







29<sup>th</sup> May, 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 292,224

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

Total number of samples sequenced: 327,665

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

Table 1: Cur	Table 1: Cumulative samples with pangolin lineage assigned (as on 26.05.2022)														
Community sample	Travelers sample	Total pangolin lineage assigned	Total VOC/VOI	Percentage											
205333	12526	217859	182540	83.8											

		-	100000		iant		Delta Varia	ant	D.1.01	/.I and	B.1.617.3		AY Series		Omicron						
Tr&Co Com Total Tr	r&Co Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total				
1002 5698 6700 2	225 175	400	2	3	5	807	77391	78198	145	9732	9877	420	33999	34419	10890	150146	161482				

Recombinant																																										
(AR XA	ΗХ	AB X	AG XA	M XA	W X	BB X	BB.1	XBB.1.	XBB.1.1	XBB.1													XBB.1.1	XBB.1.1		XBB.1.					XBB.1.	XBB.1.	XBB.1.				XBB.1.5				XBB.1.	XBB.1.
								1	1	12	11.1	13	15	.16	.16.1	16.1.1	6.1.2	16.2	.16.3	16.4	.16.5	16.6	7.1	9	19.1	2	22	22.2	2.8	22	3	4	5	.1	1.5.4	5.5	.]	5.8	.5.11	5.13	5.15	5.16
4	1	3	2	1	1 1	081	1154	4		2	)	3	3 1	7208	1379	2	1	9	2	1	1	1	1	1	1	3	3	1	1	11	8	2	486	1	3	2	4	21	1	2	4	1

X	3B.1.5.			XBB.1.5.	XBB.1	.5. XBB.	1.5 XBB.	1.5. XI	BB.1.5.	XBB.1.	XBB.1.9	XBB.1.	XBB.1.	YRR 2	(BB.2. )	(BB.2.	XBB.2.	XBB.2.	XBB.2.3	XBB.2	XBB.2	. XBB.2	XBB.2	XBB.2.	XBB.2.	VRR 2	YRR 21	YRR 4	ABB E	I YRC	IXRC 1	YRC11	YRNI	YRH Y				THERS	Recombinant	Total	XE	XM	XU	XJ	XG	Total	
	18	24	30	31	32	.33	3	9	45	9	1	9.2	22.2	VANIE	1	3	3.2	3.3	.4	3.5	3.6	3.9	4	7.1	8	היחחע	VANIÀIT	ייטטא	ליחחע	NUC.	VDC1	VhčitiT	טטא	און וועא	וטאן ונ	ADE A	UII V	IIILNA	nccompiliant	IVLai	Variant	Varian	t Varian	t Varian	t Variant	VOC/VO	) <mark>l</mark>
	3	3	1	. 1	1	2	1	1	1	108	112	38	1	653	1	1400	161	10		7 51	j	1 1	5	4	1	438	6	26	84	1	. 1	1	6	1	7 1	5	1	213	115	14950	1		2 1	.0	1 2	2 <mark>182</mark> 5	<del>340</del>









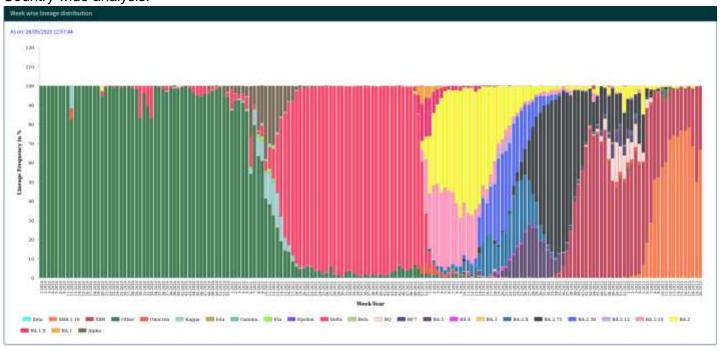
#### Global Scenario

Globally, nearly 2.3 million new cases and 15000 deaths have been reported in the last 28 days [1]. During the week 18 of the year 2023, there has been a continued decreasing trend in the proportions of recombinant lineages globally. However, the situation is mixed at the regional level, with increases in reported cases seen in the African and Western Pacific Regions and increases in deaths in the African, the Americas, South-East Asia, and Western Pacific Regions. Currently, there are two variants of interest (VOI), XBB.1.5 & XBB.1.16 and seven variants under monitoring (VUMs). The VUMs are BA.2.75, CH.1.1, BQ.1, XBB, XBB.1.9.1, XBB.1.9.2, and XBB.2.3. Globally, XBB.1.5 has been detected in 113 countries and continues to be the most prevalent variant, accounting for 41.6% of cases in epidemiological week 18. XBB.1.16 has been reported from 58 countries and accounted for 13.2% of sequences submitted till date. Isolated rise in hospitalizations and ICU admissions has been observed in some regions world-wide.

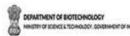
#### Indian Scenario

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 compared to last week, accounting for 68.8% of the infection till date. Among the samples collected till the second week of May 2023, other XBB sub-lineages accounted for 29.3% of the current infection. The number of samples were relatively low in some part of India. However, no increase in disease severity or hospitalization has been reported.

