









13<sup>th</sup> March, 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 <a href="https://ibdc.rcb.res.in/">https://ibdc.rcb.res.in/</a>

#### **INSACOG:**

Total number of samples sequenced is 273,645

Samples sequenced by IGSLs under State government MoUs: 34,763

Total number of samples sequenced: 308,408

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

| Table 1: Cumulative | samples with pan | golin lineage as | signed (as on | 10.03.2022) |
|---------------------|------------------|------------------|---------------|-------------|

| Community sample | Travelers sample | Total pangolin lineage assigned | Total VOC/VOI | Percentage |
|------------------|------------------|---------------------------------|---------------|------------|
| 190937           | 12382            | 203319                          | 168477        | 82.9       |

|   | Cumulative Distribution of variants and sub-lineages (as on 11-03-2023) |                 |           |          |       |           |       |       |             |         |          |     |       |        |        |          |             |          |           |         |           |           |         |           |           |         |            |           |           |       |         |       |         |       |        |          |       |         |         |         |         |         |         |
|---|---|-----------------|-----------|----------|-------|-----------|-------|-------|-------------|---------|----------|-----|-------|--------|--------|----------|-------------|----------|-----------|---------|-----------|-----------|---------|-----------|-----------|---------|------------|-----------|-----------|-------|---------|-------|---------|-------|--------|----------|-------|---------|---------|---------|---------|---------|---------|
| Alpha Variant Beta Variant Gamma Variant Delta Variant 8.1.617.1 and 8.1.617.3 AV Series Omicron* |   |                 |           |          |       |           |       |       | Recombinant |         |          |     |       |        |        |          |             |          |           |         |           |           |         |           | XE        | XM      | XU         | XJ        | XG        | Total |         |       |         |       |        |          |       |         |         |         |         |         |         |
| Tr&Co Com Total   | Tr&Co Com Total   | Tr&Co Com Total | Tr&Co Cor | n Total  | Tr&Co | Com Tota  | Tr&Co | Com   | Total Tr    | &Co Con | n* Total | XAR | XAH ) | (AB XA | XBB XB | B.1 XB8. | 1.1 XBB.1.2 | 2 XBB.1. | .3 XBB.14 | XBB.1.5 | XBB.1.5.4 | XBB.1.5.8 | XBB.1.9 | XBB.1.9.1 | XBB.1.9.2 | XBB.2 X | 18.2.1 XBI | .2.3 XBB. | 2.4 XB8.3 | XB8.3 | 1 XBB.4 | XBB.5 | (BC.1 X | BD XB | SF XBI | L OTHERS | Total | Variant | Variant | Variant | Variant | Variant | VOC/VOI |
| 577 3691 4268   | 117 105 222   | 1 2 3           | 412 412   | 16 44658 | 84    | 5540 5624 | 270   | 20357 | 20627 6     | 209 841 | 27 90659 | 3   | 1     | 1 2    | 593 4  | 9 4      | 3           | 8        | 2         | 97      | 1         | 1         | 14      | 1         | 5         | 520     | 1 :        | 7 3       | 401       | 5     | 77      | 73    | 1 7     | , 6   | 1      | 106      | 2409  | 1       | 2       | 1       | 1       | 2       | 168483  |
| Tr&Co=Travelers an  | d contacts ; Com=   | Commumity sampl | <b>5</b>  |          |       |           |       |       |             |         |          |     |       |        |        |          |             |          |           |         |           |           |         |           |           |         |            |           |           |       |         |       |         |       |        |          |       |         |         |         |         |         |         |









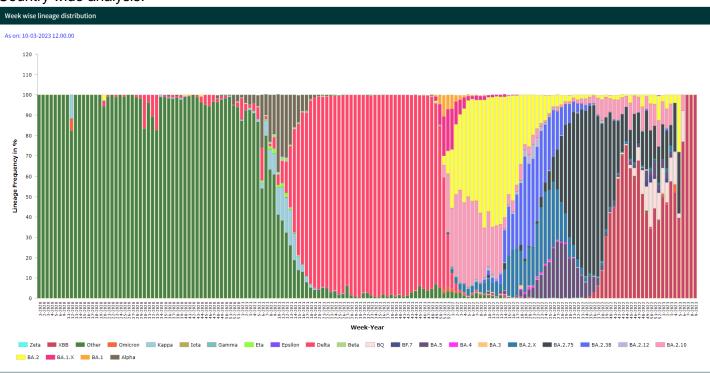
#### **Global Scenario**

Globally, nearly 4.5 million new cases and 32000 deaths have been reported in the last 28 days<sup>[1]</sup>. During the week 07 of the year 2023, there has been a continued increasing trend in the proportions of recombinant lineages globally. In epidemiological week 7, recombinant variants accounted for 44.1%. BA.5 and descendent lineages accounted for 27.2%. BA.2 and descendent lineages showed a stable trend with 14.2%. BA.1, BA.3 and BA.4 collectively accounted for less than 0.1%. Unassigned sequences (all presumed Omicron while awaiting descendent lineage assignment) accounted for 14.5% of the shared sequences in week 7. However, there is no indication of increased severity associated with these variants under monitoring compared to the former Omicron lineages.

#### **Indian Scenario**

Omicron and its sub-lineages continue to be the dominant variants in India. Among the samples collected till the first week of March 2023, XBB continued to be the most commonly circulating Omicron sub-lineages. A few BQ.1 sub-lineage was detected in northern part and BA.2.75 was detected in eastern part of India, whereas other part of India, XBB was the most prevalent sub-lineage of omicron variant.

