INSACOG BULLETIN

24th April, 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:

Total number of samples sequenced is 280,891

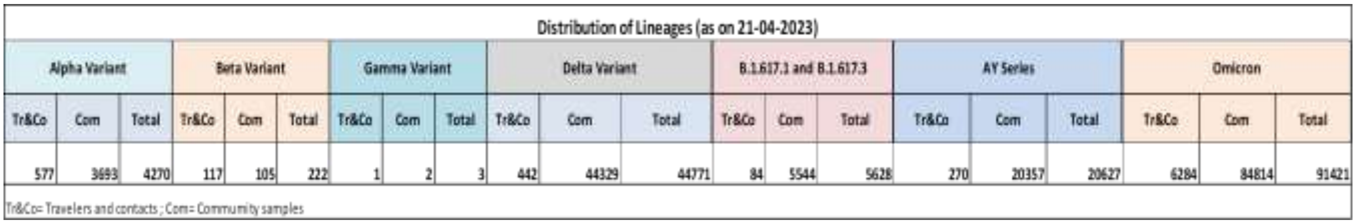
Samples sequenced by IGSLs under State government MoUs: 34,763

Total number of samples sequenced: 315,654

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

Table 1: Cumulative samples with pangolin lineage assigned (as on 24.03.2022)

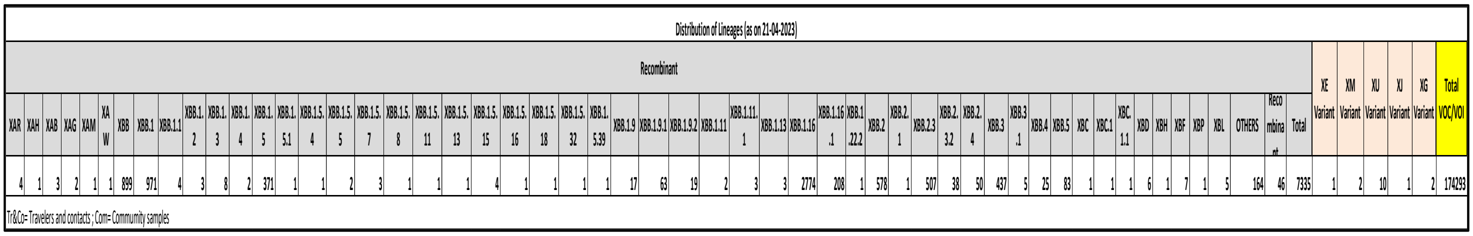
Community sample	Travelers sample	Total pangolin lineage assigned	Total VOC/VOI	Percentage
196924	**12505**	**209429**	**174266**	**83.2**



Distribution of Lineages (as on 21-04-2023)

Alpha Variant			Beta Variant			Gamma Variant			Delta Variant			B.1.617.1 and B.1.617.3			AY Series			Omicron		
Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total
577	3693	4270	117	105	222	1	2	3	442	44329	44771	84	5544	5628	270	20357	20627	6284	84814	91421

Tr&Co= Travelers and contacts ; Com= Community samples



Distribution of Lineages (as on 21-04-2023)

Recombinant																																																						XE Variant	XM Variant	XU Variant	XJ Variant	XG Variant	Total VOC/VOI
XAR	XAH	XAB	XAG	XAM	XAW	XBB	XBB.1	XBB.1.1	XBB.1.2	XBB.1.3	XBB.1.4	XBB.1.5	XBB.1.5.1	XBB.1.5.4	XBB.1.5.5	XBB.1.5.7	XBB.1.5.8	XBB.1.5.11	XBB.1.5.13	XBB.1.5.15	XBB.1.5.16	XBB.1.5.18	XBB.1.5.32	XBB.1.5.39	XBB.1.9	XBB.1.9.1	XBB.1.9.2	XBB.1.11	XBB.1.11.1	XBB.1.13	XBB.1.16	XBB.1.16.1	XBB.1.22.2	XBB.2	XBB.2.1	XBB.2.3	XBB.2.3.2	XBB.2.4	XBB.3	XBB.3.1	XBB.4	XBB.5	XBC	XBC.1	XBC.1.1	XBD	XBH	XBF	XBP	XBL	OTHERS	Recombinant	Total						
4	1	3	2	1	1	899	971	4	3	8	2	371	1	1	2	3	1	1	1	4	1	1	1	1	17	63	19	2	3	3	2774	208	1	578	1	507	38	50	437	5	25	83	1	1	1	6	1	7	1	5	164	46	7335	1	2	10	1	2	174293

