

INSACOG BULLETIN

15 December 2023

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 297,940

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: 333,381

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

Table 1: Cumulative samples with pangolin lineage assigned				
Community sample	Travelers sample	Total pangolin lineage assigned	Total VOC/VOI	Percentage
210065	12564	222629	186625	83.8

Global Scenario

Globally, over half a million new cases and 2400 new deaths were reported during the 28-day period from 23 October to 19 November 2023, a decrease of 13% and 72%, respectively, compared to the previous 28 days¹. During the week 40-44 of 2023, recombinant lineages continued to be the most prevalent variants globally. During this reporting period, BA.2.86 was reclassified from a variant under monitoring (VUM) to a variant of interest (VOI). So, currently there are four variants of interest (VOI), XBB.1.5, XBB.1.16 & EG.5, & BA.2.86 and five variants under monitoring (VUMs): DV.7, XBB, XBB.1.9.1, XBB.1.9.2, and XBB.2.3. 3109 sequences of the BA.2.86 variant reported from 41 countries. There has been stable trend of the prevalence of XBB.1.5 globally (128 Countries), accounting for 8.3% of sequences in week 44 compared to 8.5% of sequences in week 40. The prevalence of XBB.1.16 has decreased from 15.9% in week 40 to 8.2% in week 44. EG.5 is still the most prevalent VOIs worldwide, accounted for 51.6% of sequences from 89 countries.

Recently, JN.1 is causing a growing number of cases around the world. JN.1 is a descendent lineage of BA.2.86, with the earliest sample collected on 25 August 2023 from Luxembourg and as of now 7,344

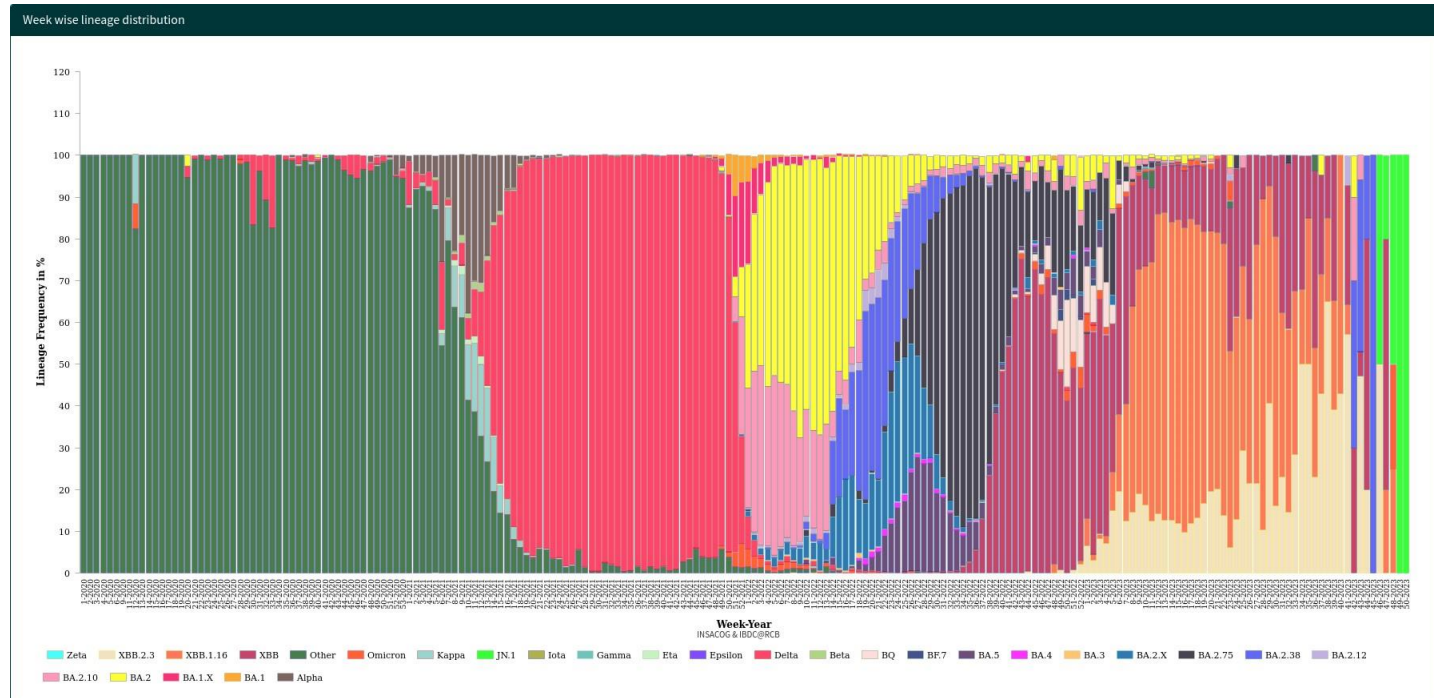
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sequences of JN.1 have been submitted in GISAID from 41 countries². There is only a single change between JN.1 and BA.2.86 in the spike protein, meaning vaccines should work against JN.1 and BA.2.86 similarly. However, JN.1, by inheriting BA.2.86's antigenic diversity and acquisition of L455S, rapidly achieved extensive resistance across receptor binding domain of class 1, 2, and 3 antibodies. It showed higher immune evasion compared with BA.2.86 and other resistant strains like HV.1 and JD.1.1, at the expense of reduced human ACE2 binding³.

