INSACOG BULLETIN

31 March 2024

The INSACOG reports genomic surveillance of SARS-CoV-2 by whole genome sequencing of samples from sentinel sites across the country and international passengers arriving in India. A summary of the cumulative data of INSACOG and other state sequencing initiatives can be found in the INSACOG data portal along with other INSACOG related information at https://ibdc.rcb.res.in/

INSACOG:

Number of samples sequenced by IGSLs 300,788

Samples sequenced by IGSLs under State government MoUs: 35,441

Total number of samples sequenced by labs associated with INSACOG including their efforts under MoU with States: 336,229

The number of samples with pangolin lineages assigned are given below:

Table 1: Cumulative samples with pangolin lineage assigned (as on 29-03-2024)

Community sample	Travelers sample	Total pangolin lineage assigned	Total VOC/VOI	Percentage
213267	**12564**	**225831**	**189602**	**84.0**

Global Scenario

Over 292,000 new cases and 6,200 new deaths were reported during the last 28-day period (from 5 February, 2024 to 3 March, 2024), globally. The number of reported new cases and reported deaths has decreased by 44% and 51% respectively compared to the previous 28 days[1]. WHO is currently tracking several SARS-CoV-2 variants: five variants of interest (VOIs) – XBB.1.5, XBB.1.16, EG.5, BA.2.86 and JN.1; and three variants under monitoring (VUMs): XBB, XBB.1.9.1 and XBB.2.3. As of 31st March, 2024, 68,680 JN.1 sequences have been submitted to GISAID from 109 countries[2]. Globally, JN.1 is now the most reported VOI, accounting for 90.3% of sequences in week 9 compared to 89.4% in week 6. Its parent lineage, BA.2.86, is declining and accounted for 2.2% of sequences in week 9. However, the JN.1 is of perceived as of low public health risk at the global level based on available evidence. The other VOIs, XBB.1.5, XBB.1.16 and EG.5, have decreased in global prevalence during the same period. XBB.1.5, XBB.1.16 and EG.5 accounted for 0.6%, less than 0.1% and 2.2% of sequences respectively in week 9 of 2024. All the VUMs have also showed a decreasing trend.