Tr&Co= Travelers and contacts ; Com= Community samples

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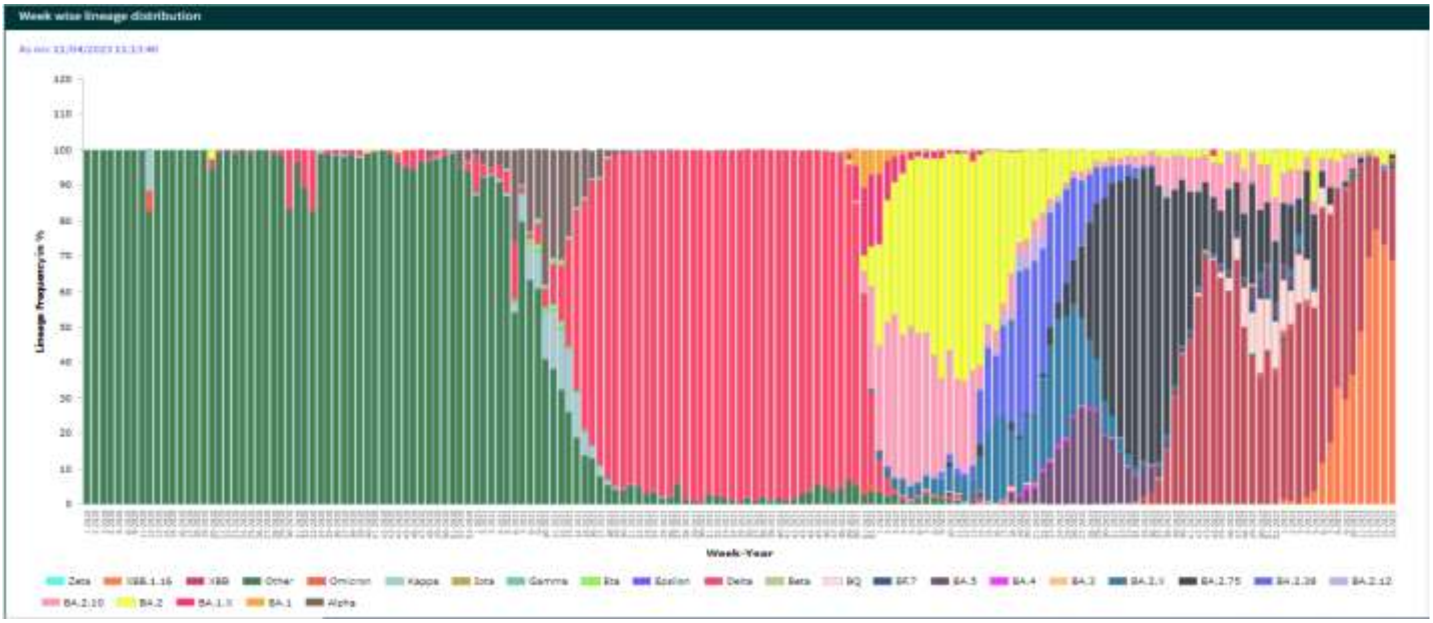
Global Scenario

Globally, nearly 2.8 million new cases and 18000 deaths have been reported in the last 28 days [1]. During week 13 of the year 2023, there has been a continued increasing 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). The VUMs are BQ.1, BA.2.75, CH.1.1, BQ.1, XBB, and XBF. Globally, XBB.1.5 has been detected in 96 countries and continues to be the most prevalent variant. XBB.1.16 has been reported in 31 countries. However, at present, there is no early signal of an increase in severity.

