INSACOG BULLETIN

15 April 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 301,019

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: 336,460

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

Table 1: Cumulative samples with pangolin lineage assigned (as on 15-04-2024)

Community sample	Travelers sample	Total pangolin lineage assigned	Total VOC/VOI	Percentage
213442	**12564**	**226006**	**189776**	**84.0**

Global Scenario

Over 275,553 new cases and 4,200 new deaths were reported during the last 28-day period (from 4 March, 2024 to 31 March, 2024), globally. The number of reported new cases and reported deaths has decreased by 11% and 41% 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. All the most recent variants under monitoring (VUMs) (XBB, XBB.1.9.1 and XBB.2.3) have been de-escalated after having less than 1% global prevalence for eight epidemiological weeks. Globally, JN.1 is now the most frequentlyreported VOI, accounting for 95.1% of sequences in week 13 compared to 93.0% in week 10. As of 15th April, 2024, 72,520 JN.1 sequences have been submitted to GISAID from 112 countries[2]. Its parent lineage, BA.2.86, is stable and accounted for 1.6% of sequences in week 13. 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 either decreased or remained stable in global prevalence during the same period. XBB.1.5 and EG.5 have not been reported, whereas, XBB.1.16 is reported by 0.4% sequences in week 13.

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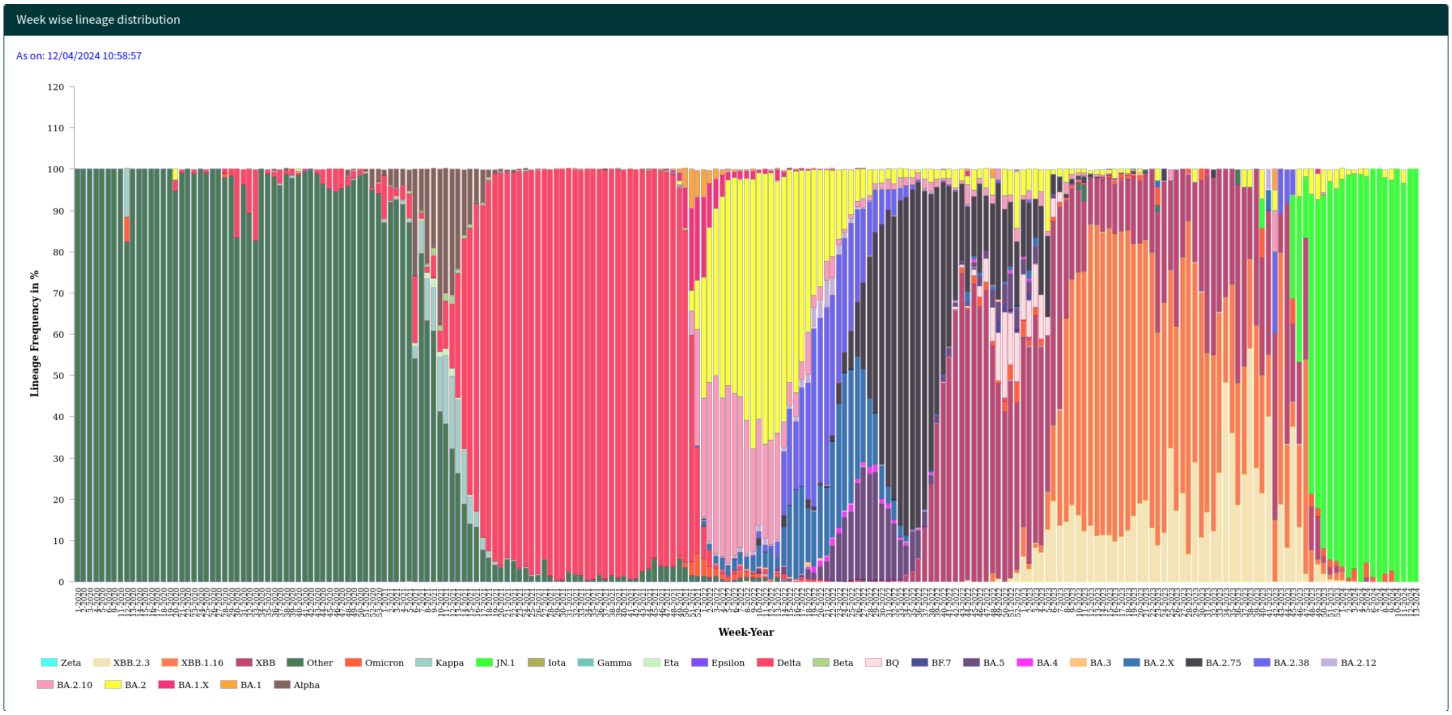
Indian Scenario