Indian Scenario

Omicron and its recombinant variants XBB and XBB.1.16 used to be the dominant variants in India. But, as of 15 December 2023, 20 cases of JN.1 variants also have been identified from Western and Southern part of India. Since, the sequencing frequency is very less for other parts of India, the overall scenario might not be clear enough. INSACOG is keep continuing the surveillance for the emerging variants all over India. However, no increase in disease severity or hospitalization has been observed yet.

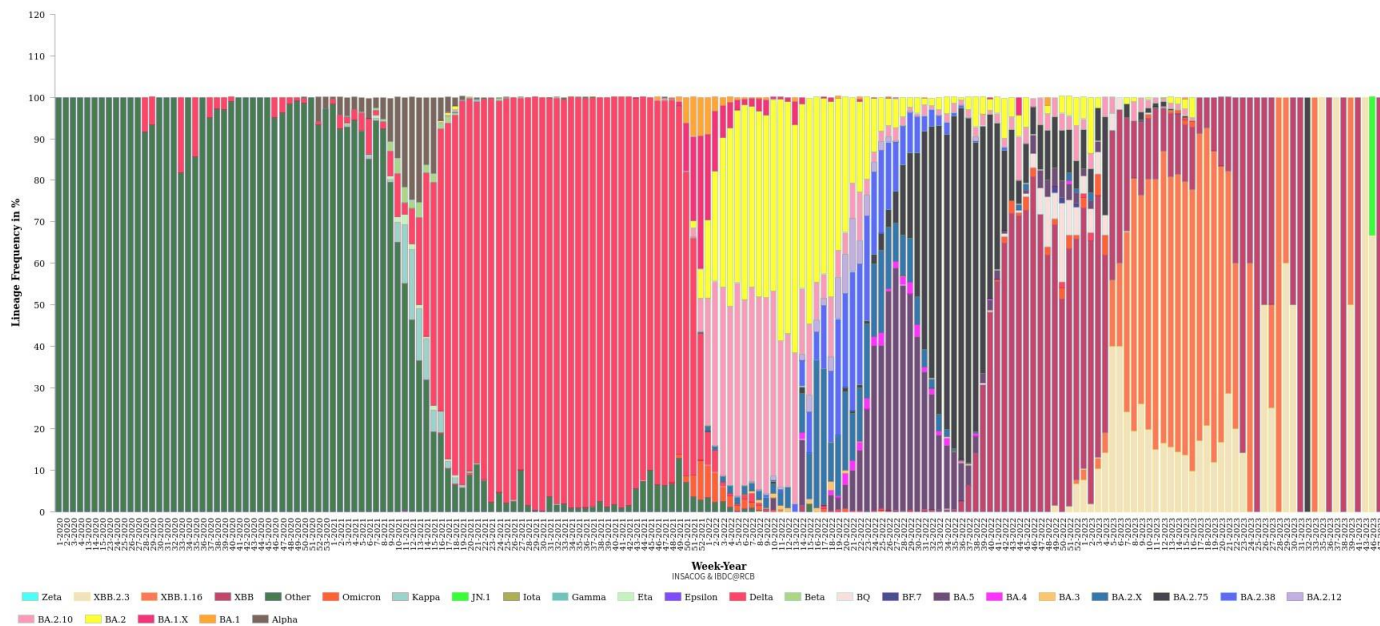
Country wide analysis:



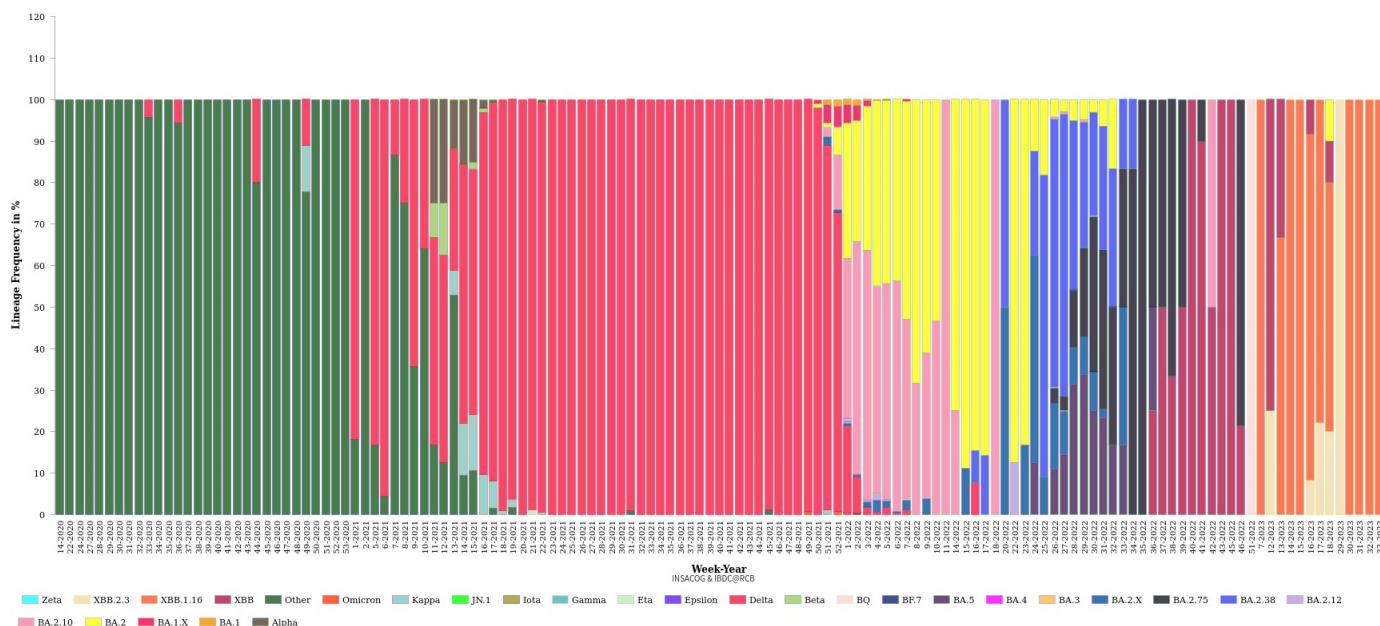
Region-wise analysis:

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South India - Week wise lineage distribution