#### Country wide analysis:



Region-wise analysis:

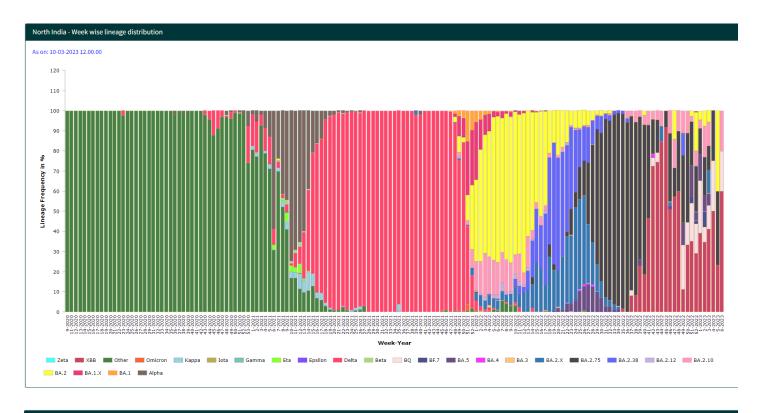




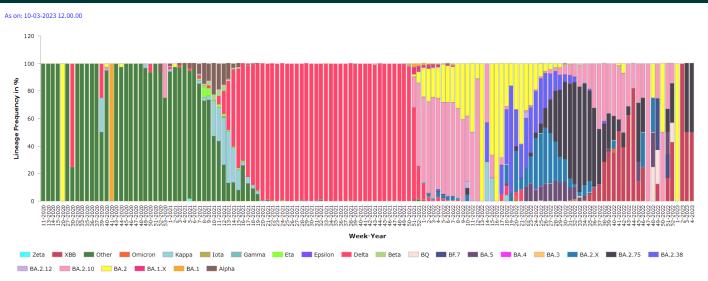




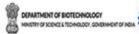








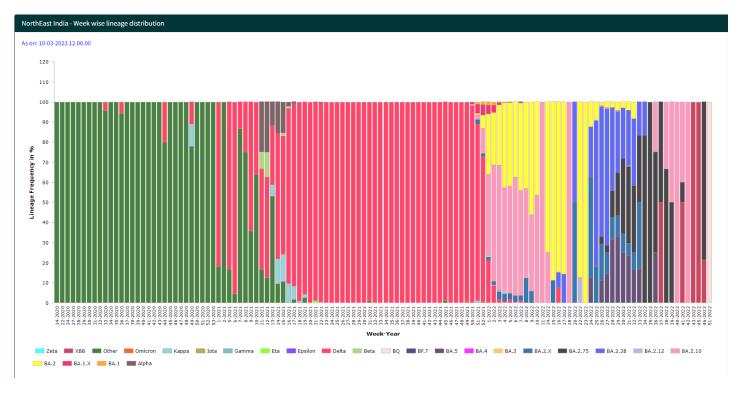


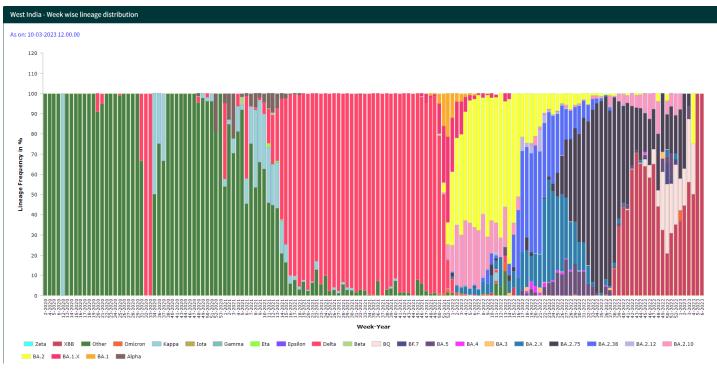




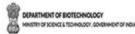








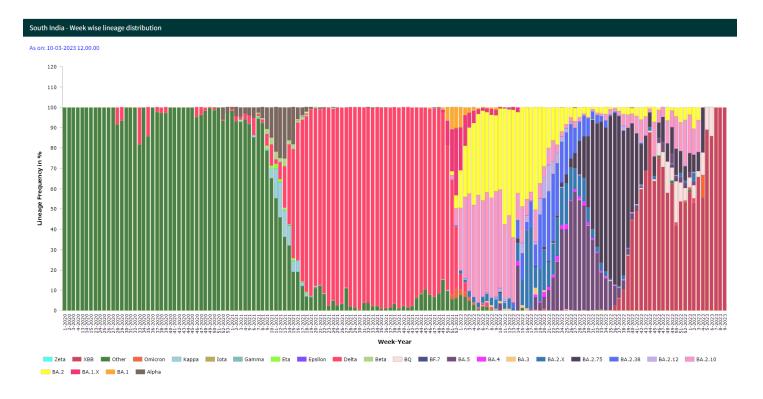


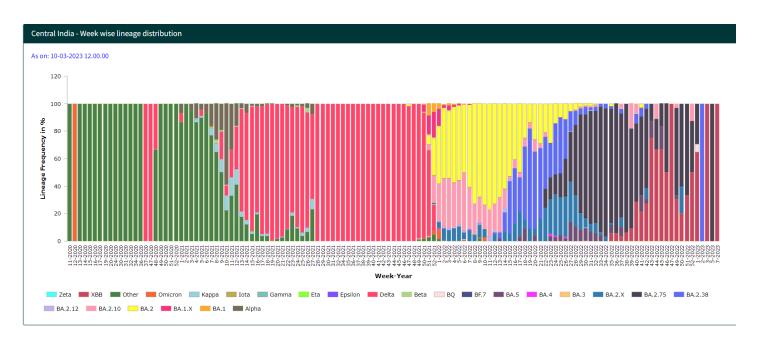




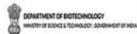


















### Reference:

1. WHO weekly epidemiological report.