

INSACOG BULLETIN

15 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 300,494

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: 335,935

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

Table 1: Cumulative samples with pangolin lineage assigned (as on 14-03-2024)				
Community sample	Travelers sample	Total pangolin lineage assigned	Total VOC/VOI	Percentage
213138	12564	225702	189476	83.9

Global Scenario

During the last 28-day period (from 5 February, 2024 to 3 March, 2024), over 292,000 new cases and 6,200 new deaths were reported globally. The number of reported new cases has decreased by 44% while the number of reported deaths has decreased by 51% compared to the previous 28 days¹. On 18 December 2023, JN.1, a sub-lineage of the BA.2.86 Omicron variant was designated a separate variant of interest (VOI), due to its rapid increase in prevalence in recent weeks. As of 15th March, 2024, 73,556 JN.1 sequences have been submitted to GISAID from 114 countries². 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. 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. The other VOIs, XBB.1.5, XBB.1.16 and EG.5, have decreased in

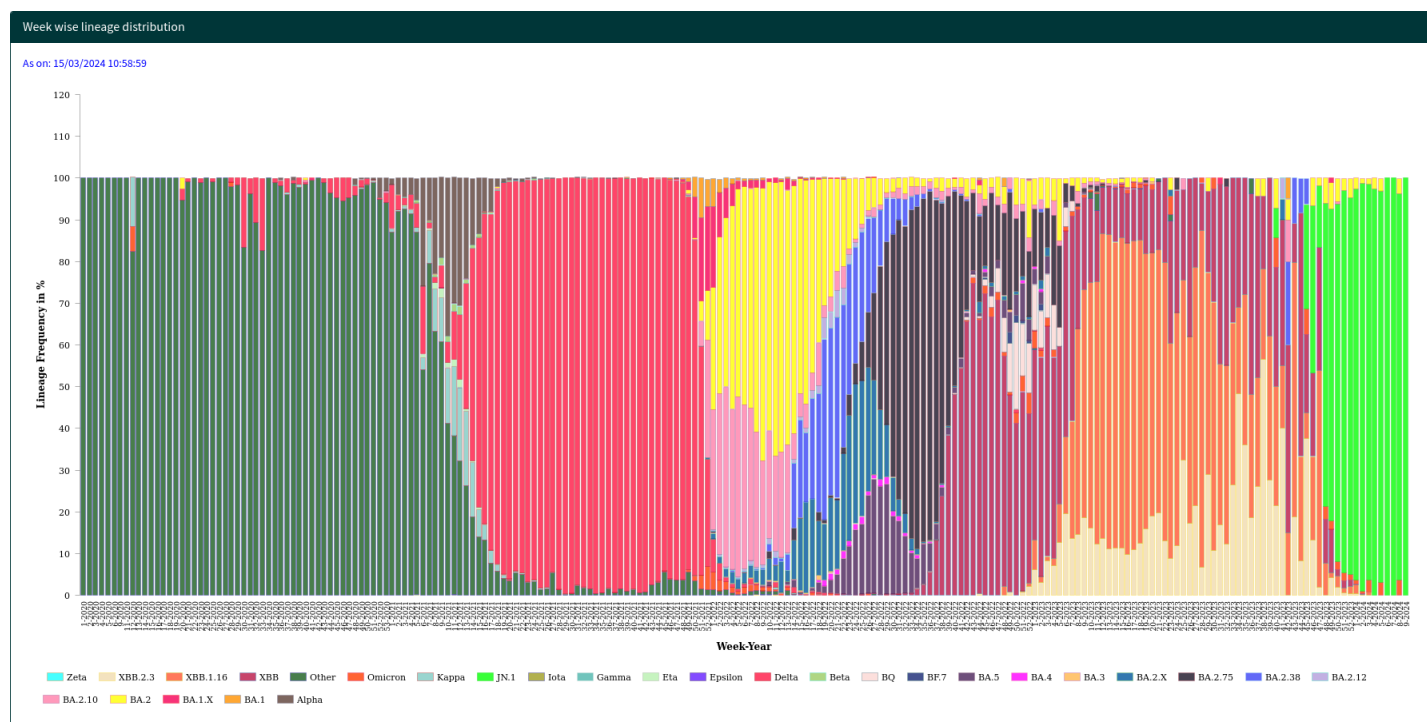
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global prevalence during the same period. XBB.1.5, XBB.1.16 and EG.5 accounted for 0.6%, less than 0.1% and 2.2% of sequences respectively in week 9 of 2024. All the VUMs have also showed a decreasing trend.