Indian Scenario

Omicron and its sub-lineages continue to be the dominant variants in India. There is a continuous increase in infection rate has been observed. The recombinant variant XBB.1.16 has accounted for 68.7% of the infection till date. Among the samples collected till the second week of April 2023, other XBB sub-lineages accounted for 26.5% of the current infection. A few BA.2.75 sub-lineage was detected in some part of India, whereas XBB.1.16 was the most prevalent sub-lineage of omicron variant. However, no increase in disease severity or hospitalization has been observed.

Country wide analysis:



Region-wise analysis:

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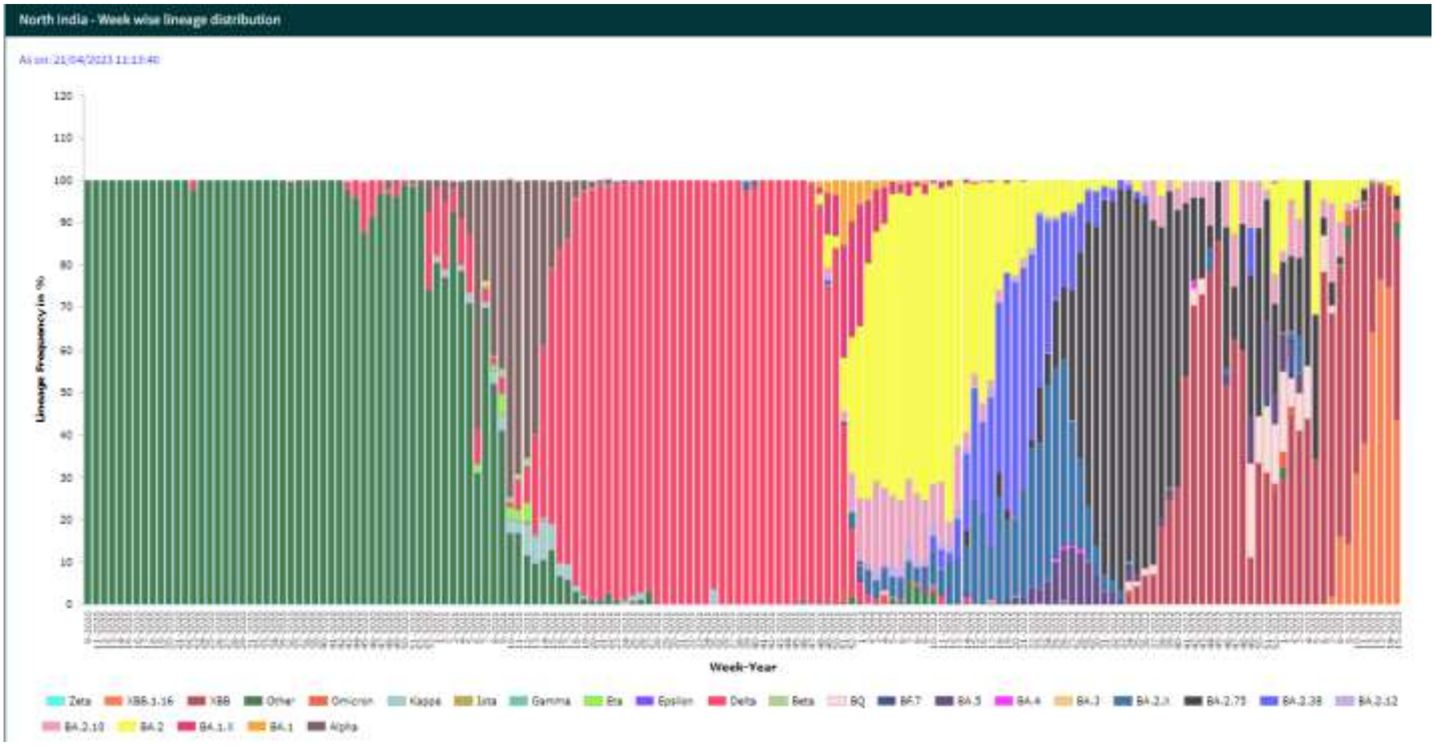