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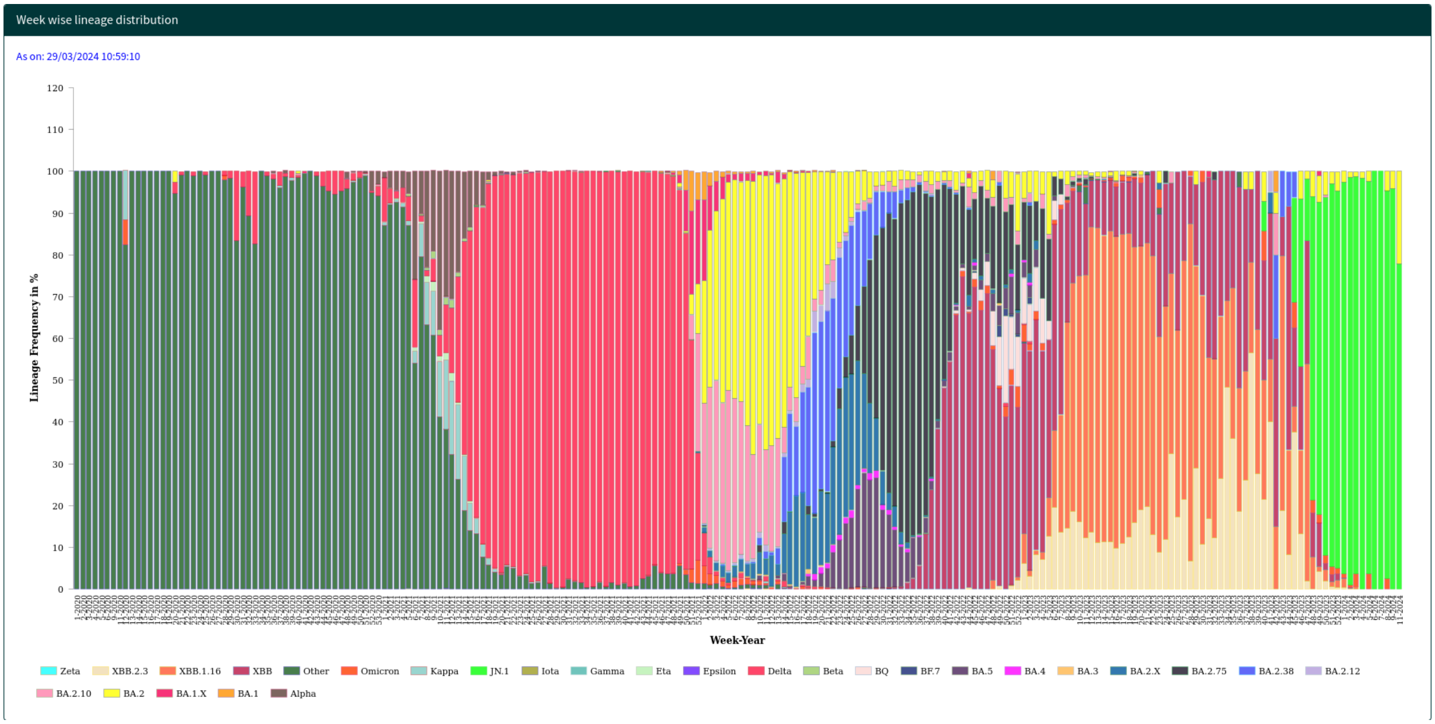
Indian Scenario

During this reporting period, 80% of the submitted sequences were of JN.1 sub-variants. However, reported cases do not accurately represent infection rates due to the reduction in overall testing and reporting. INSACOG is continuing the surveillance of the emerging variants. However, no increase in disease severity or hospitalization has been observed with JN.1 sub-variants so far.

Country wide analysis:



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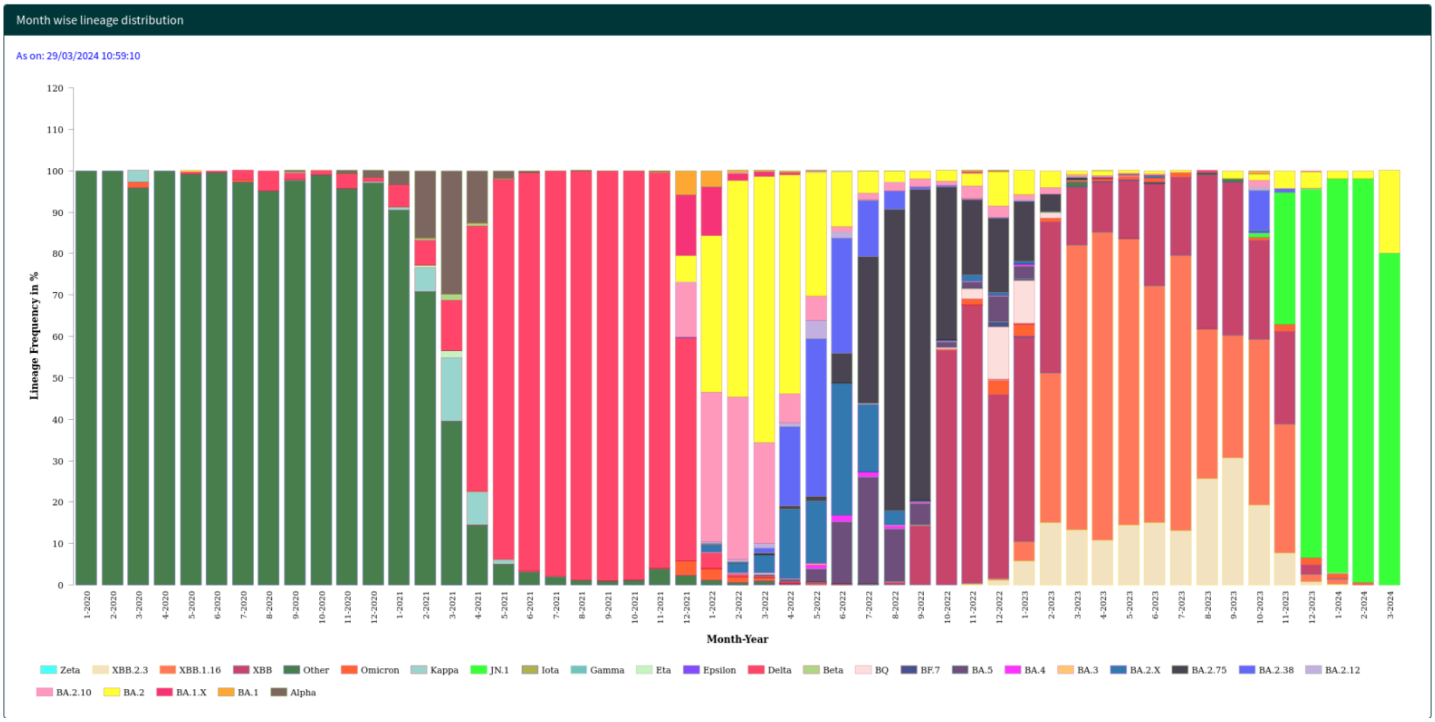
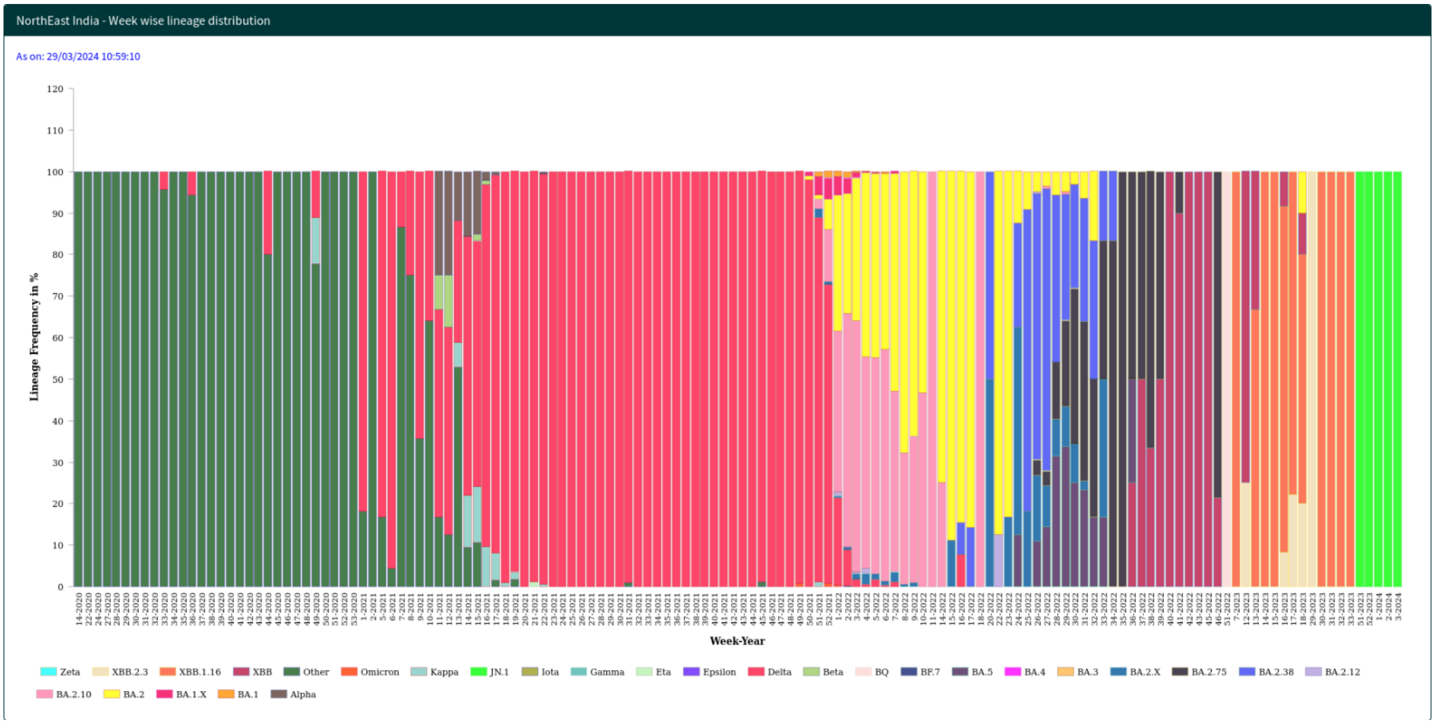