Indian Scenario

During this reporting period, 100% of the submitted sequences were of JN.1 sub-variants. Since the testing and the sampling frequency is less for some other parts of India, the overall scenario might not be clear yet. 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.

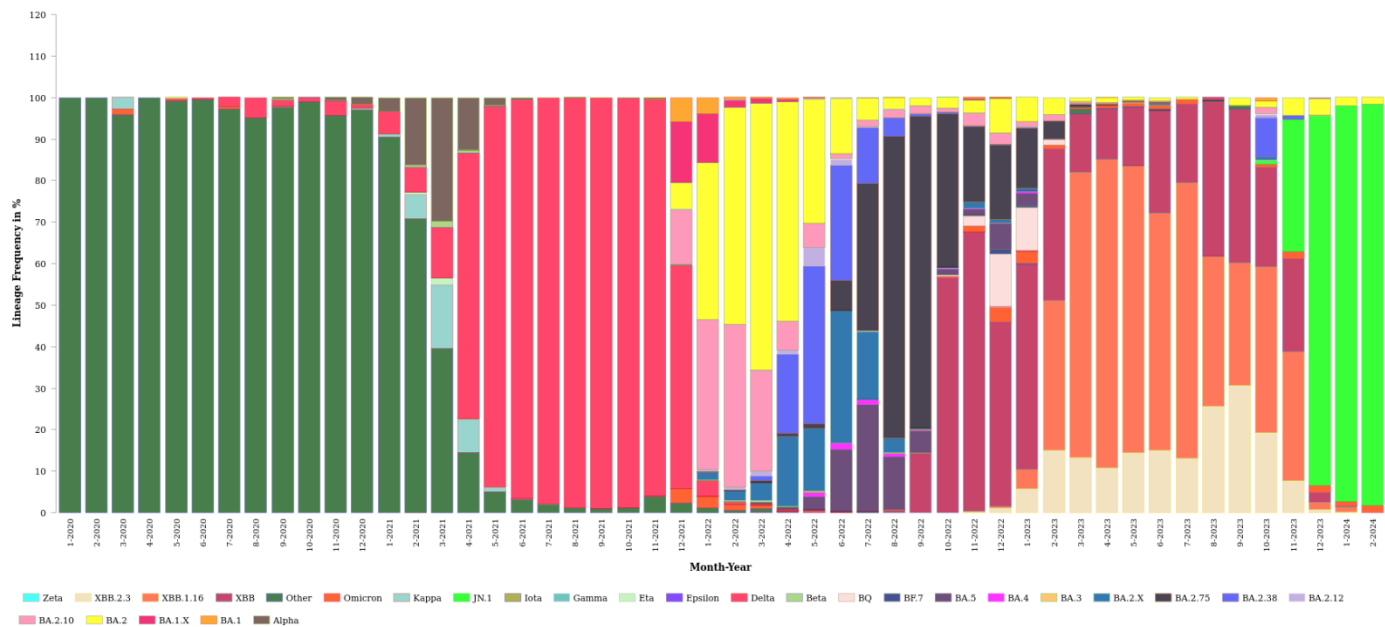
Country wide analysis:



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Month wise lineage distribution