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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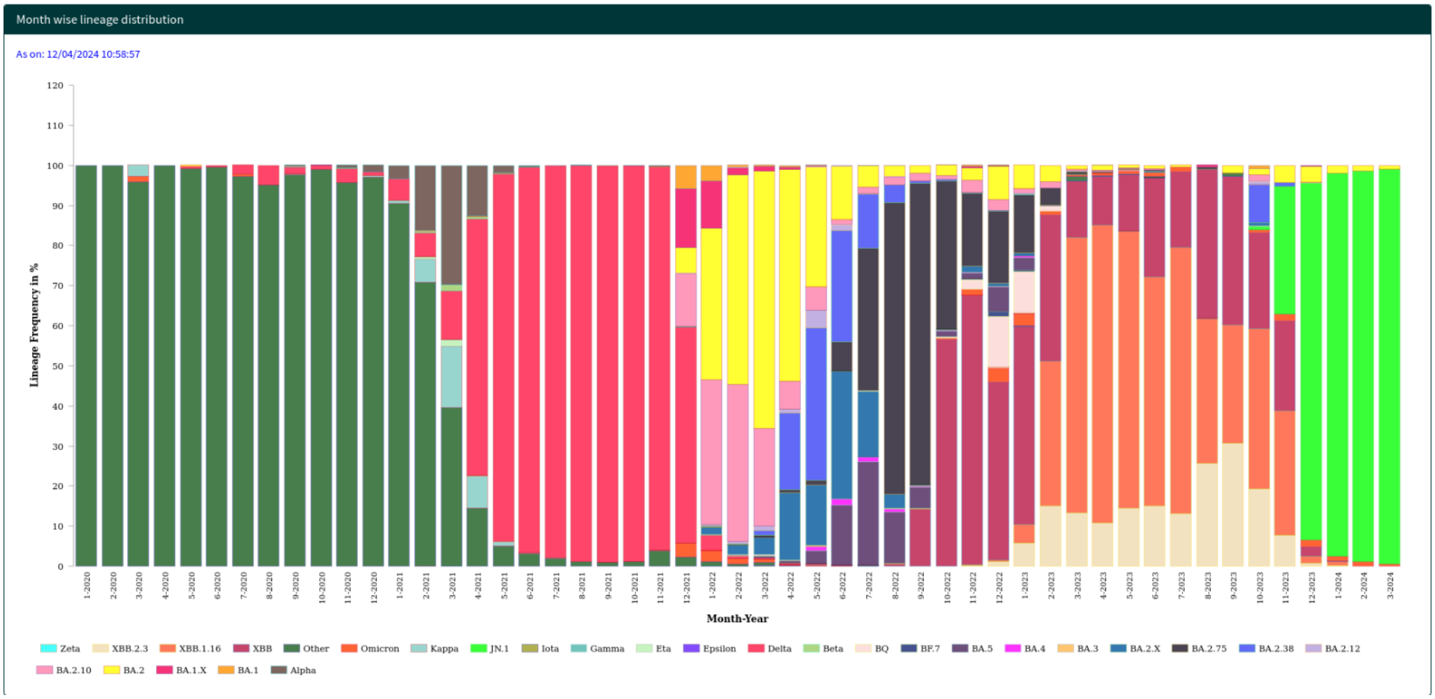
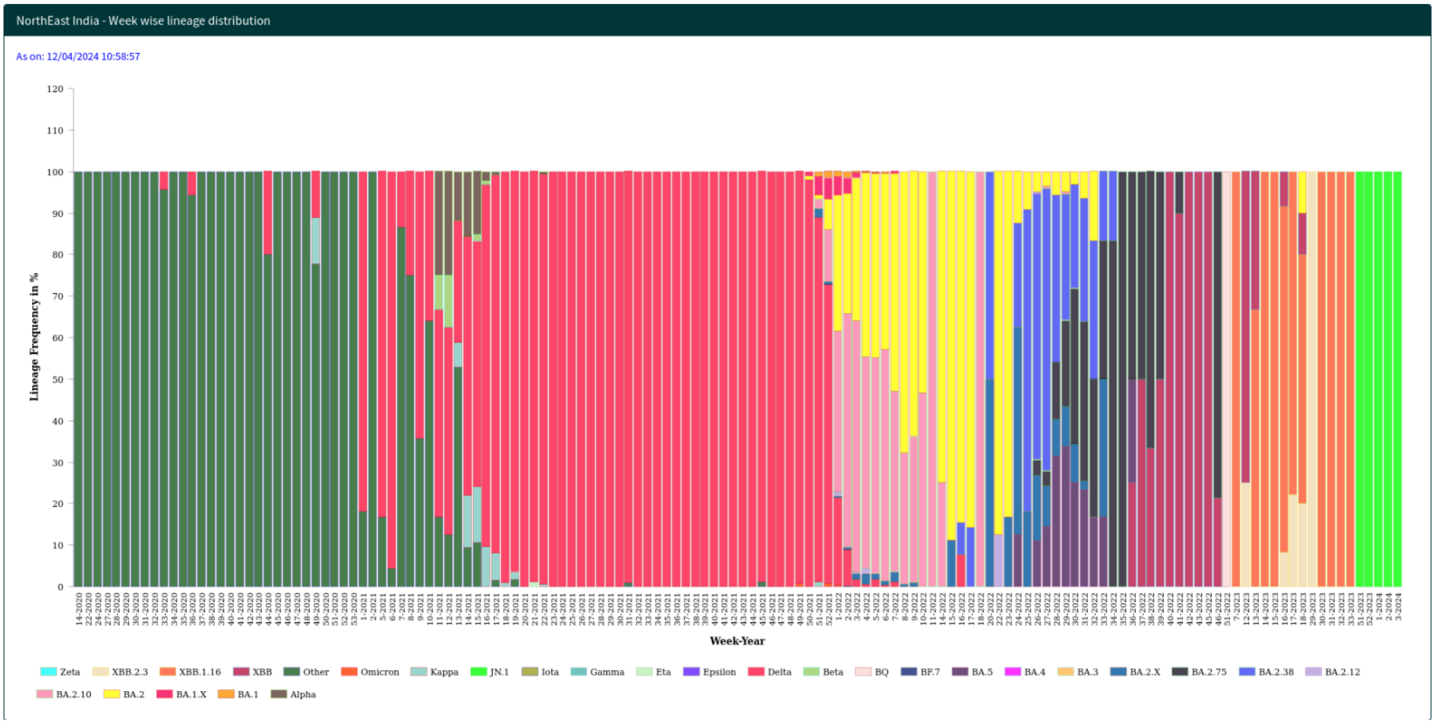

