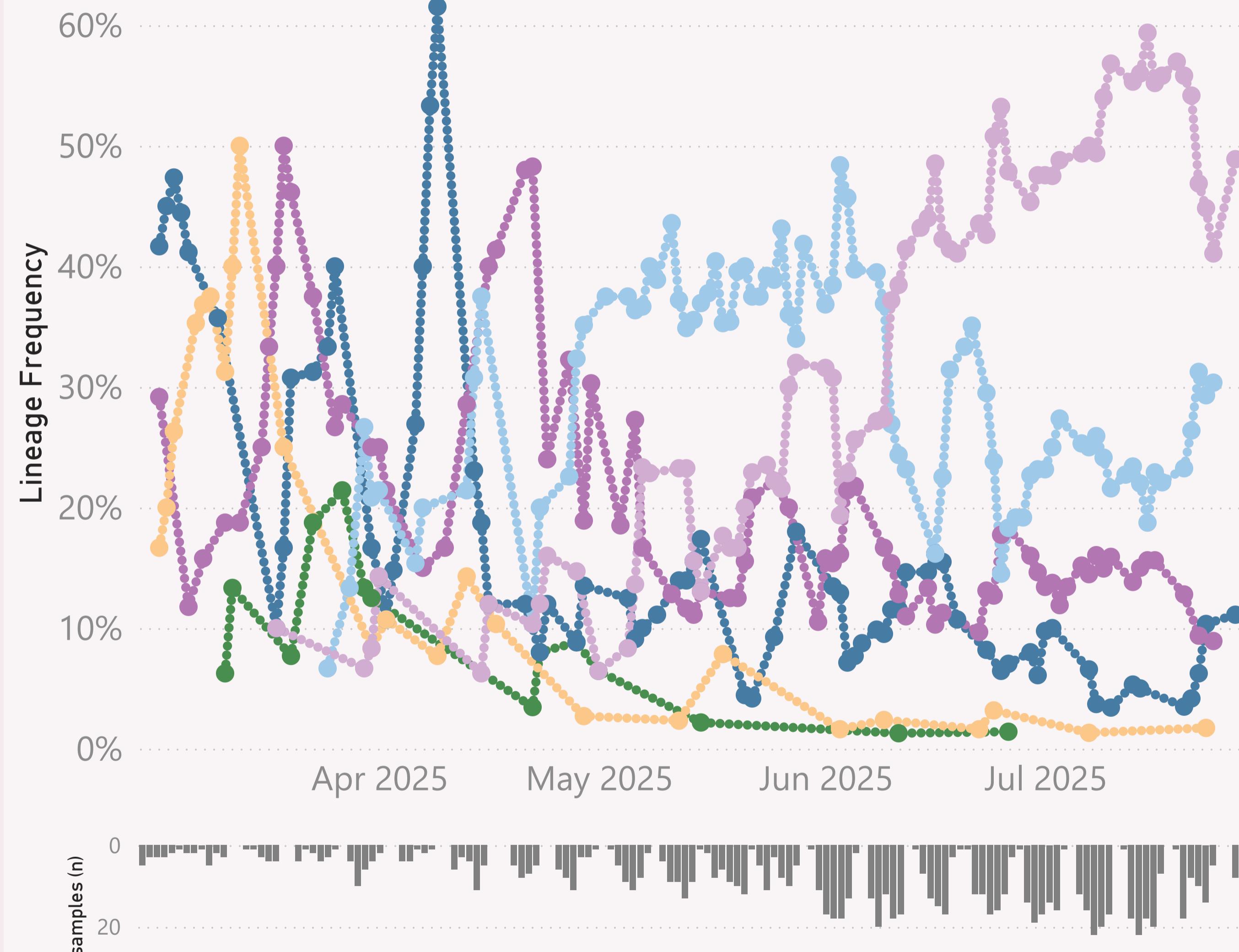
The full picture is typically quite busy, so insignificant Lineages (with few samples, or at the extreme top or bottom of the hierarchy) are not shown.

