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26<sup>th</sup> June, 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 <u>https://ibdc.rcb.res.in/</u>

### INSACOG:

Total number of samples sequenced is 294,955

Samples sequenced by IGSLs under State government MoUs: 35,441

### Total number of samples sequenced: 330,396

| The number of samp | les with pangolin | lineages assigned | are given below: |
|--------------------|-------------------|-------------------|------------------|
|                    |                   |                   |                  |

| Table 1: Cumulative samples with pangolin lineage assigned (as on 23.06.2022) |                     |                                    |               |            |  |
|-------------------------------------------------------------------------------|---------------------|------------------------------------|---------------|------------|--|
| Community sample                                                              | Travelers<br>sample | Total pangolin lineage<br>assigned | Total VOC/VOI | Percentage |  |
| 208131                                                                        | 12548               | 220679                             | 184711        | 83.7       |  |

#### Global Scenario

Globally, nearly 1.2 million new cases and 7100 deaths have been reported in the last 28 days<sup>[1]</sup>. During the week 22 of the year 2023, there has been a continued decreasing trend in the proportions of recombinant lineages globally. Currently, there are two variants of interest (VOI), XBB.1.5 & XBB.1.16 and six variants under monitoring (VUMs) and their descendent lineages. The VUMs are BA.2.75, CH.1.1, XBB, XBB.1.9.1, XBB.1.9.2, and XBB.2.3. The variant BQ.1 has been removed from the VUM list due to its low global prevalence (below 1% over the past month). Globally, XBB.1.5 has been detected in 116 countries and continues to be the most prevalent variant, accounting for 23.3% of cases in epidemiological week 22. XBB.1.16 has been reported from 85 countries and accounted for 21.9% of sequences submitted till date. An analysis of available data indicates that countries with a low prior prevalence of XBB.1.5 have experienced an increase in the prevalence of XBB.1.16, while countries that had a high prevalence of XBB.1.5 have reported low circulation of XBB.1.16.





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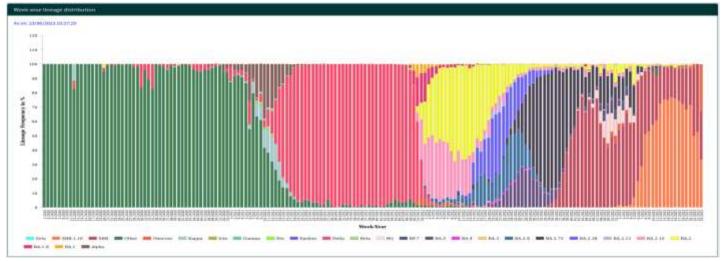
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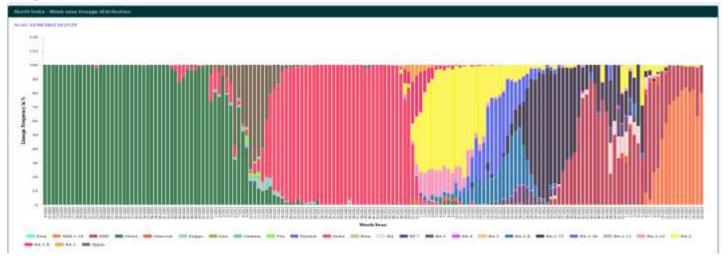
### **Indian Scenario**

Omicron and its sub-lineages continue to be the dominant variants in India. The prevalence of recombinant variant XBB.1.16 has been observed in different parts of India, accounting for 56.4% of the infection till date. Among the samples collected till the second week of June 2023, other XBB sub-lineages accounted for 43.6% of the current infection. No increase in disease severity or hospitalization has been observed.