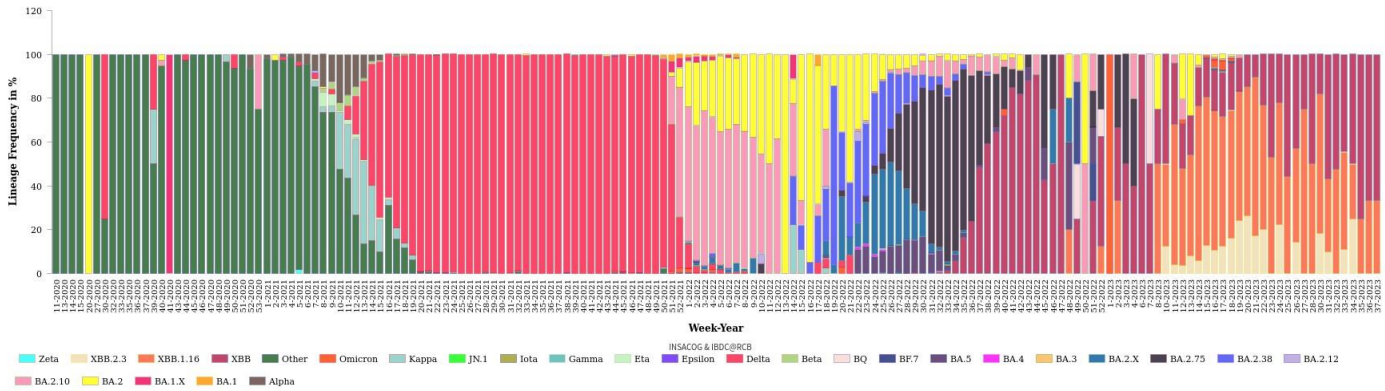


NorthEast India - Week wise lineage distribution

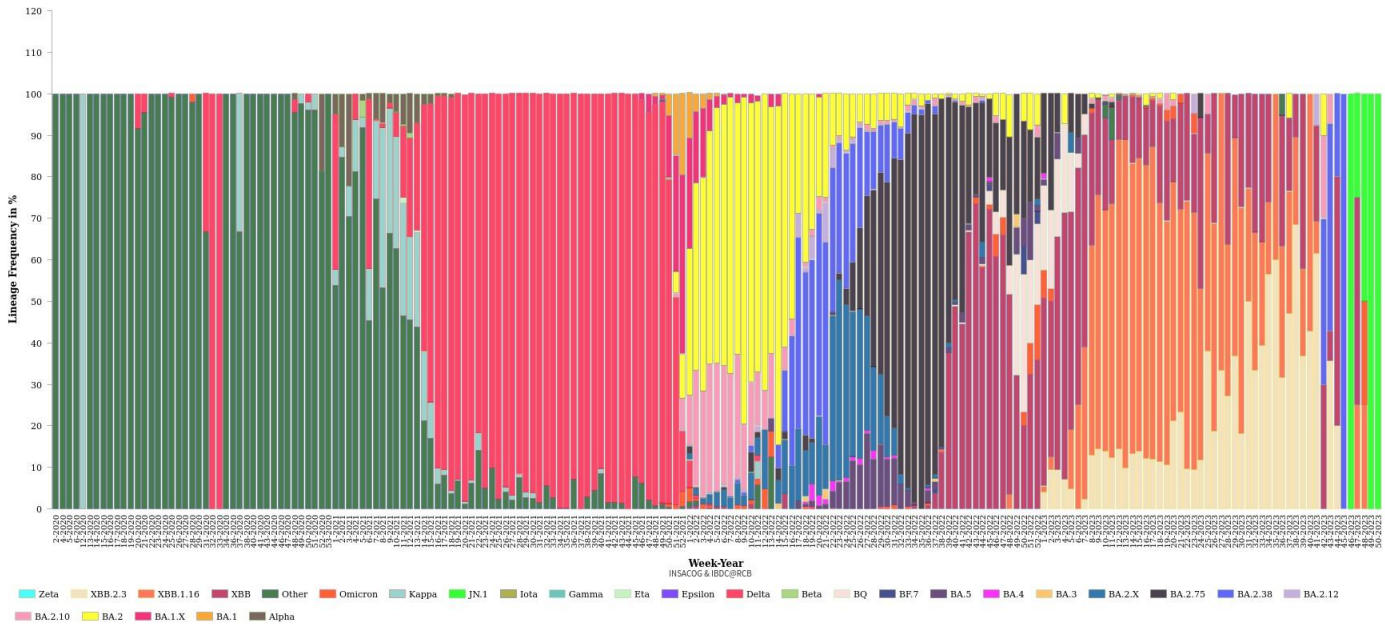


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East India - Week wise lineage distribution