The Lineage classifications are provided by Nextclade.

n=964 sequenced genomes, from 2 March 2025 up to 27 July 2025

**Global**

- JN.1.\* +DeFLuQE
- JN.1.\* +FLiRT
- LP.8.1.\*
- NB.1.8.1.\* Nimbus
- XEC.\*
- XFG.\*

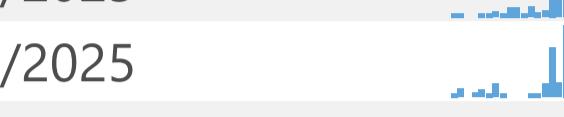
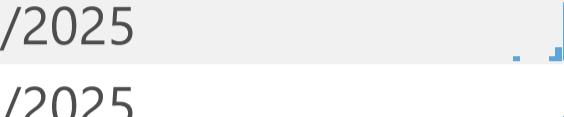
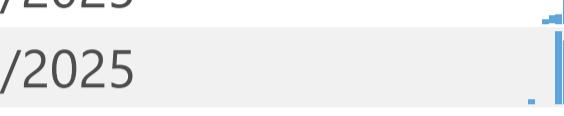
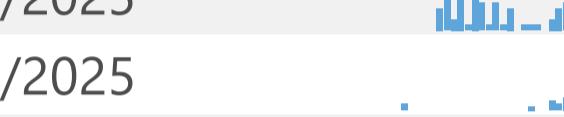
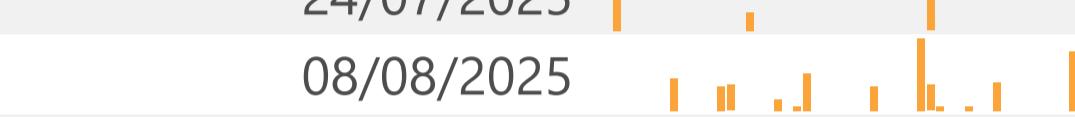
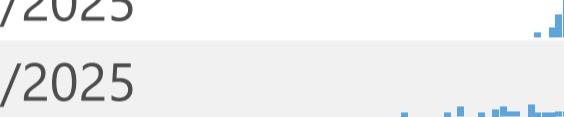
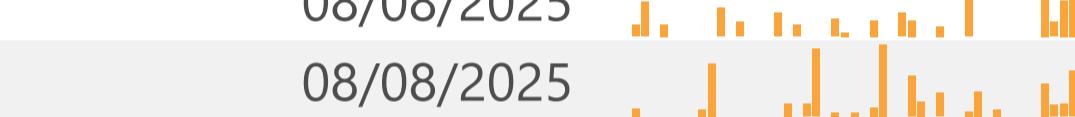
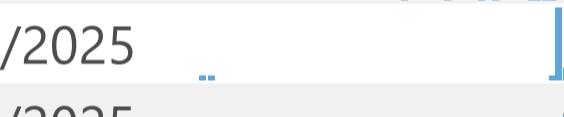
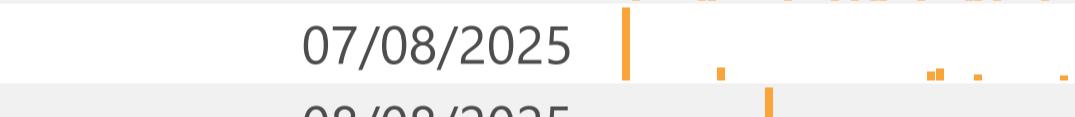
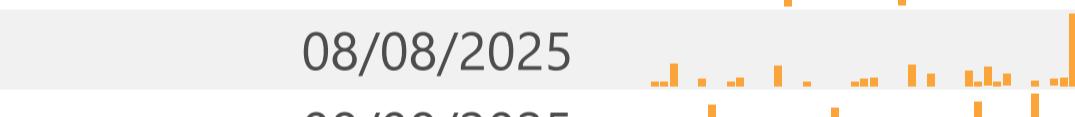
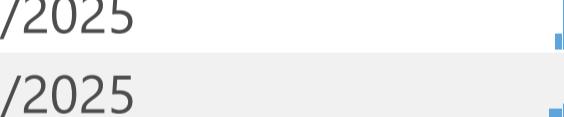
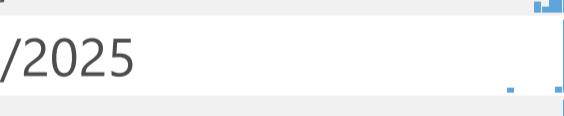
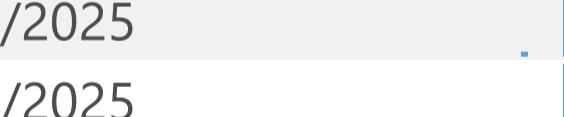
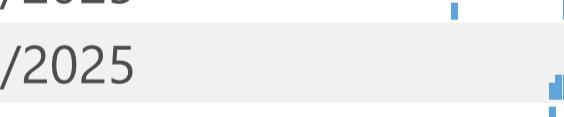
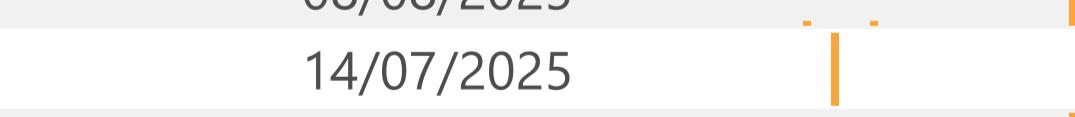
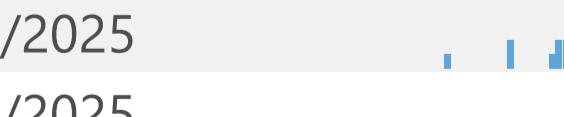
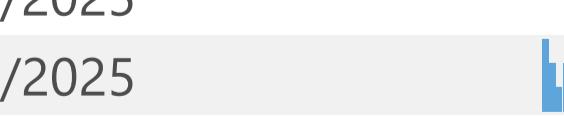