Month wise lineage distribution

As on: 12/04/2024 10:58:57

Region-wise analysis:


NorthEast India - Week wise lineage distribution

As on: 12/04/2024 10:58:57

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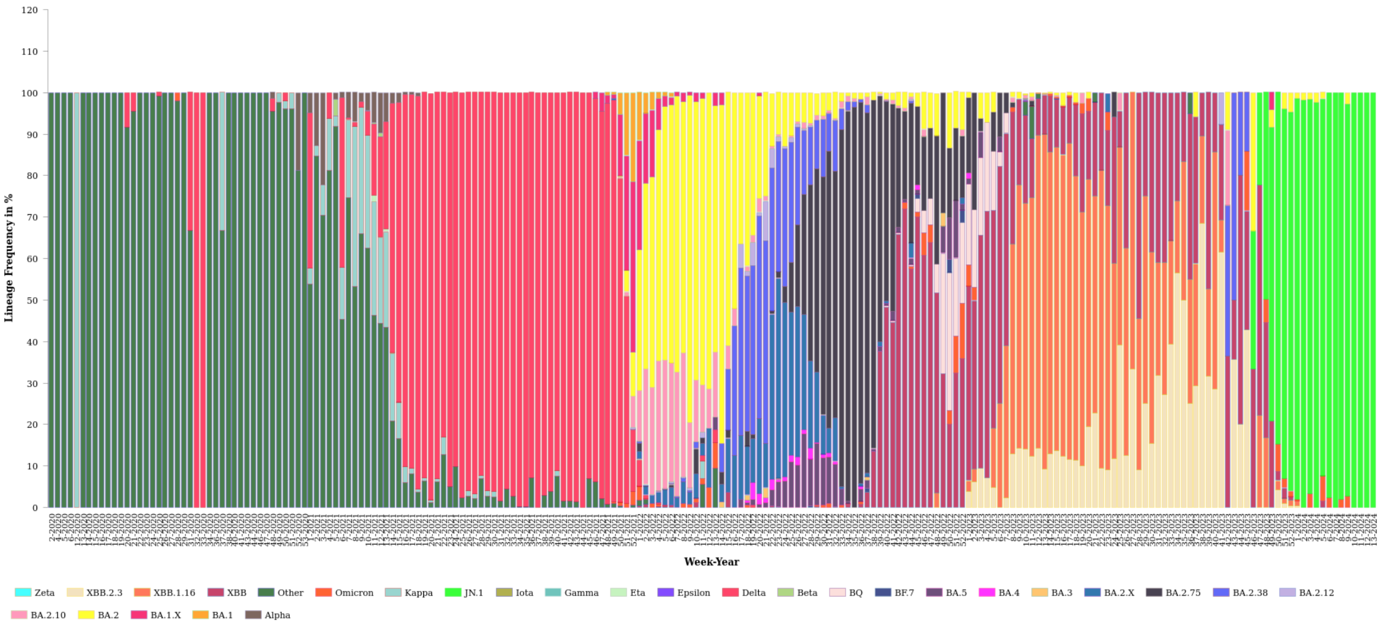
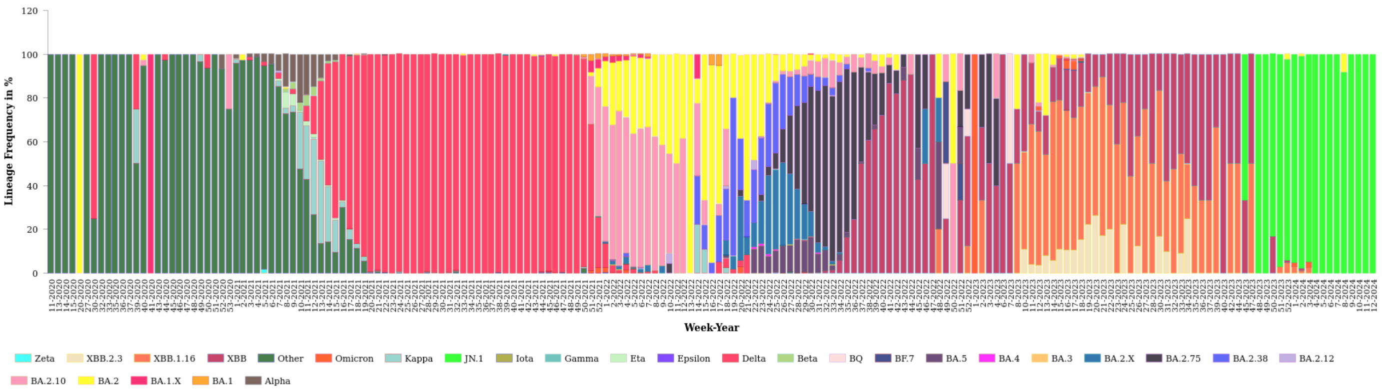