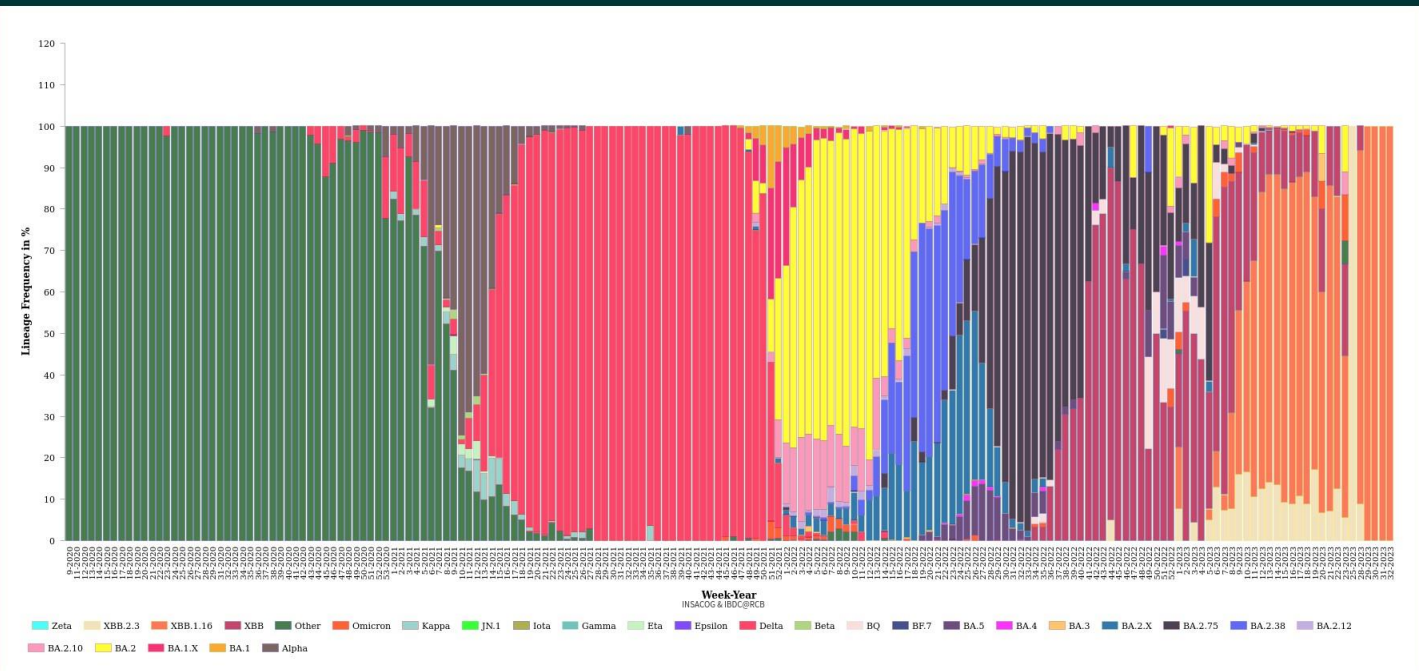


West India - Week wise lineage distribution

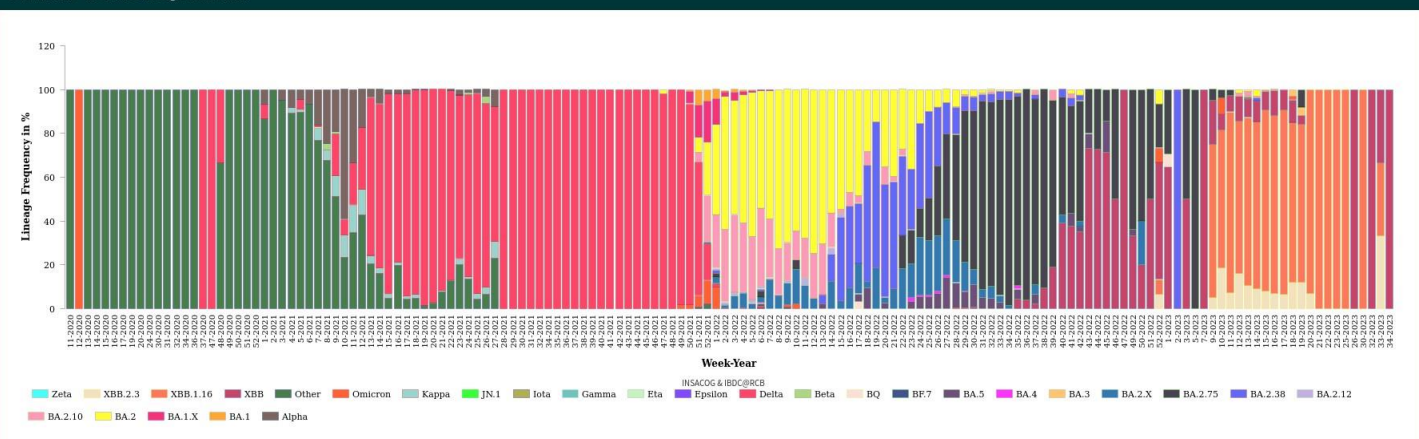


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North India - Week wise lineage distribution



Central India - Week wise lineage distribution



Reference:

1. WHO weekly epidemiological report.
2. GISAID. Available from: <https://gisaid.org/hcov19-variants/>
3. Yang S. *et. al.*, *The Lancet Infectious Disease*, December 15, 2023.