Region-wise analysis:



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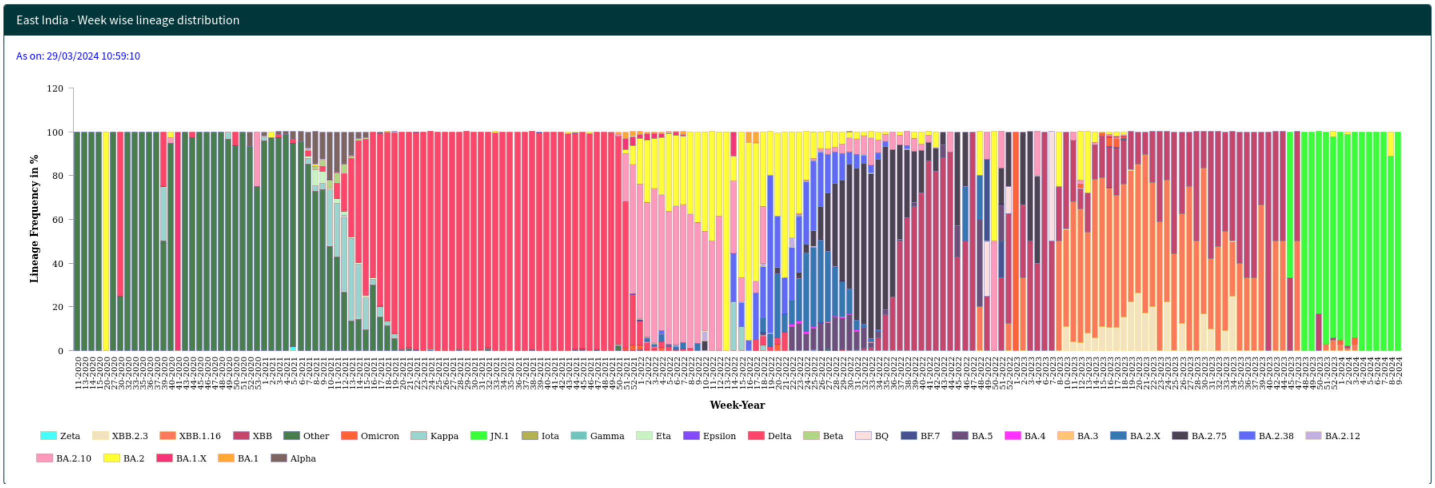
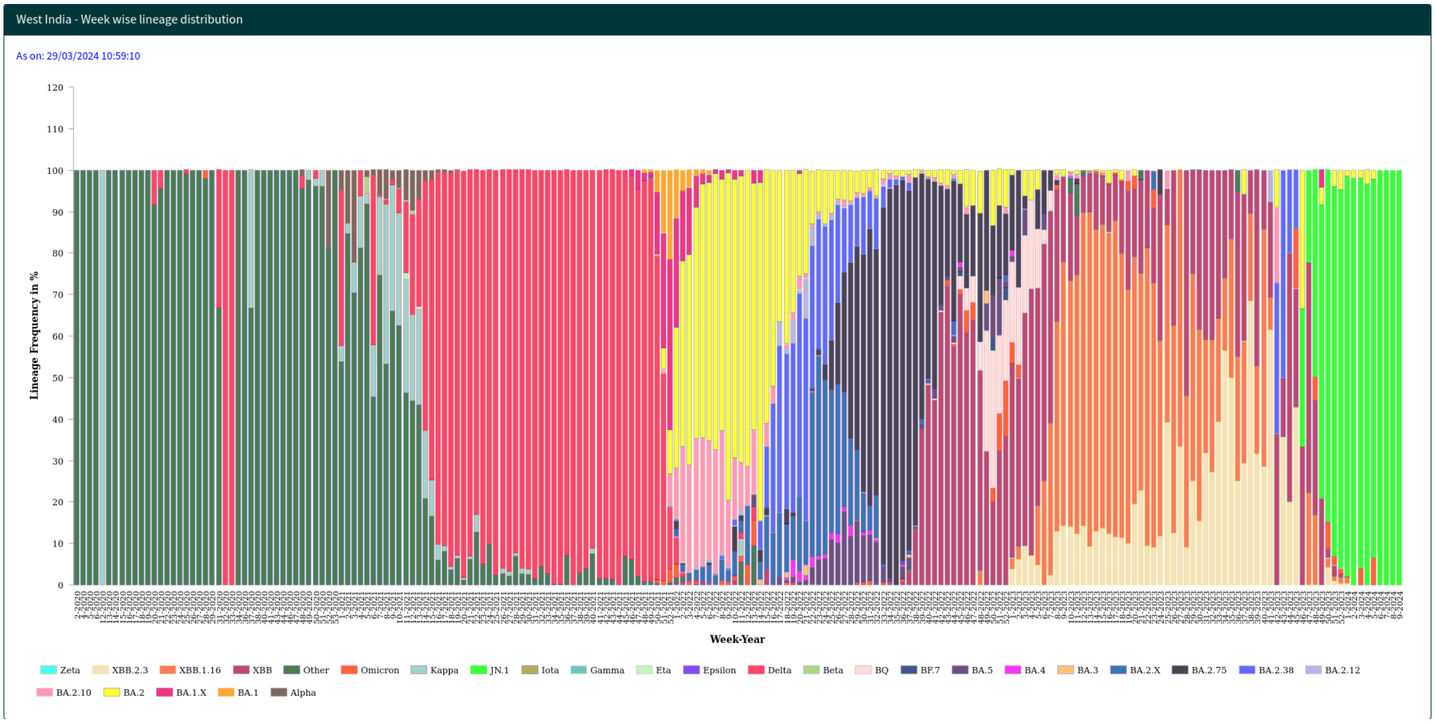