West India - Week wise lineage distribution

As on: 12/04/2024 10:58:57



East India - Week wise lineage distribution

As on: 12/04/2024 10:58:57



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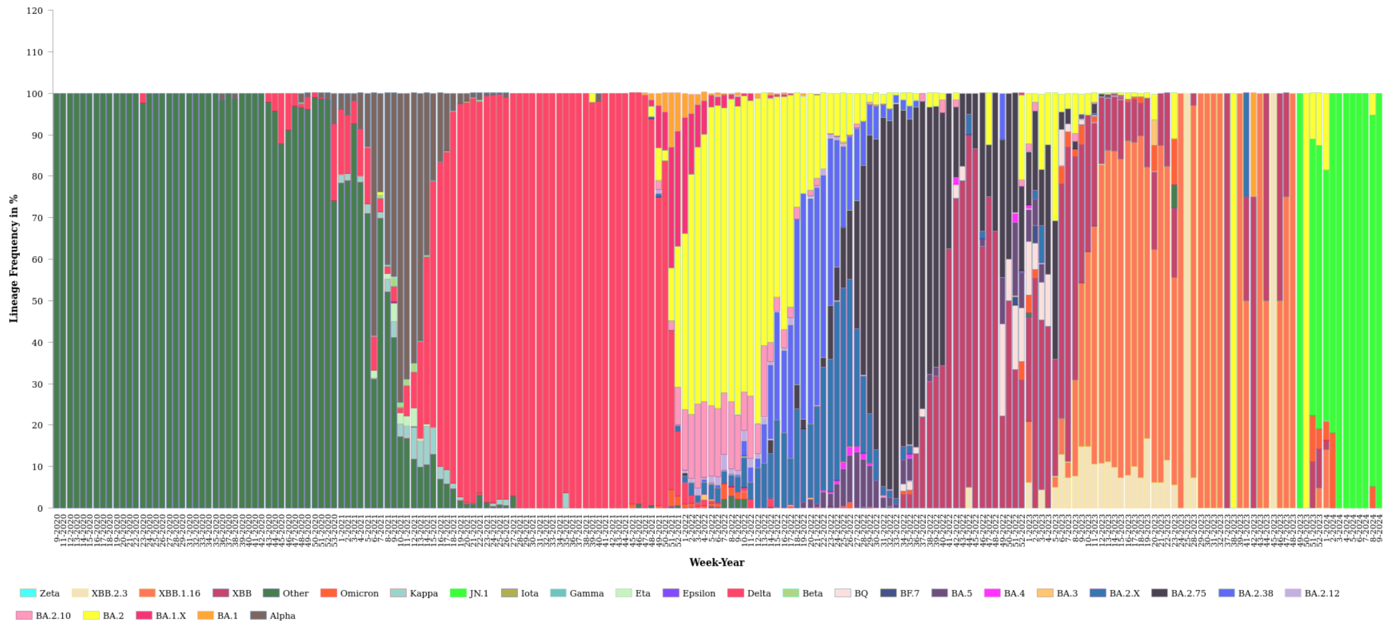
North India - Week wise lineage distribution

