







15 February 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, 277

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, 718

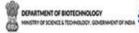
The number of samples with pangolin lineages assigned are given below:

Table 1: Cumulative samples with pangolin lineage assigned (as on 08-02-2024)				
Community sample	Travelers sample	Total pangolin lineage assigned	Total VOC/VOI	Percentage
212804	12564	225368	189148	83.9

Global Scenario

During the last 28-day period, the number of reported cases and deaths have decreased, with over 503000 new cases and 10000 new deaths, a decrease of 58% and 31%, respectively, compared to the previous 28 days¹. Globally, JN.1 is the most reported VOI (now reported by 99 countries), accounting for 88.2% of sequences in week 5 of 2024 compared to 77.1% in week 2 of 2024². Its parent lineage, BA.2.86, is declining and accounted for 3.7% of sequences in week 5 of 2024 compared to 5.4% in week 2 of 2024. The updated risk evaluation for JN.1 was published on 9 January 2024, with an overall evaluation 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 three VUMs: XBB, XBB.1.9.1, and XBB.2.3







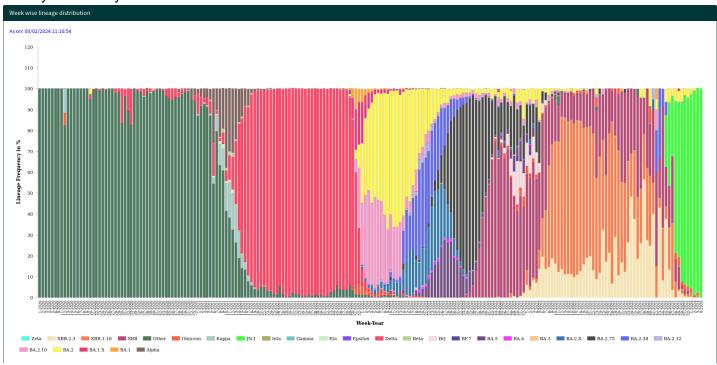




Indian Scenario

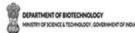
During this reporting period, all of the submitted sequences were of JN.1 sub-variants. INSACOG is continuing the surveillance of the emerging variants. However, no increase in disease severity or hospitalization has been observed with JN.1 sub-variants so far.

Country wide analysis:

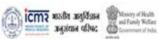


Region-wise analysis:

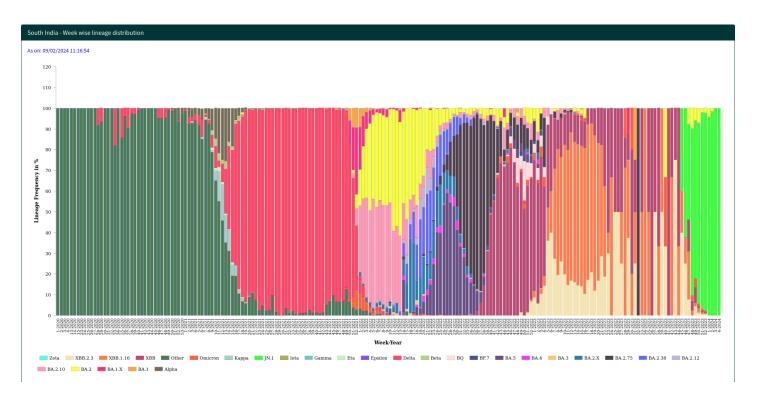








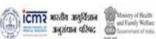




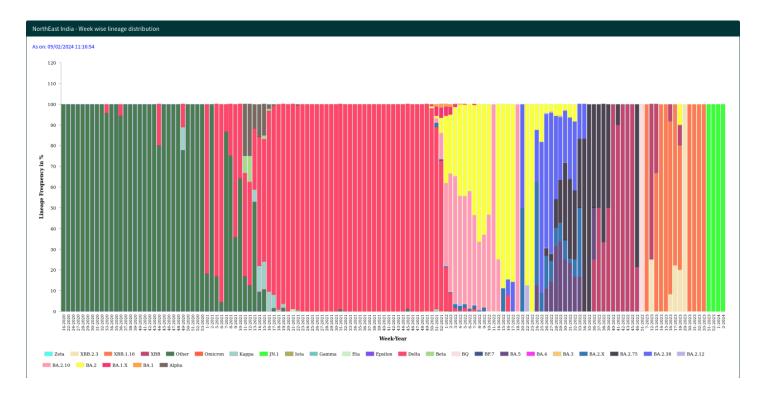


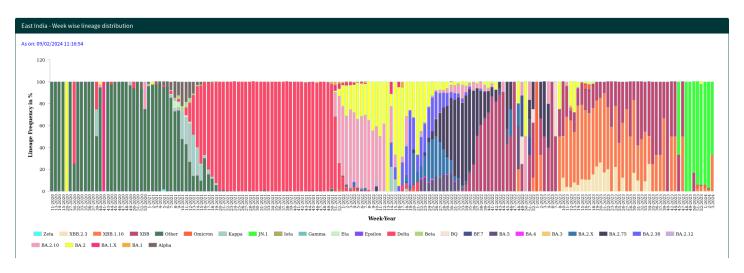




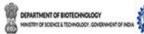








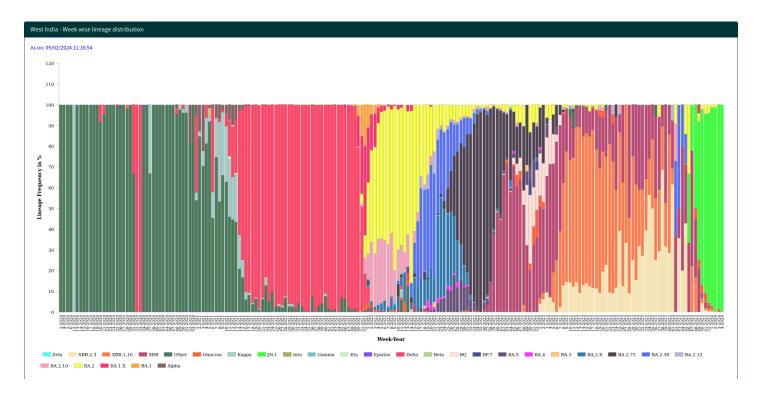


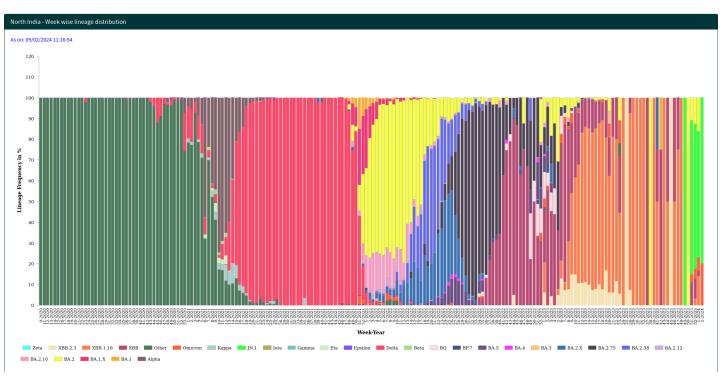












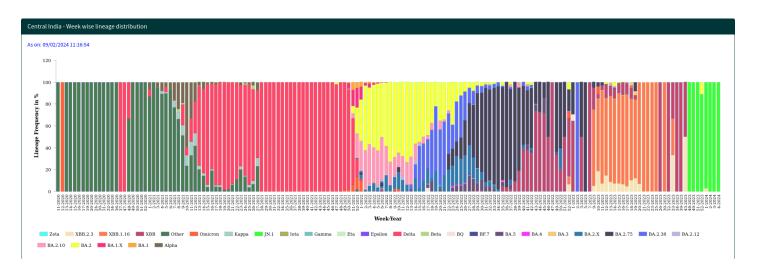












Reference:

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