

# INSACOG BULLETIN

31 January 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 299,955

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: 335,396**

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

Table 1: Cumulative samples with pangolin lineage assigned (as on 25-01-2024)				
Community sample	Travelers sample	Total pangolin lineage assigned	Total VOC/VOI	Percentage
212218	12564	224782	188631	83.9

## Global Scenario

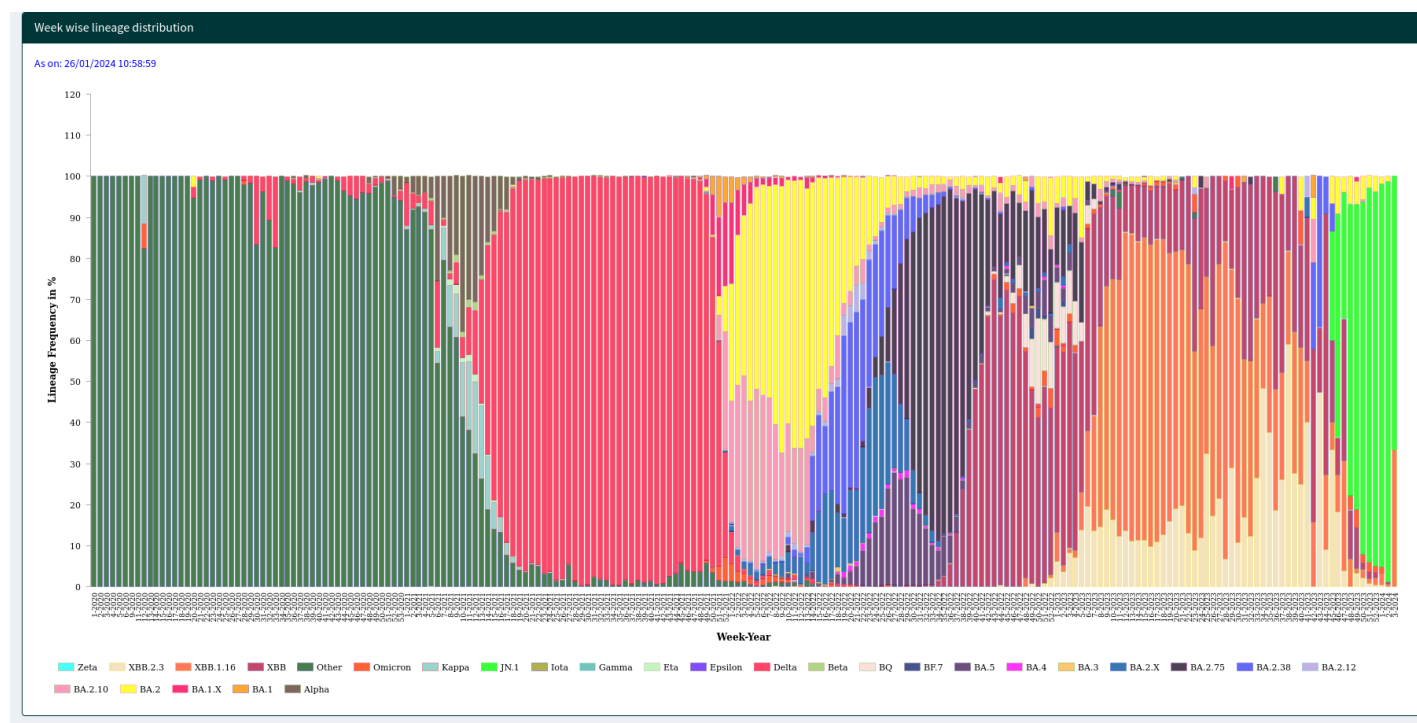
During the last 28-day period (from 11 December 2023 to 7 January 2024), over 1.1 million new cases and 8,700 new deaths were reported globally. The number of reported new cases has increased by 4% while the number of reported deaths has decreased by 26% compared to the previous 28 days<sup>1</sup>. 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 31<sup>st</sup> January, 2024, 42,757 JN.1 sequences have been submitted to GISAID from 91 countries<sup>2</sup>. Globally, JN.1 is now the most reported VOI, accounting for 65.5% of sequences in week 52 compared to 24.8% in week 48. Its parent lineage, BA.2.86, is stable and accounted for 7.8% of sequences in week 52. 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 VOIs – XBB.1.5, XBB.1.16, EG.5 BA.2.86 and JN.1; and five VUMs: DV.7, XBB, XBB.1.9.1, XBB.1.9.2 and XBB.2.3.

