





20<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 273,825

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

Total number of samples sequenced: 308,588

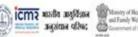
The number of samples with pangolin lineages assigned are given below:

Table 1: Cumulative samples with pangolin lineage assigned (as on 17.03.2022)													
Community sample	Travelers sample	Total pangolin lineage assigned	Total VOC/VOI	Percentage									
191041	12383	203424	168587	82.9									

	Cumulative distribution of variants and sub-lineages (as on 1749-2023)																																																		
Alpha Variant	Be	leta Variant		Gamma\	/ariant		Delta	Variant		B.1.617	.1 and B.1.8	17.3		AYSeries		Onicron Recombinant																																			
Tr&Co Com Tot	tal Tr&Co	Com	Total Tr	&Co Cor	n Tota	l Tr&Co	o Com	To	otal	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	To	tal )	AR XAL	XAB	XAG X	8 X88.1	X88.1.1	XB8.1.2 )	IBB.13 XBI	B.14 XBB.13	XB8.1.5 4	5. XB8.1.5. X	88.1.5. 8	38.1.9 XBB.	8.1.9. XBB.1 1 2	19. XBB1.1	16 XB8.2	X88.2.1 X	B82.3 XBI	3.2.4 XBI	B3 XB8.	3.1 XB8.4	X88.5	XBC1 1	XBO XBF	XBL	OTHERS		XE Variant	XM Variant	XV Variant	XI Variant	XG Varia	int Total VOC/V
577 3691 42	68 117	105	m	1 2	3	442	44216	4	658	84	5540	5624	270	20357	20627	6210	8413	2 90	665	3 1	1	2 5	9 522	4	3	8	2 119	1	2	1	14 9	9 5	11	521	1	48	3 40	01 5	27	73	1	7 6	1	106	2507	1	2	1	1	2	168587
Tr&Co=Travelers and o	contacts ; Co	om=Comm	numity sar	ples																																															







#### **Global Scenario**

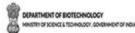
Globally, nearly 4.1 million new cases and 28000 deaths have been reported in the last 28 days<sup>[1]</sup>. During the week 08 of the year 2023, there has been a continued increasing trend in the proportions of recombinant lineages globally. The global variant landscape is characterized by a continuous increase in prevalence of the recombinant variant XBB and its descendent lineages. At a global level, XBB\* (XBB and its descendant lineages, excluding XBB.1.5) and XBB.1.5 are increasing in prevalence in all over the world. Due to the growth advantage of this recombinant variant, the replacement of former circulating variants was anticipated. BA.1, BA.3 and BA.4 collectively accounted for less than 0.1% of sequences in week 8. BA.2 and BA.5 have both declined in prevalence; they accounted for 13.1% and 20.1% in week 8. The pooled class of recombinants has increased in prevalence to 46.7%. Unassigned sequences (all presumed Omicron while awaiting descendent lineage assignment) accounted for 20.1% of the shared sequences. 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. An increase in infection rate has been observed, especially in Western, Southern and Northern part of India as well as a newly emerged recombinant variant XBB.1.16, accounting for 27% of the infection till date. Among the samples collected till the second week of March 2023, XBB continued to be the most commonly circulating Omicron sub-lineages. A few BQ.1 and BA.2.75 sub-lineage was detected in some part of India, whereas XBB was the most prevalent sub-lineage of omicron variant.

Country wide analysis:

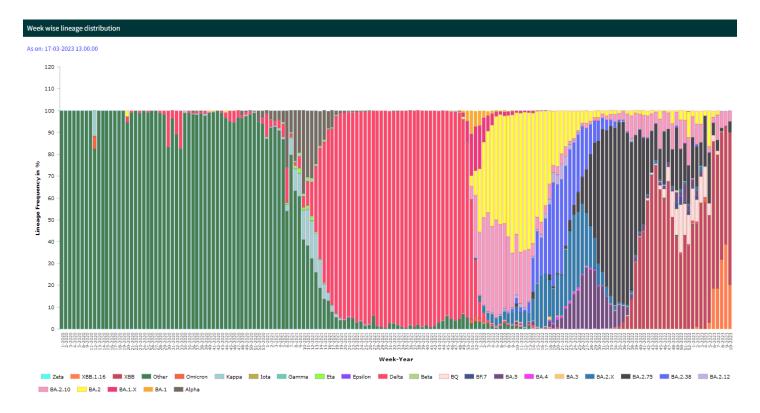






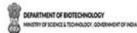






Region-wise analysis:

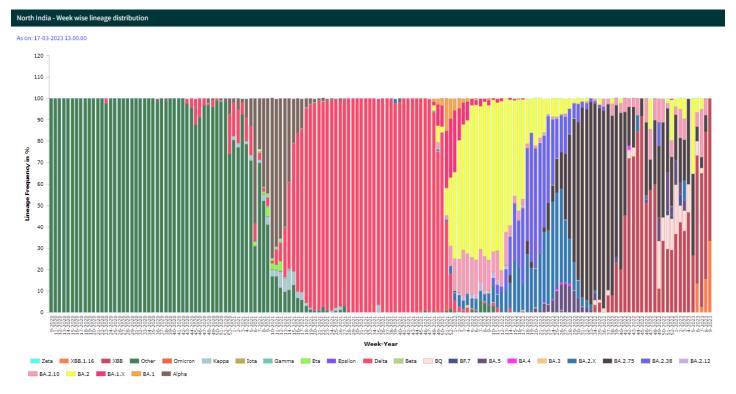


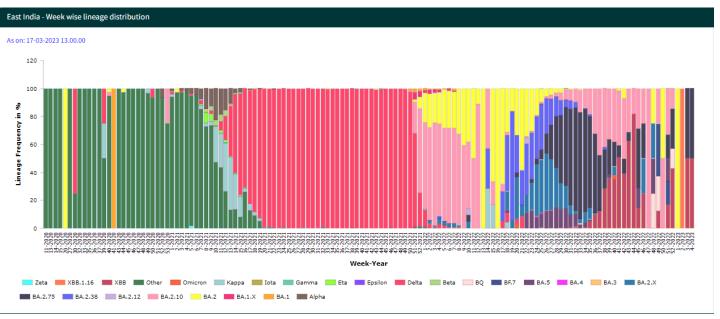












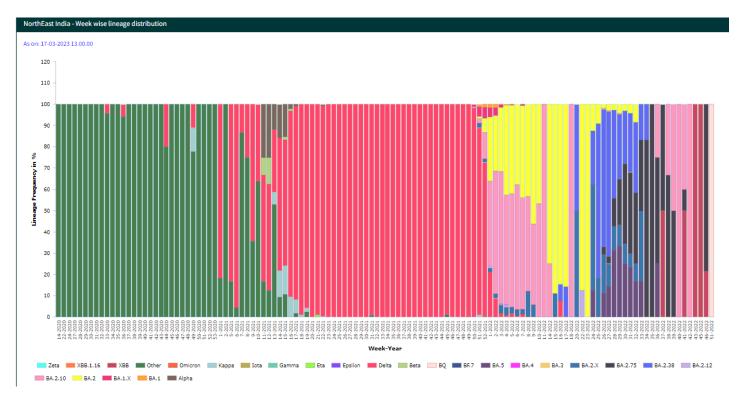


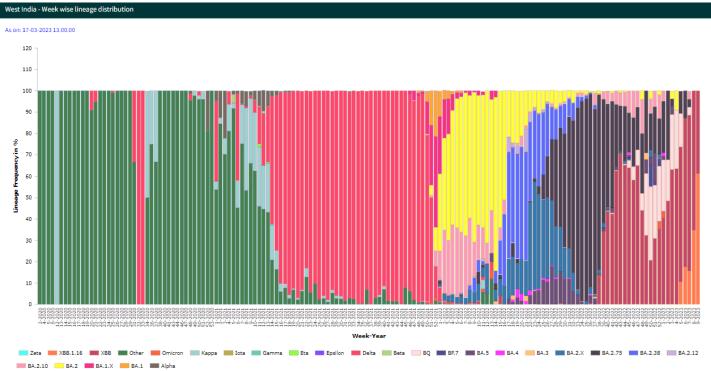






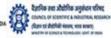






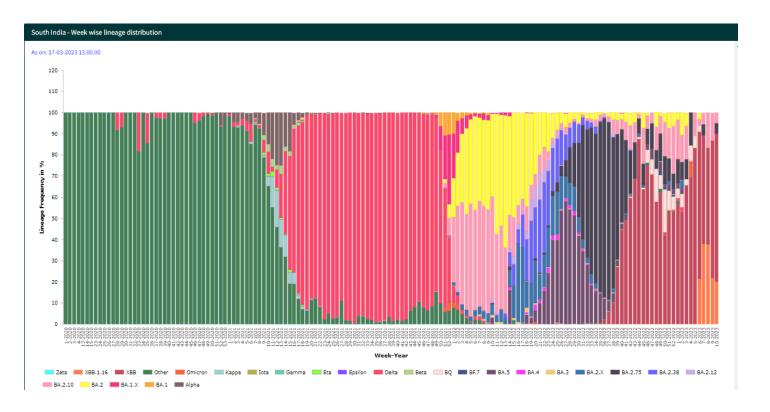


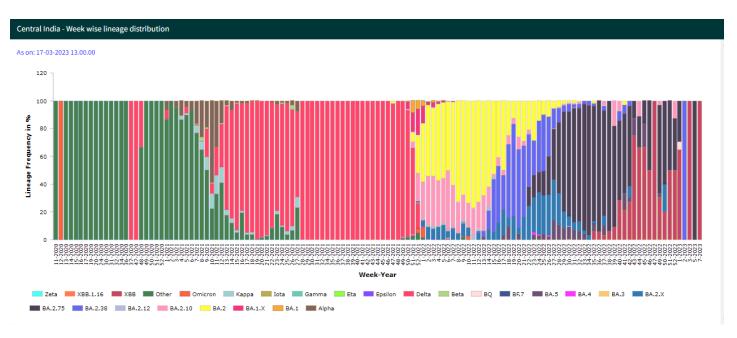




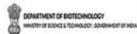


















### Reference:

1. WHO weekly epidemiological report.