As on: 12/04/2024 10:58:57

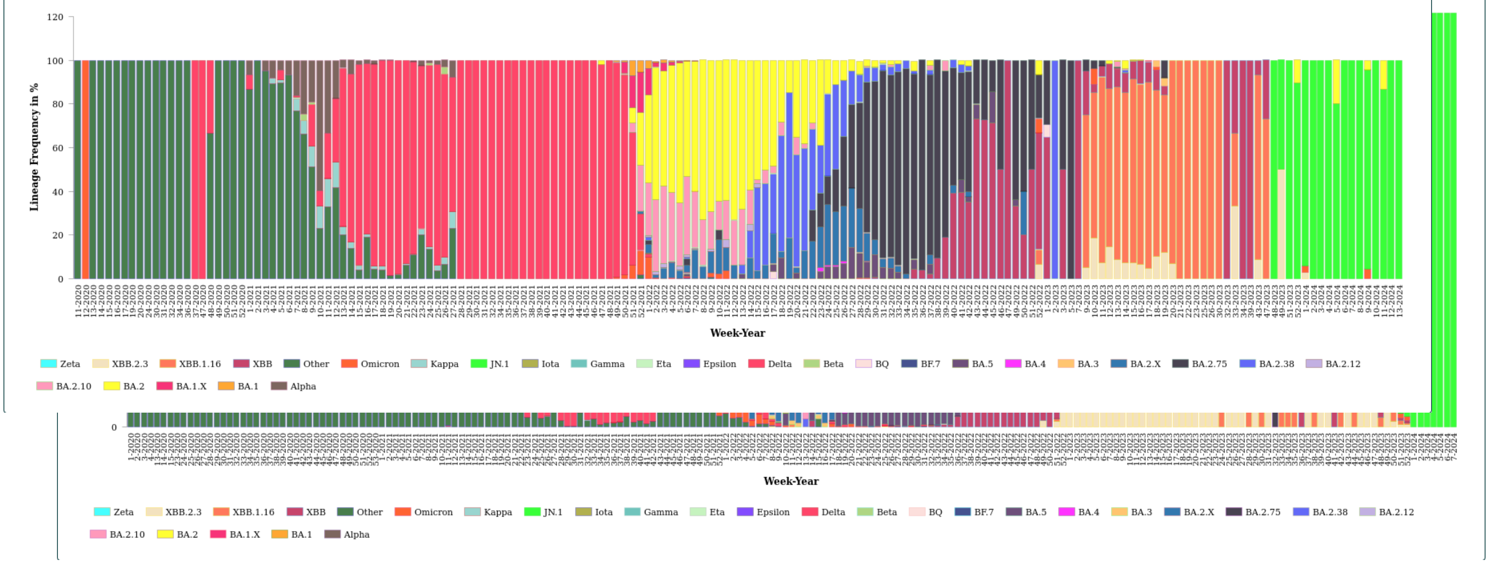


South India - Week wise lineage distribution

As on: 12/04/2024 10:58:57

Central India - Week wise lineage distribution

As on: 12/04/2024 10:58:57



Reference:

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