Country wide analysis:



### Region-wise analysis:





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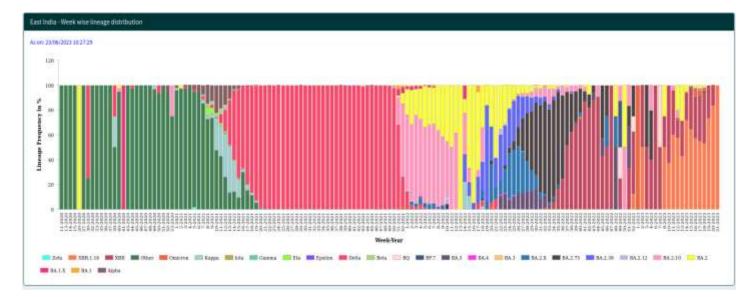
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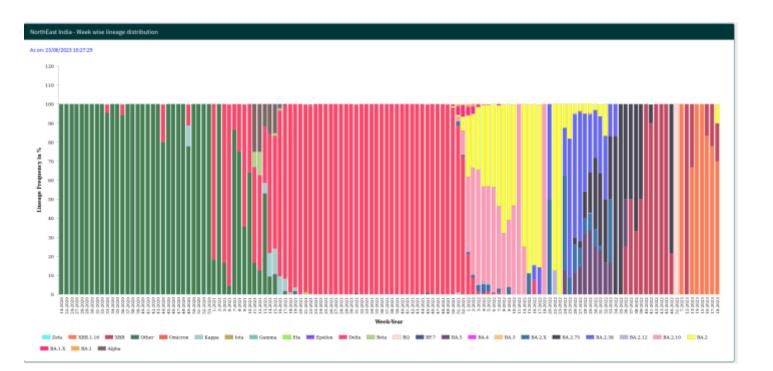
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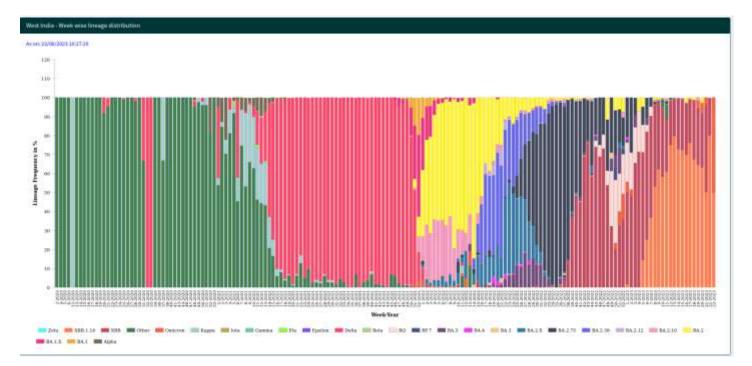
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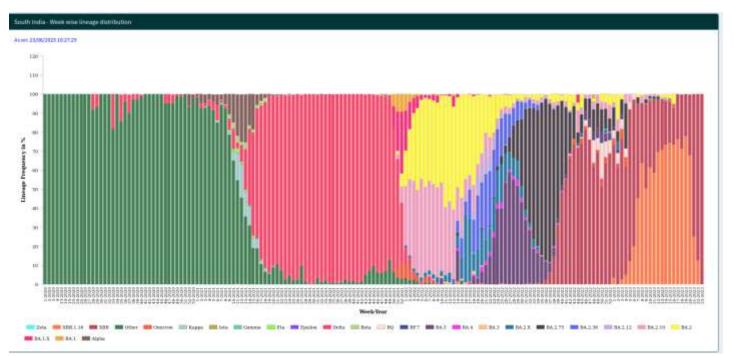
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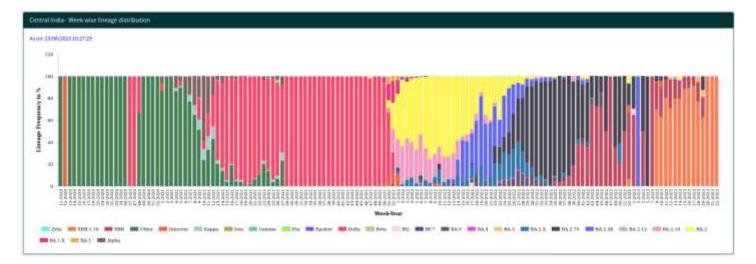
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Reference:

1. WHO weekly epidemiological report.