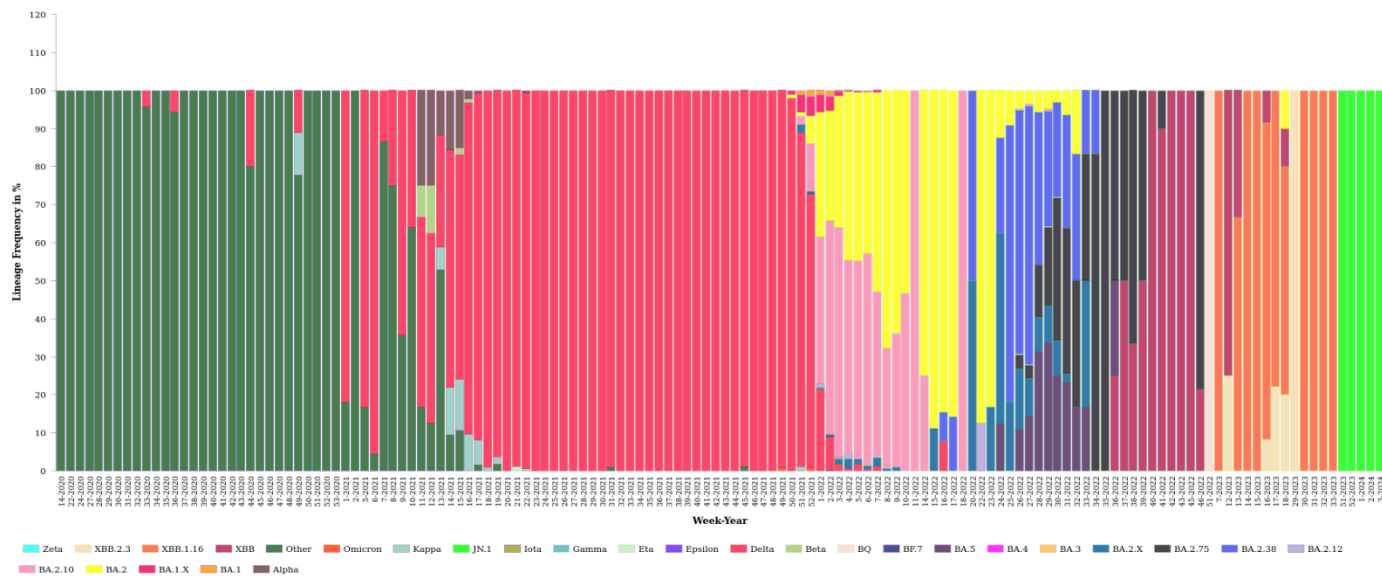
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Region-wise analysis:

NorthEast India - Week wise lineage distribution

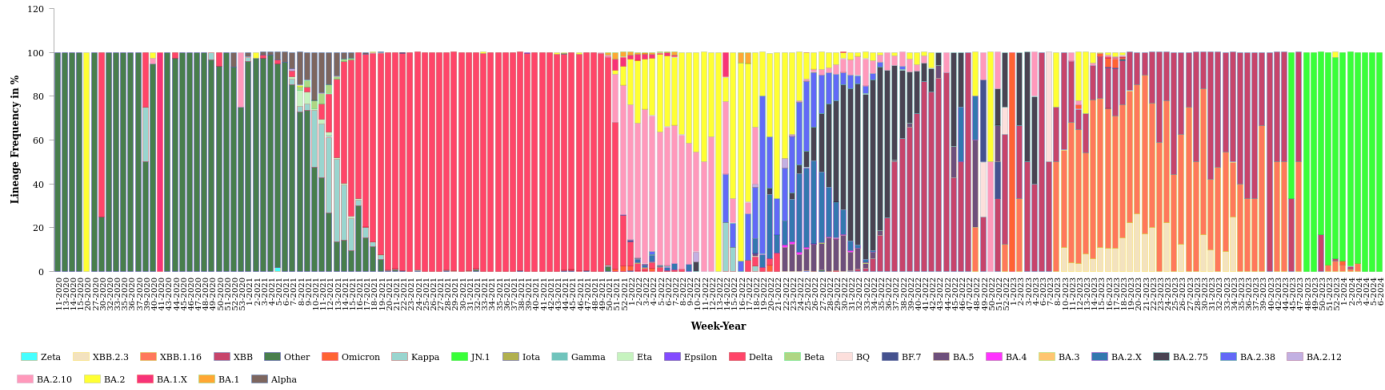
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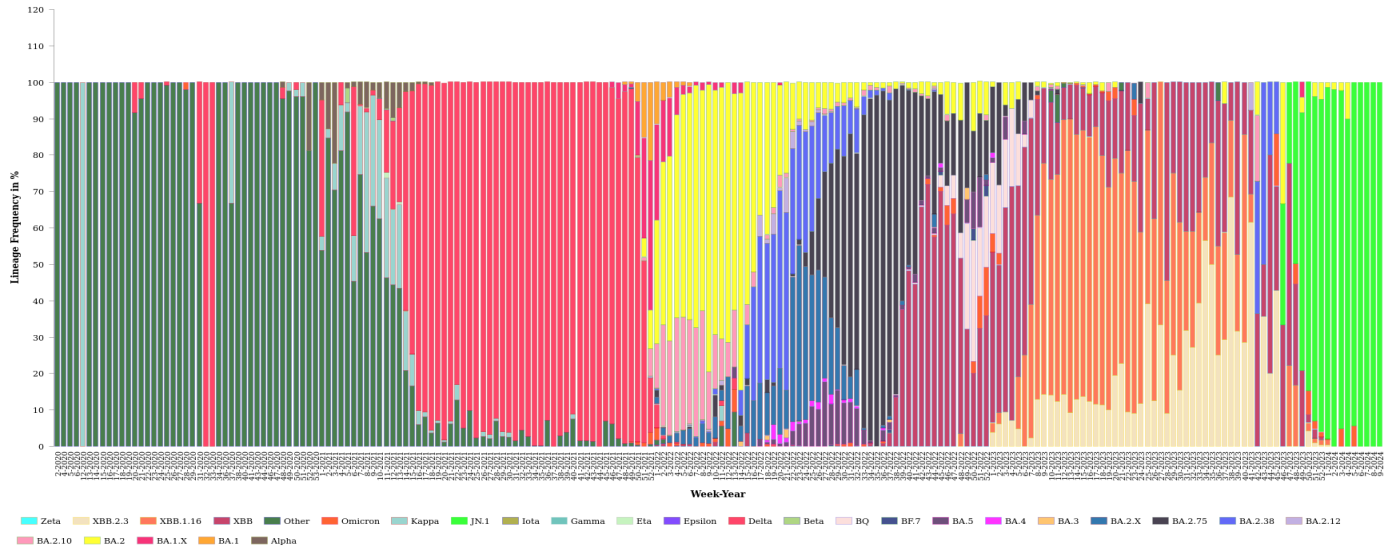
East India - Week wise lineage distribution