# INSACOG BULLETIN

## Indian Scenario

During this reporting period, 94% of the submitted sequences were of JN.1 sub-variants. As of 31<sup>st</sup> January 2024, 21,200 cases of JN.1 and its sub lineages have been detected in India. 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:

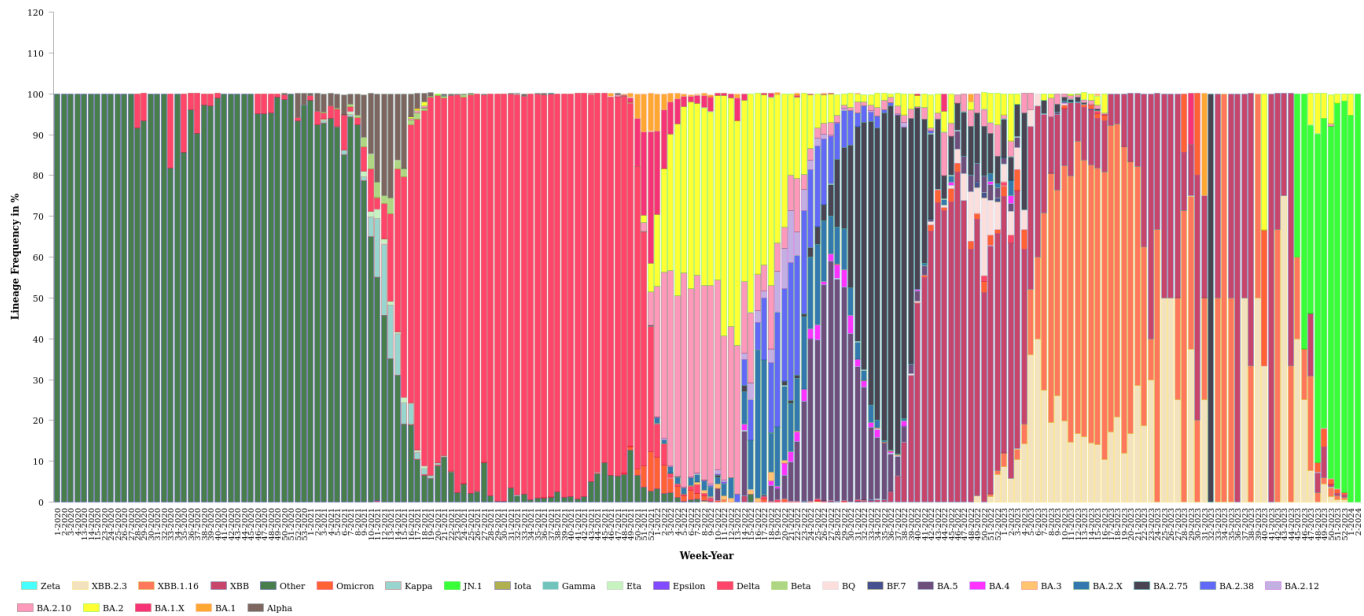


## Region-wise analysis:

# INSACOG BULLETIN

South India - Week wise lineage distribution

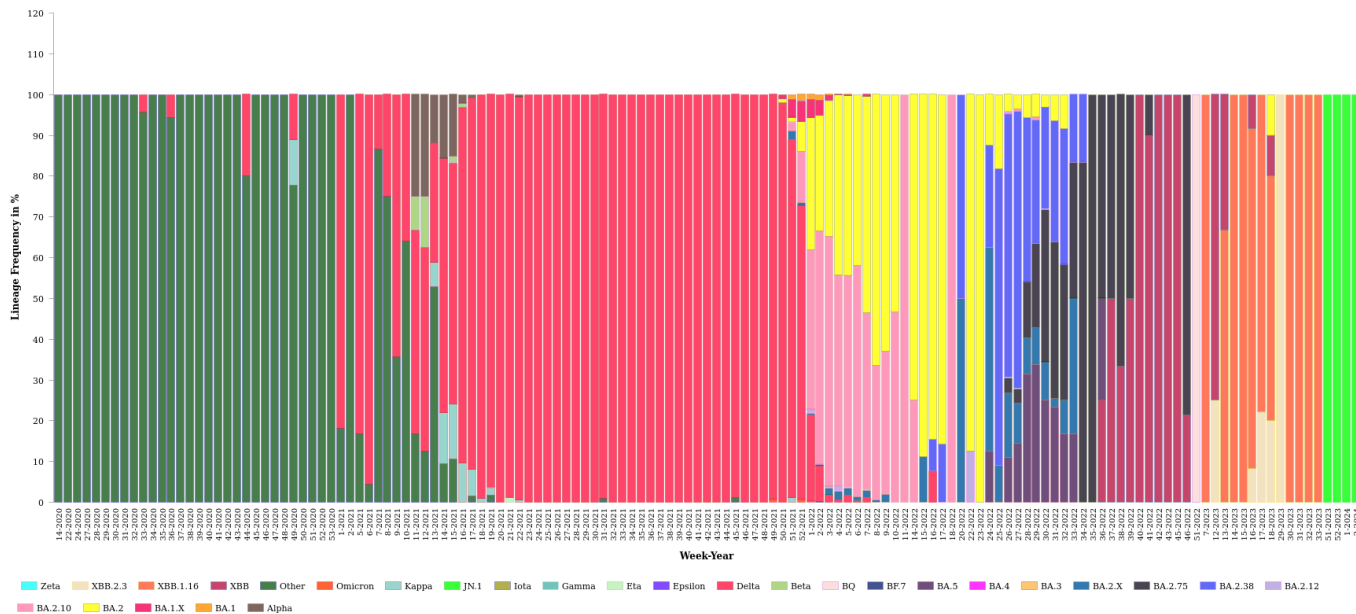
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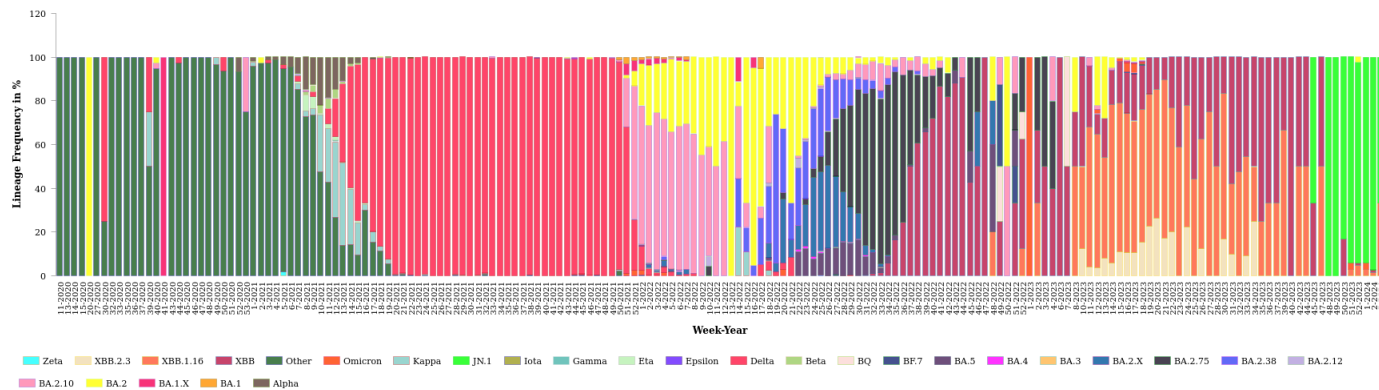
NorthEast India - Week wise lineage distribution

