









12 December, 2022

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 269,145

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

Total number of samples sequenced: 303,908

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

Table 1: Cumulative samples with pangolin lineage assigned (as on 09.12.2022
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Community sample	Travelers sample	Total pangolin lineage assigned	Total VOC/VOI	Percentage
184651	12285	196936	162343	82.4

Distribution of VOC/VOI and B.1.617.1 & B.1.617.1 & B.1.617.3 (as on 09-12-2022)																																																		
A	lpha Va	ariant	t	Beta Variant			t	Gamma Vari		nma Variant			D	Delta Varia		ĺ	B.1.61	B.1.617.1 and B.1.617.				AY Series	S			Omicron									Re	ecombir	nant							XE	XM	XT	XU	XJ		<b>Total</b>
Tr&Co	Con	n T	iotal	Tr&C	o Co	m i	Total	Tr&C	io Ci	Com	Tota	al Tr	r&Co	Com	1	Total	Tr&Co	Corr	ı Te	otal	Tr&Co	Com	Tot	tal	Tr&Co	Com	Total	XAR	XA	НХ	(BB X	BB.1	XBB.1.	XBB.1	L XBB	XBB.	3 XBB.3	3. XBE	i.4 XB	B.5 )	(BD	OTHERS	S Total	Variant	t Varian	t Varia	nt Varian	t Varian	nt VO	IC/VOI
577	36	590 4	4267	111	7 1	.05	222		1	2		3	387	435	75 (	43962	. 84	554	.O	5624	227	2024	8 2	0475	5952	80520	8679	5 :	2	1	348	121	2		2 16	0 28	18	5	8	25	6	10	.6 98	<b>14</b>	1	2	0	6	2	162343
Tr&Co	= Trave	elers a	and cr	ontact	s;Cor	n= Co	ommu	mity	samp	ples																																								





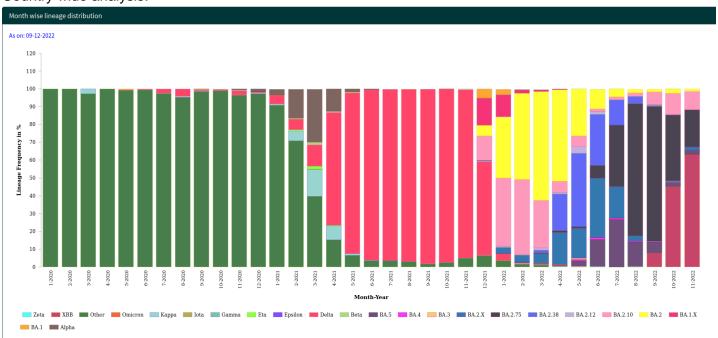
#### **Global Scenario**

Globally, the number of new weekly cases decreased by 3% during last week as compared to the previous week, with over 2.4 million new cases reported. The number of new weekly deaths decreased by 17% as compared to the previous week<sup>[1]</sup>. During last week, BA.5 descendent lineages remained dominant, with a prevalence of 70.1%; followed by BA.2 descendent lineages, with a prevalence of 10.5%. BA.4 descendent lineages continued to decline in prevalence, going from 2.8% to 2.0% during the same reporting period. Among the Omicron subvariants under monitoring, an increase from 27.6% to 36.2% for BQ.1 and its descendent lineages was observed. During the same period, the prevalence of XBB and its descendent lineages increased from 4.2% to 5.0%. BA.2.75 increased from 6.8% to 7.8%, while BA.4.6 decreased from 2.5% to 1.7%.

#### Indian Scenario

Omicron and its sub-lineages continue to be the dominant variant in India. XBB is the most prevalent sub lineage (63.2%) circulating all over India. BA.2.75 and BA.2.10 were also circulating in lesser extent. Especially, in North-East India, BA.2.75 is the prevalent sub lineage. However, any increase in disease severity or hospitalization has not been observed over this period.

#### Country wide analysis:



\*BA.5 in the graph includes its sub-lineages also.