East India - Week wise lineage distribution

As on: 29/03/2024 10:59:10



West India - Week wise lineage distribution

As on: 29/03/2024 10:59:10

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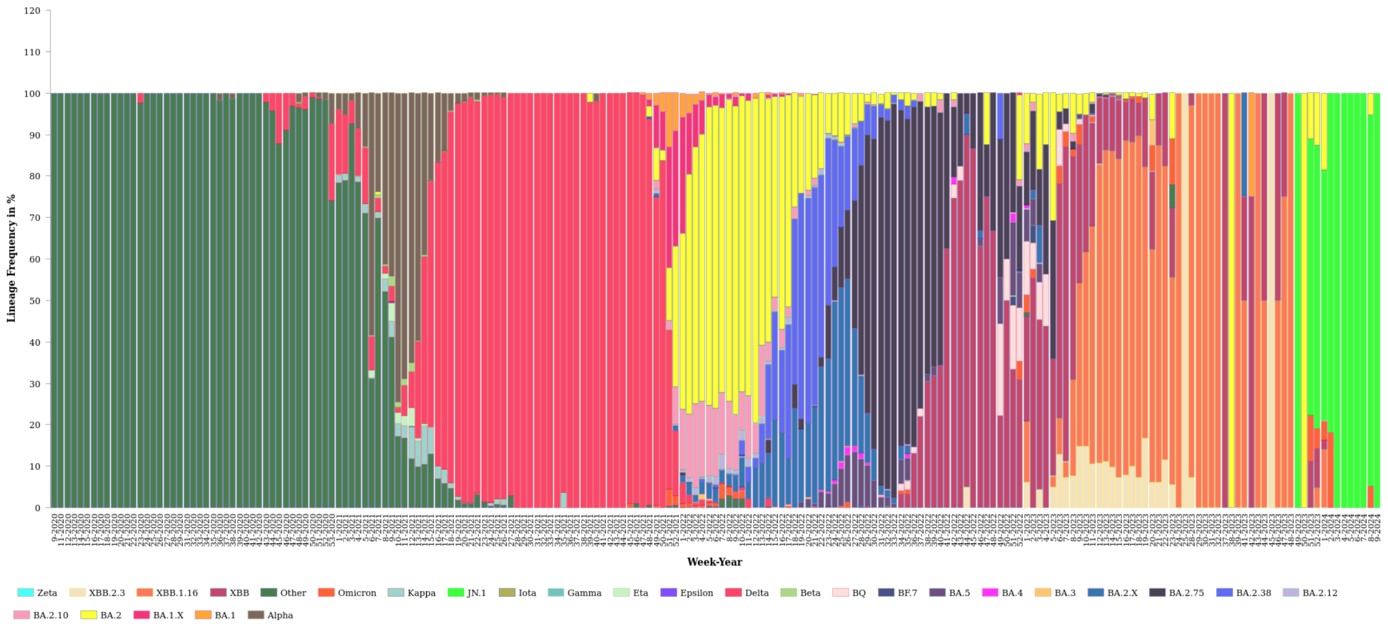
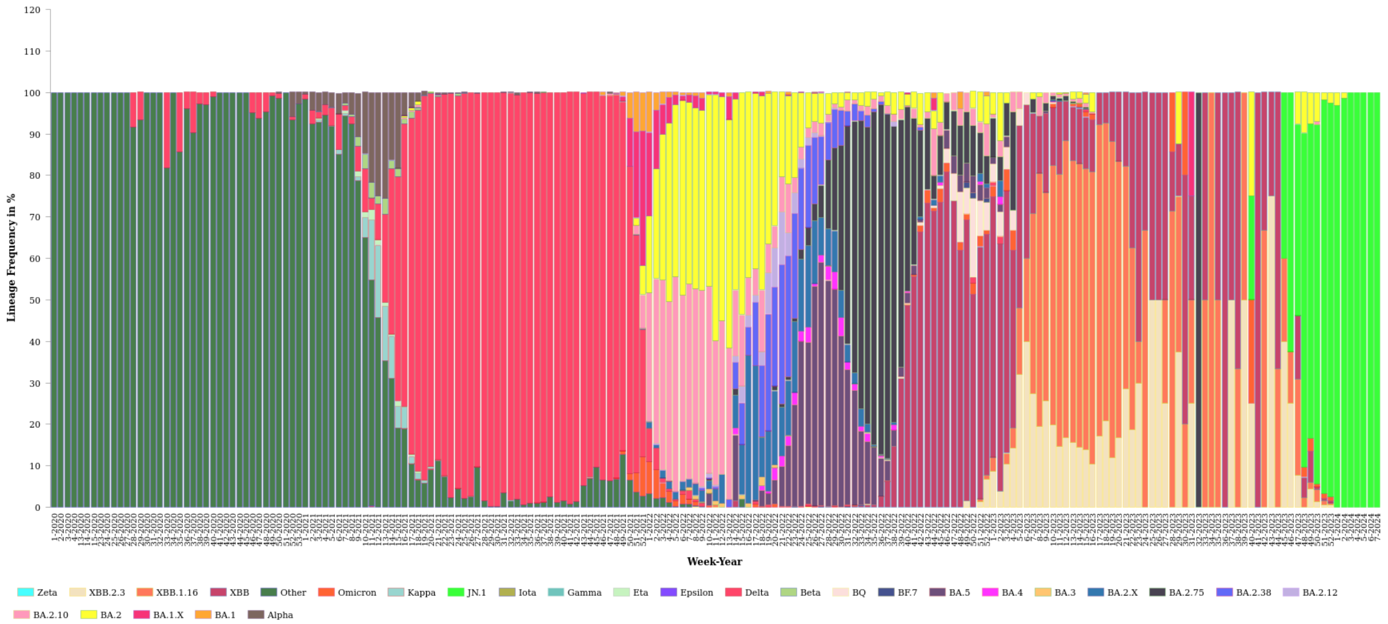
North India - Week wise lineage distribution