North India - Week wise lineage distribution

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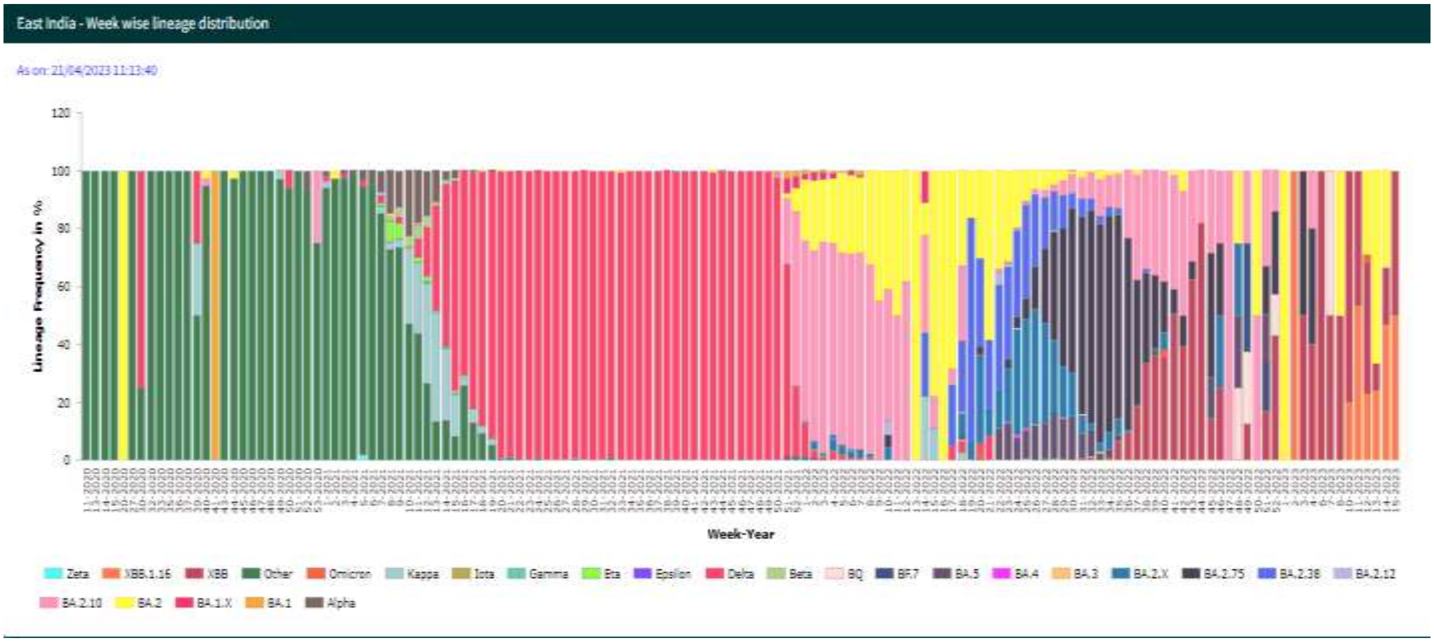