This page shows the frequency of the top 6 "L2" lineages, across recent months, for "International Traveller" samples.

This is probably a more randomised sample than the "Global" aggregate of all samples submitted to GISAID, as those are dominated by the US and Canada

These samples are mainly collected from arrivals into the US and Japan.

## Data Submitted in the last 8 weeks

Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
United States	6,405	27/07/2025		08/08/2025	
Spain	3,817	27/07/2025		08/08/2025	
China	1,811	21/07/2025		08/08/2025	
United Kingdom	1,640	27/07/2025		08/08/2025	
Australia	1,484	27/07/2025		08/08/2025	
Singapore	1,467	25/07/2025		05/08/2025	
Canada	1,287	22/07/2025		06/08/2025	
Russia	772	01/07/2025		24/07/2025	
France	756	26/07/2025		08/08/2025	
Netherlands	587	20/07/2025		08/08/2025	
Ireland	578	27/07/2025		08/08/2025	
Brazil	556	24/07/2025		08/08/2025	
India	529	02/07/2025		07/08/2025	
New Zealand	505	27/07/2025		08/08/2025	
Kenya	453	27/06/2025		21/07/2025	
Japan	424	26/07/2025		08/08/2025	
Costa Rica	343	15/07/2025		08/08/2025	
Portugal	327	01/07/2025		29/07/2025	
South Korea	321	16/07/2025		08/08/2025	
Taiwan	307	23/07/2025		01/08/2025	
Malaysia	304	18/07/2025		08/08/2025	
Germany	281	24/07/2025		07/08/2025	
Mexico	275	18/06/2025		22/07/2025	
Reunion	235	24/06/2025		08/08/2025	
Thailand	235	19/06/2025		14/07/2025	
Italy	198	27/07/2025		08/08/2025	
Luxembourg	181	07/07/2025		18/07/2025	
Sweden	145	27/07/2025		08/08/2025	
<b>Total</b>	<b>28,131</b>	<b>27/07/2025</b>		<b>08/08/2025</b>	

This page shows the volume and currency/timeliness of the genomic sequencing data shared via GISAID, over the last 8 weeks, for the countries sharing the most samples.

Each sample shared comes with a Collection date - when the PCR test for that sample was collected. The GISAID system also records a Submission date for each sample, which is typically the date that sample was uploaded.

The latest date of each type is shown, along with "sparkline"-style mini charts to give a flavour for the spread of recent data by Collection date and by Submission date.