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West India - Week wise lineage distribution

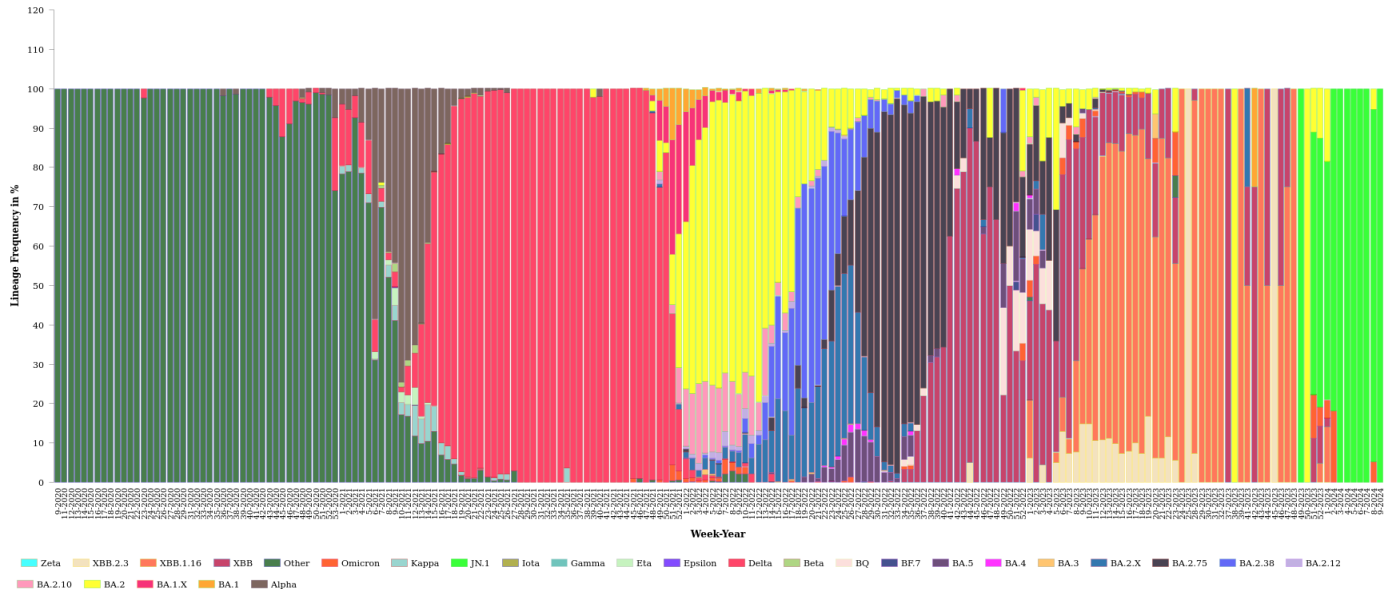
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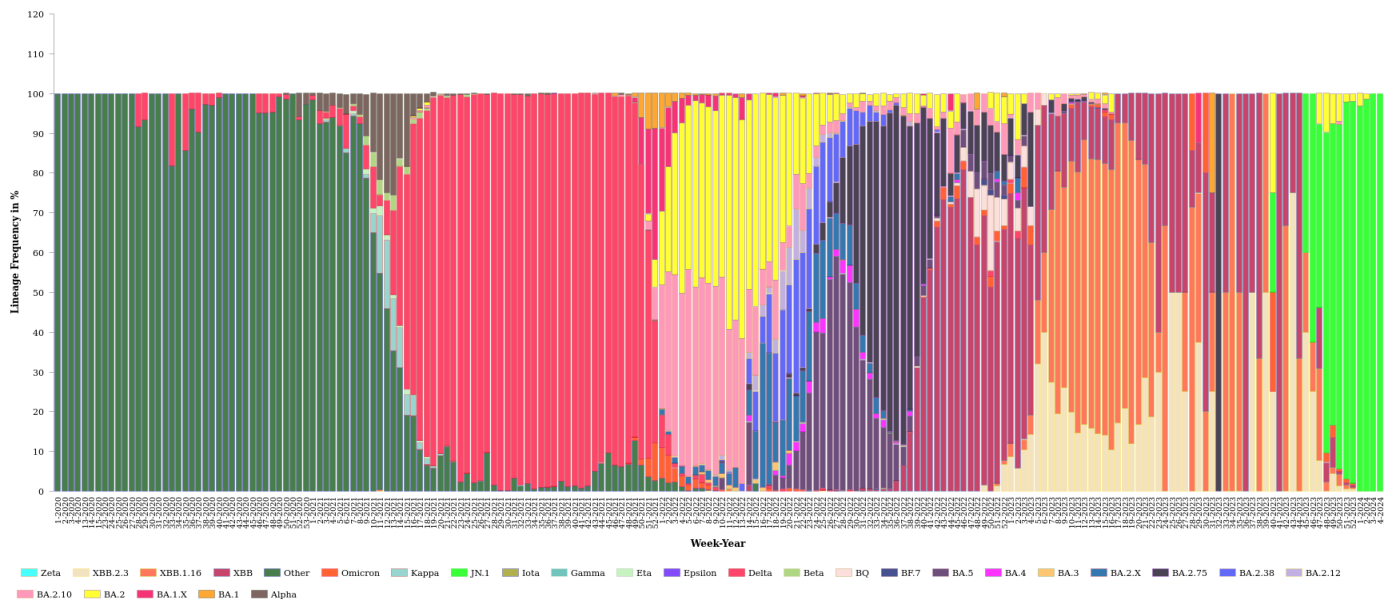
North India - Week wise lineage distribution