East India - Week wise lineage distribution

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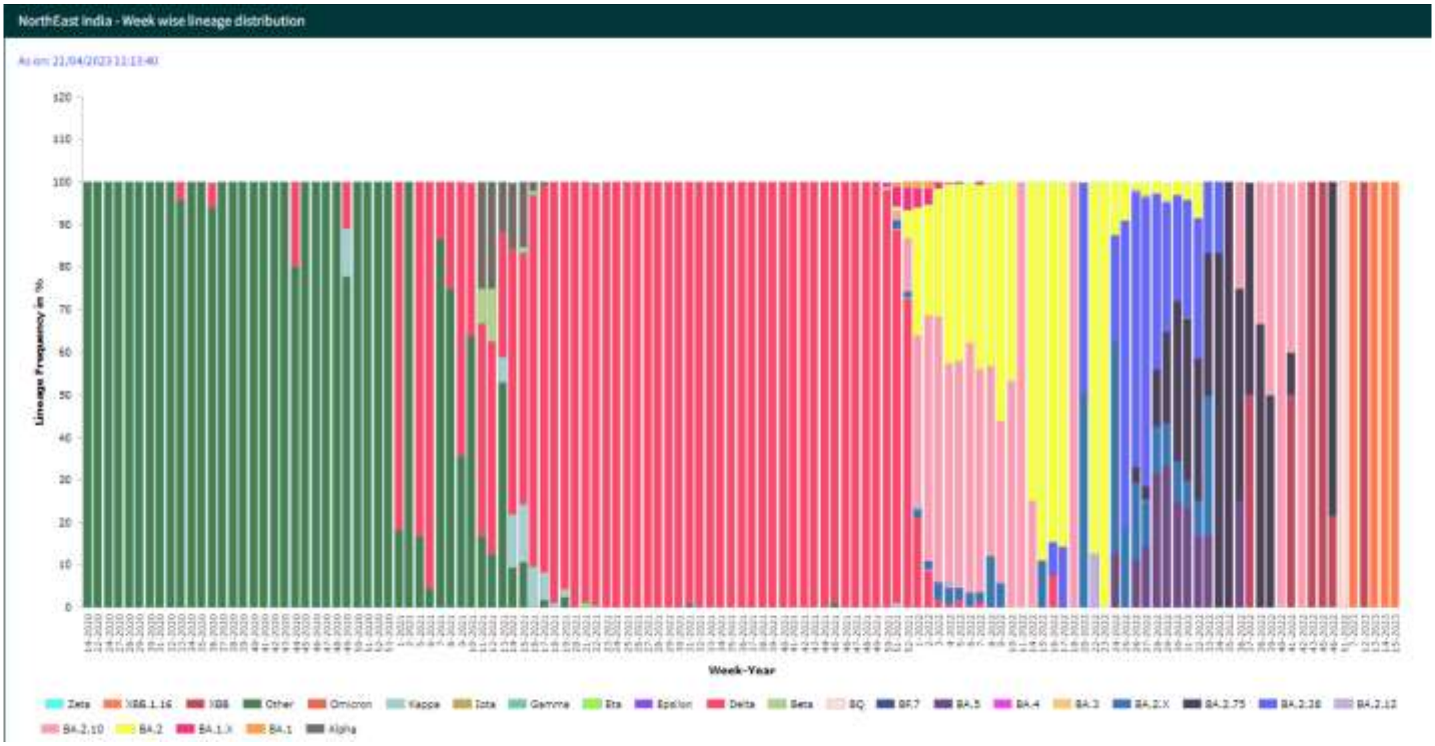