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East India - Week wise lineage distribution

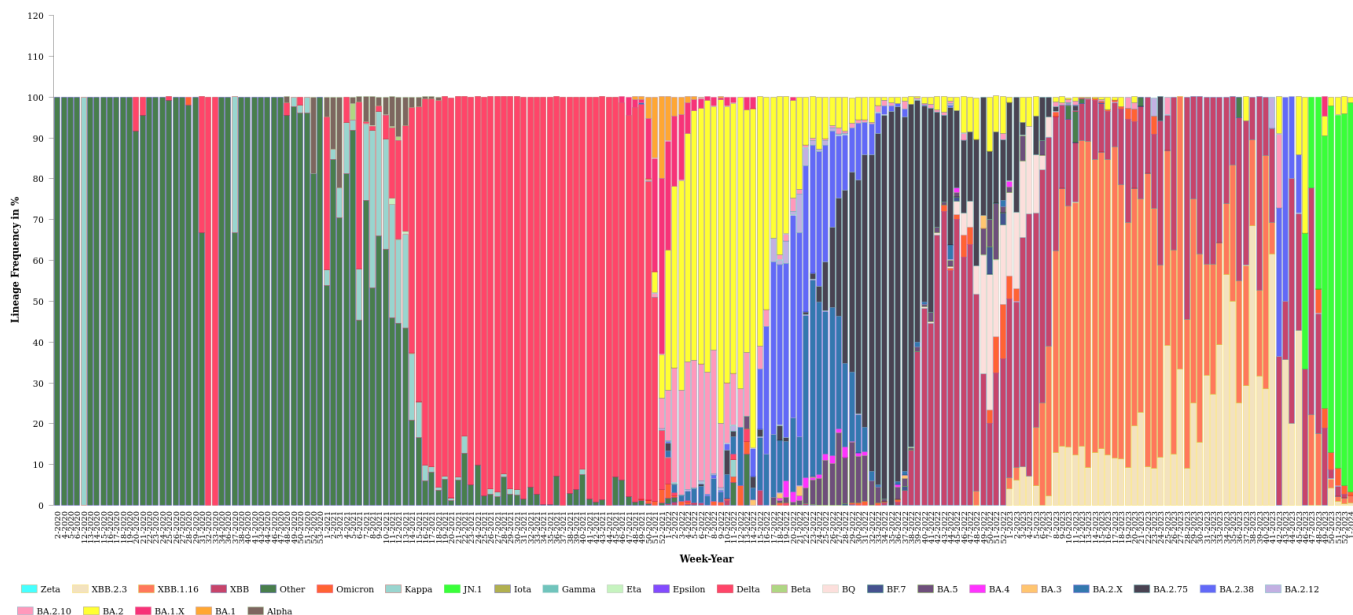
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# INSACOG BULLETIN