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South India - Week wise lineage distribution

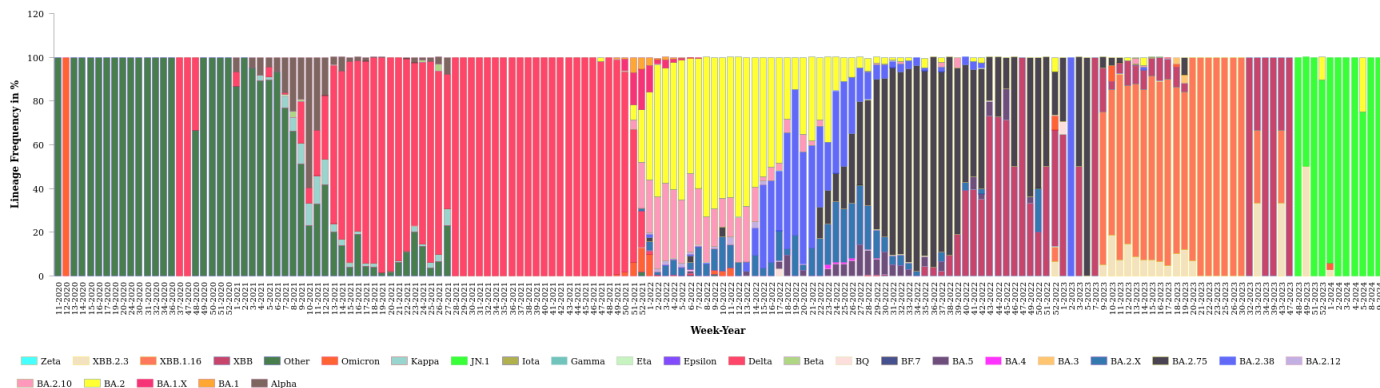
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Central India - Week wise lineage distribution

As on: 15/03/2024 10:58:59



Reference:

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