



30 November 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 297,861

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: 333,302

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

Table 1: Cumulative samples with pangolin lineage assigned (as on 24.11.2023)				
Community sample	Travelers sample	Total pangolin lineage assigned	Total VOC/VOI	Percentage
209993	12564	222557	186553	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 days [1]. 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.





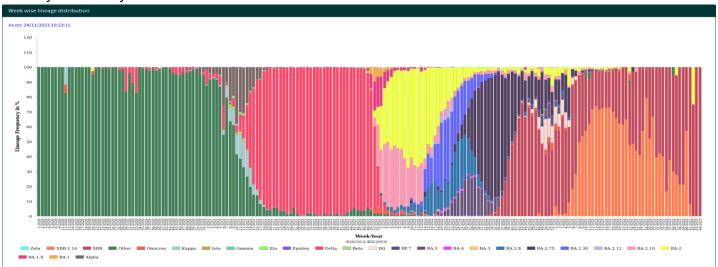




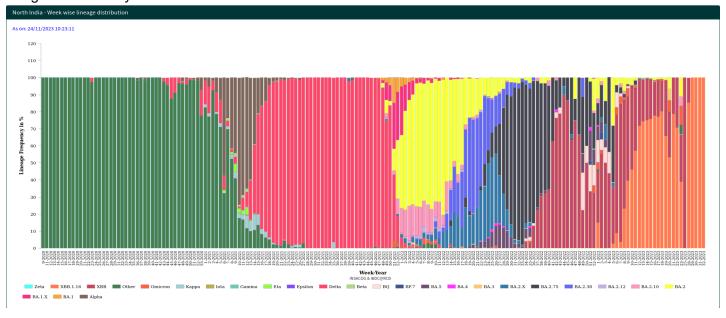
Indian Scenario

Omicron and its sub-lineages continue to be the dominant variants in India. Recombinant variants XBB and XBB.1.16 have been observed in different parts of India. Six cases of EG.5.1 variant have been identified from Maharashtra, Gujarat, and Karnataka. However, till date BA.2.86 variant has not been reported from India. No increase in disease severity or hospitalization has been observed yet.

Country wide analysis:



Region-wise analysis:



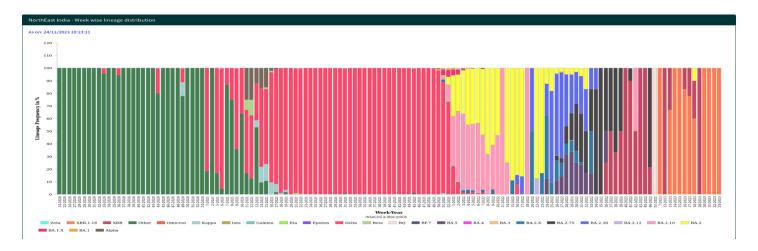


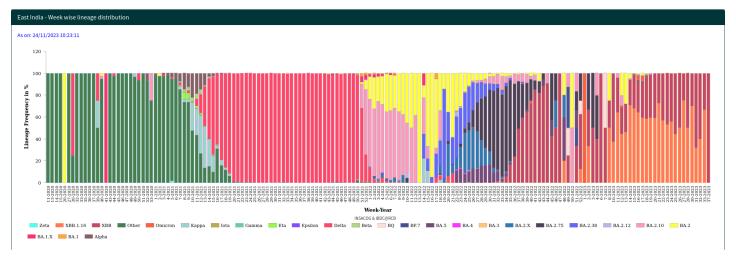


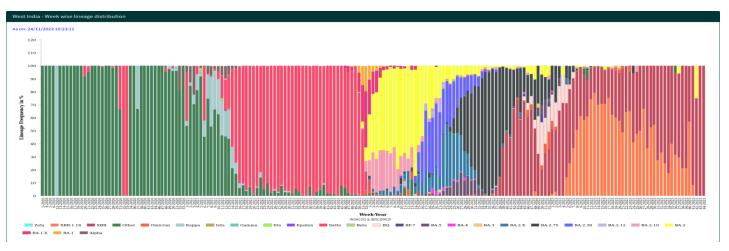












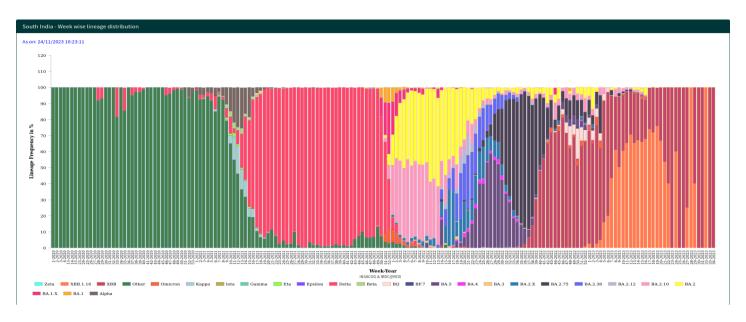


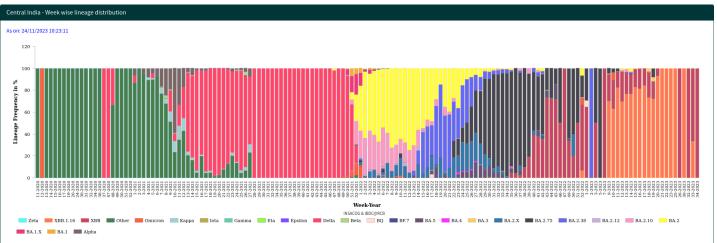












Reference:

1. WHO weekly epidemiological report.