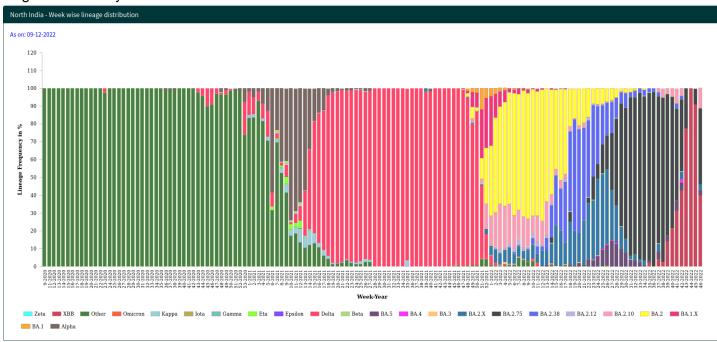


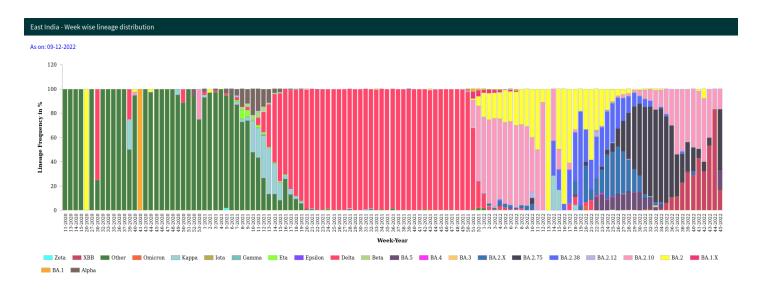






### Region-wise analysis:





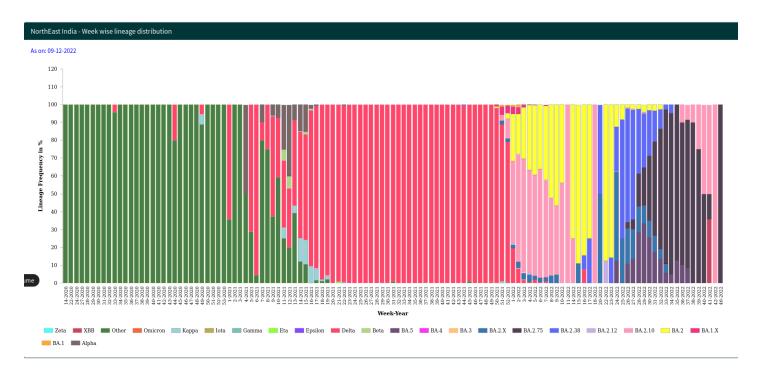


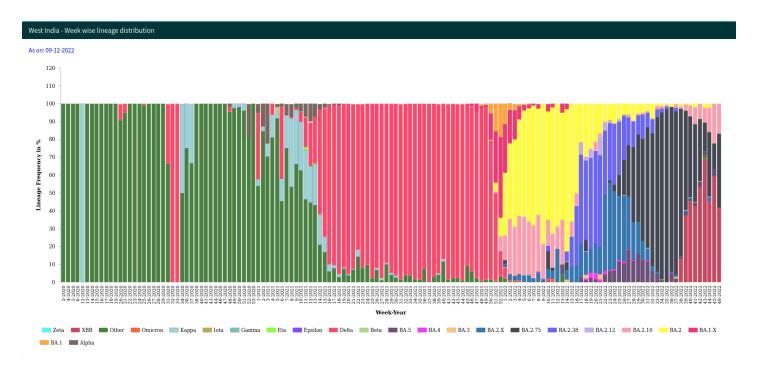




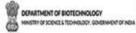








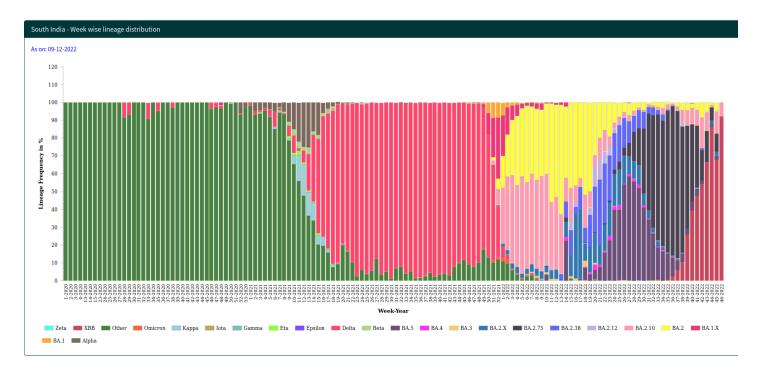


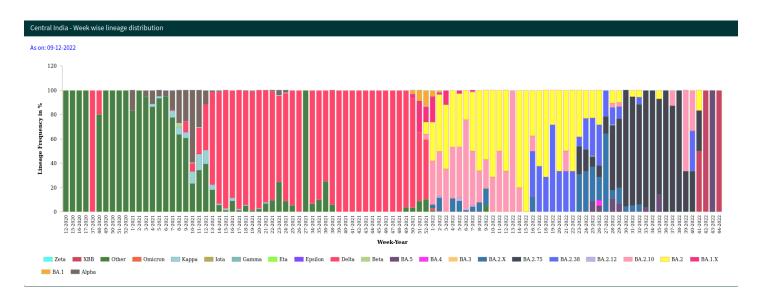












### Reference:

1. WHO weekly epidemiological report.