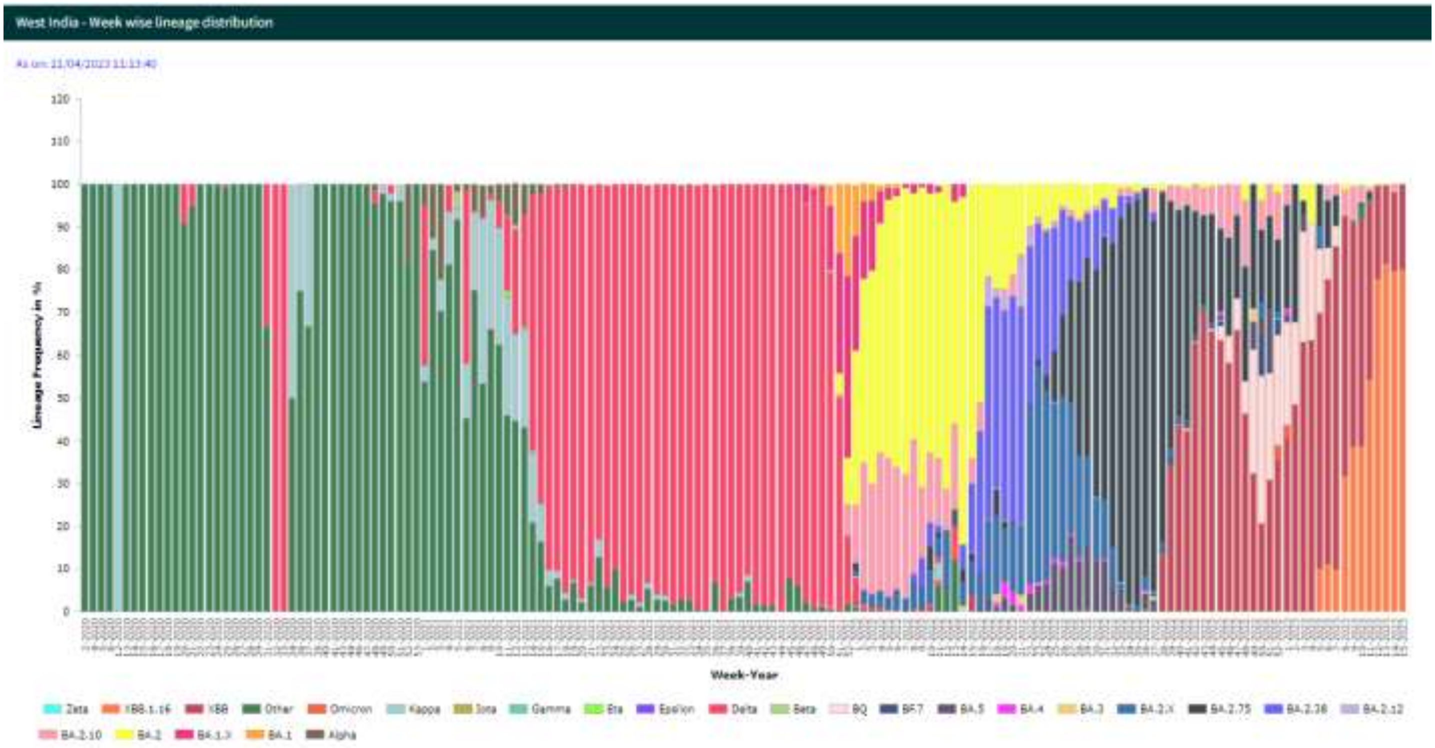

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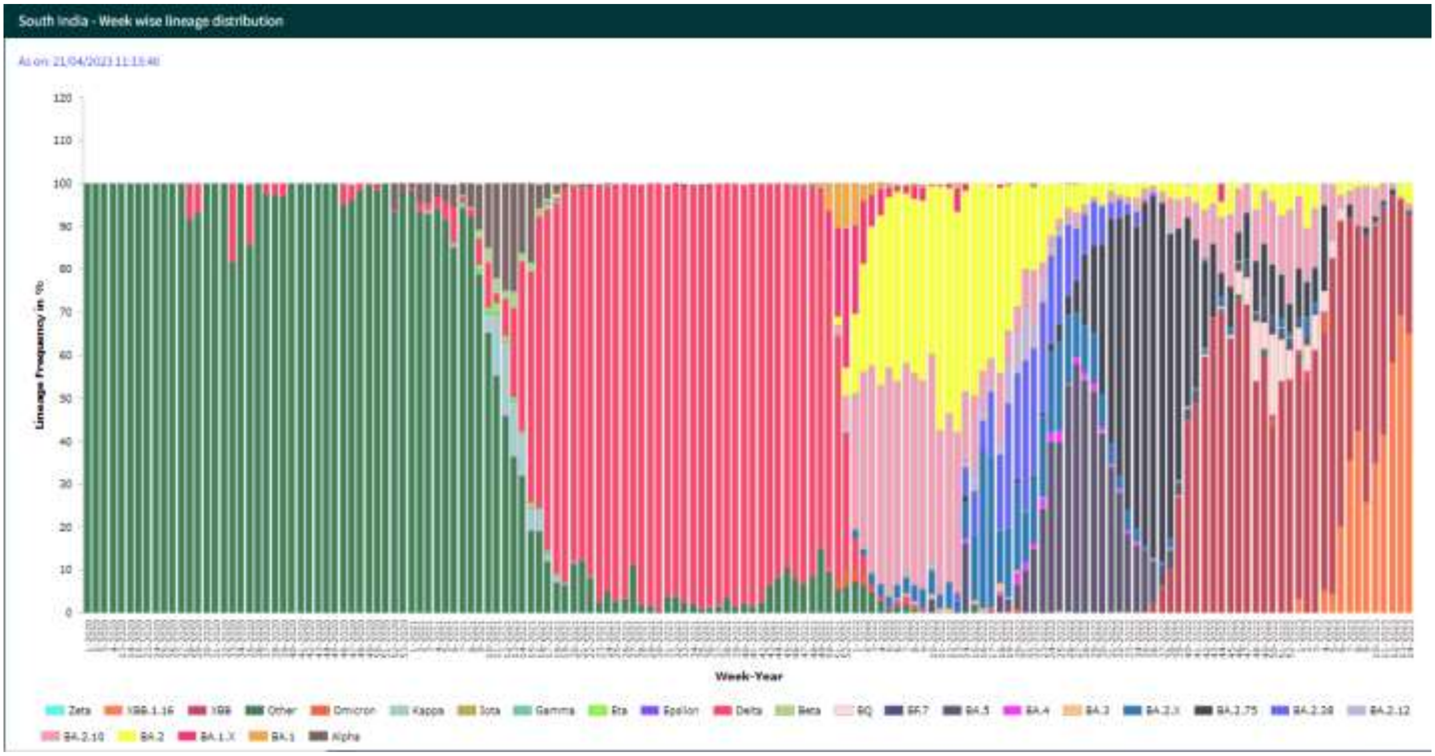