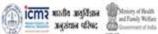
### Country wide analysis:





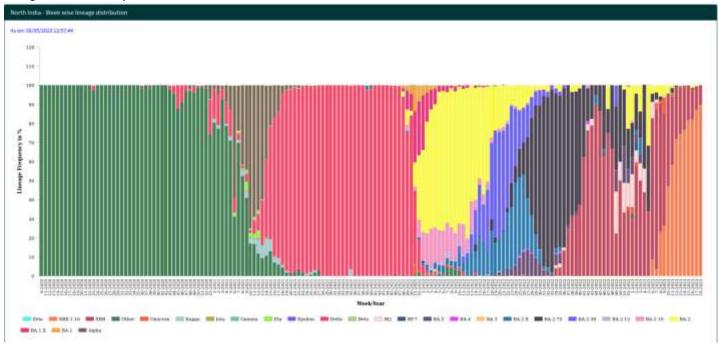


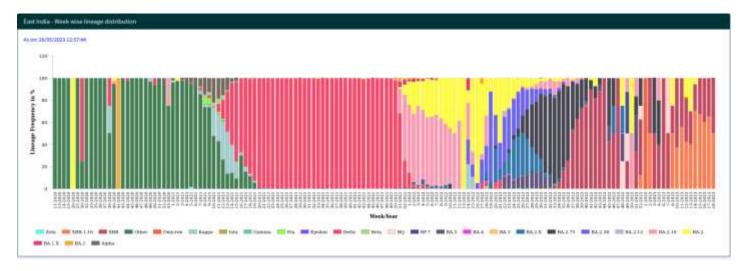




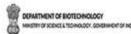


### Region-wise analysis:





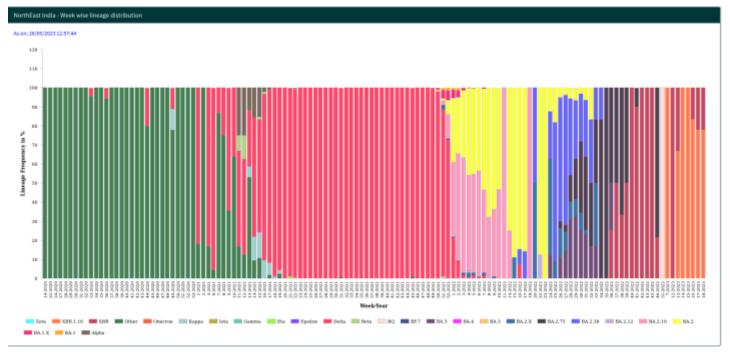


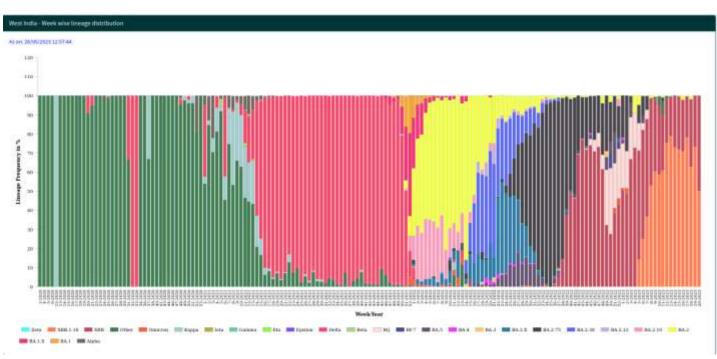












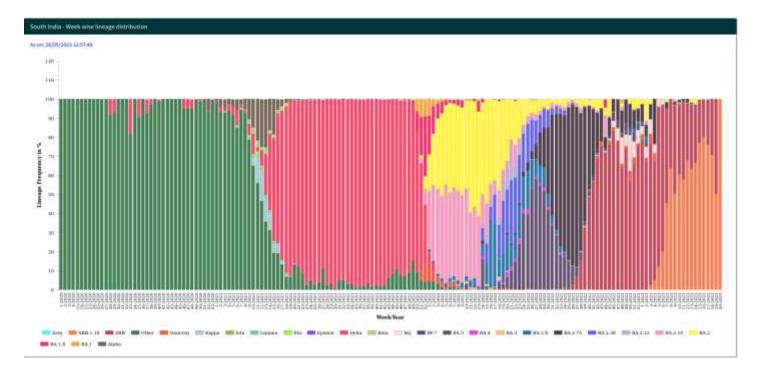


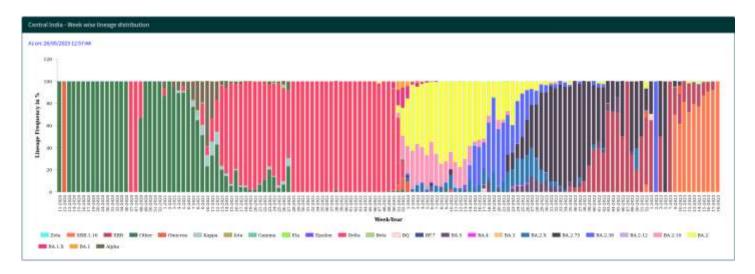












#### Reference:

1. WHO weekly epidemiological report.