As on: 29/03/2024 10:59:10



South India - Week wise lineage distribution

As on: 29/03/2024 10:59:10



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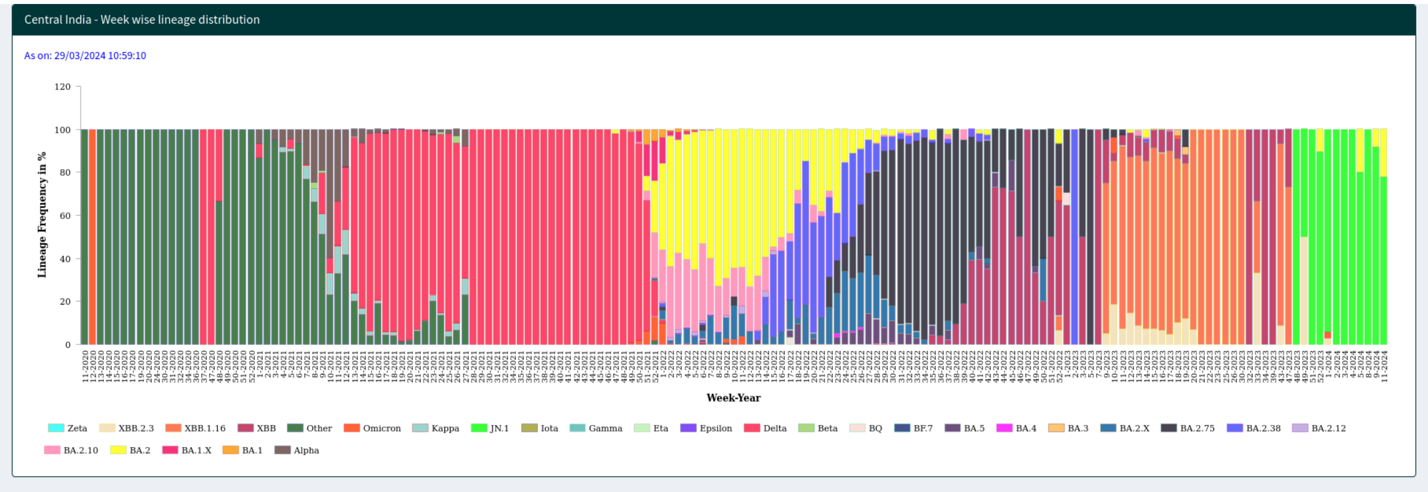

Reference:

1. WHO weekly epidemiological report.
2. GISAID. Available from: https://gisaid.org/hcov19-variants/