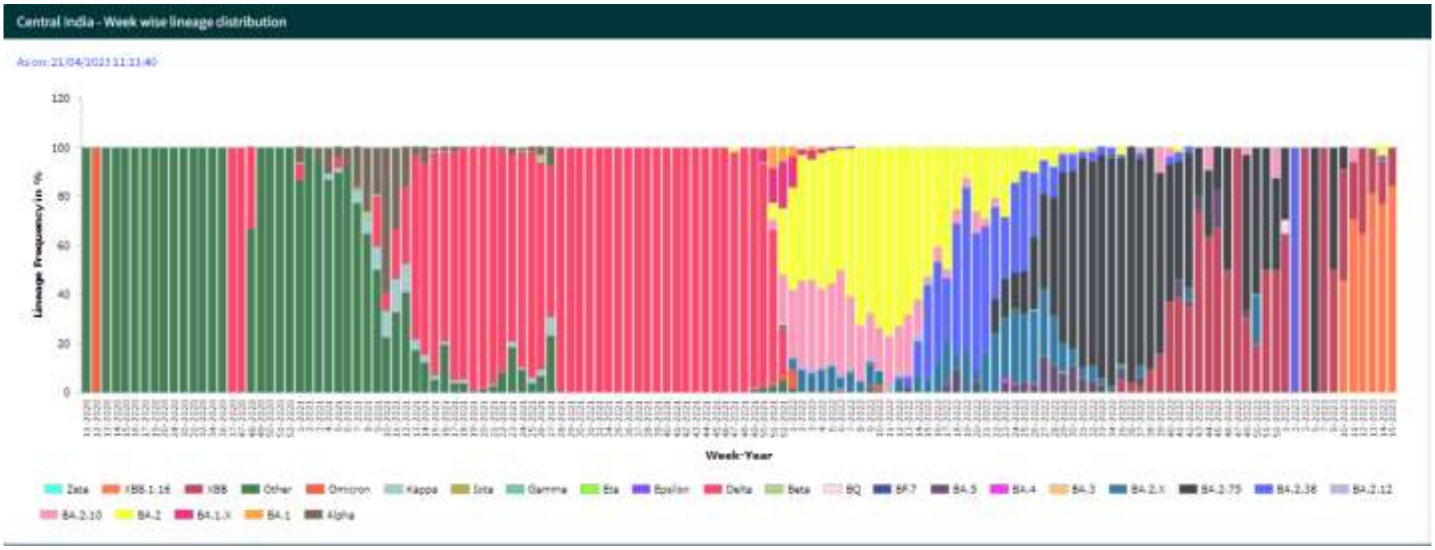

Reference:

1. WHO weekly epidemiological report.