West India - Week wise lineage distribution

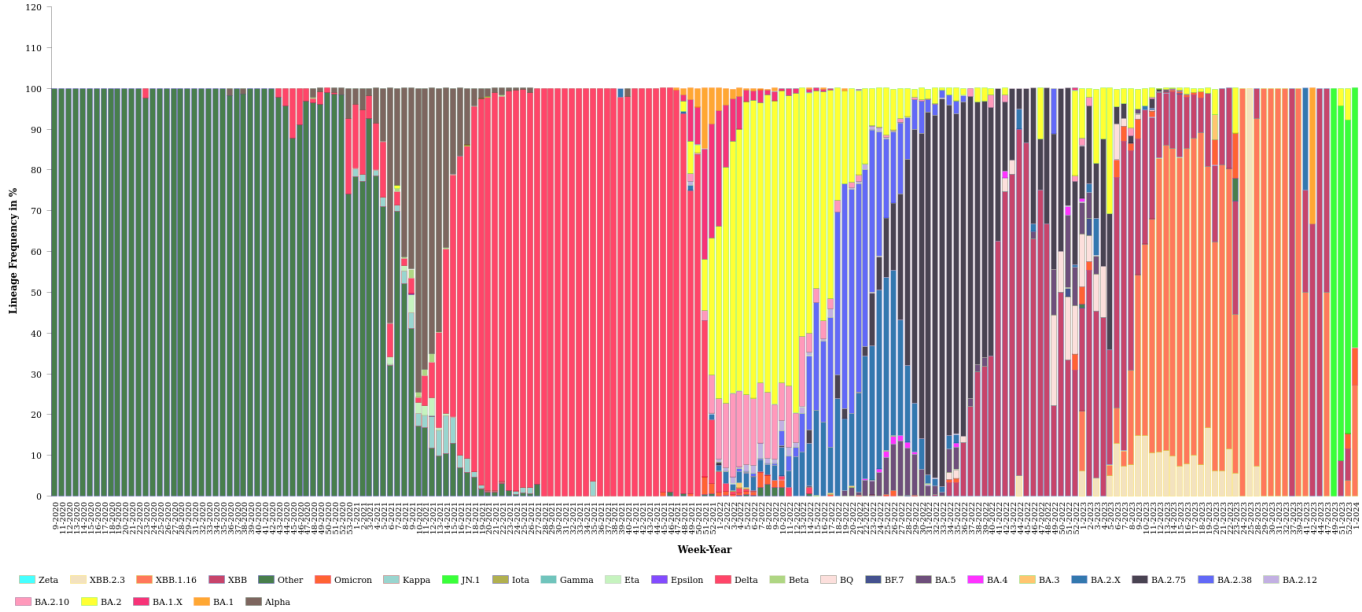
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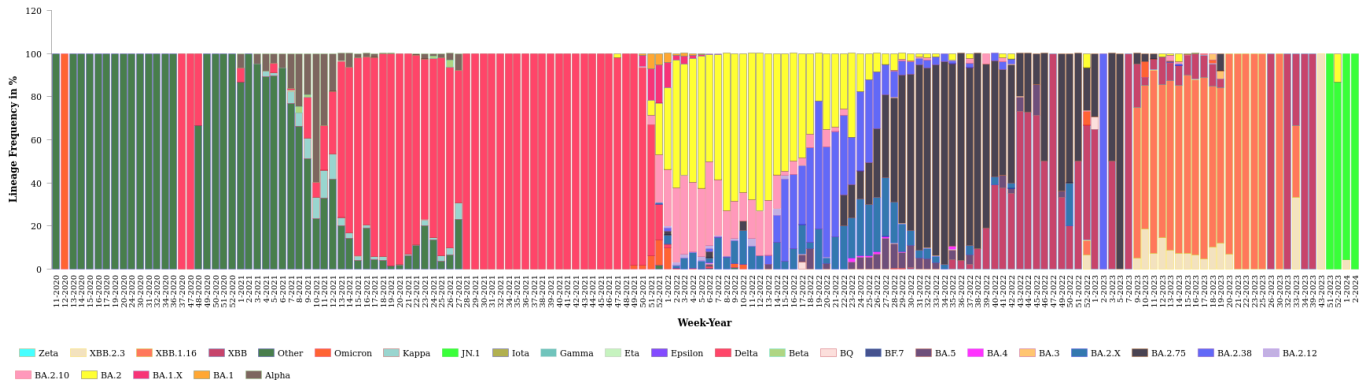
## North India - Week wise lineage distribution

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## Central India - Week wise lineage distribution

As on: 26/01/2024 10:58:59



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## Reference:

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