









26 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 269,932

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

Total number of samples sequenced: 304,695

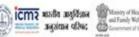
The number of samples with pangolin lineages assigned are given below:

Table 1: Cui	mulative samples wi	th pangolin lineage assign	ed (as on 23.12.20	022)
Community sample	Travelers sample	Total pangolin lineage assigned	Total VOC/VOI	Percentage
185821	12285	198106	163438	82.5

																									Distribu	tion of V	OC and	B.1.	617.1 &	B.1.617	.3 (as	on 2	3-12-	2022)													_					
A	Alpha Varinat			Beta Variar			nt		Gamma		mma Variant			Delta Variant			B.1.617.1 and B.1.617.3		AY Series			Omicron*				Recombinant											Х	E )	KT	XU	XJ	Total										
Tr&Co	Com	n T	otal	Tr&C	io Ci	om	Tota	l Tri	&Co	Com	n 1	Total	Tr8	&Co	Co	m	To	ital	Tr&C	io Ca	om	Total	Tr&0	Co	Com	Total	Tr&C		Com*	Total	XAR	XAH	XBB	XBB.1	XBB.1.	XBB.	1.3 )	KBB.2	XBB.3	XBB.3.	1 XBE	3.4 XI	3B.5	XBD	OTHER	IS Tota	al Vari	ant Va	riant \	/ariant	Variant	VOC/VO
577	36	590	4267	11	.7	105	22	2	1		2	3		387	4	3575		43962	8	4 5	540	5624		227	20248	20475	59	52	81187	87462	2	1	412	210		2	3	281	333		5	20	63	1		73 141	12	1	0	6	2	1634
Tr&Co	= Trav	elers	and	cont	acts	; Co	m= 0	omn	numi	ity sa	amp	les																																								







#### **Global Scenario**

Globally, the number of new weekly cases was similar to last week (+3%), with over 3.7 million new cases reported. The number of new weekly deaths decreased by 6% as compared to the previous week<sup>[1]</sup>. During last week, BA.5 and its descendent lineages are still dominant globally, accounting for 68.4% of sequences submitted to GISAID. The prevalence of BA.2 and its descendent lineages is rising, mainly due to BA.2.75; together they account for 12.6% of sequences submitted. BA.4 and its descendent lineages are declining with a prevalence of 1.2%. At the global level, six variants currently under monitoring account for 72.9% of prevalence, and have replaced the former BA.5 descendent lineages. These six variants under monitoring (and the respective prevalence) are BQ.1\* (42.5%), BA.5 with one or several of five mutations (S:R346X, S:K444X, S:V445X, S:N450D, S:N460X) (13.4%), BA.2.75\* (9.8%), XBB\* (6.1%), BA.4.6\* (1%), and BA.2.30.2\* (0.1%). Based on current evidence, 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 continued to be the dominant variant in India. Overall, the infection rate was around 200 per day. Among the samples collected till the end of November 2022, the prevalence of XBB and its sub-lineages was 62.6%, for BA.2.75, it was 18.7% whereas, BA.2.10 was 11.0% and those were continued to be the most commonly circulating Omicron sub-lineage. In northern half of India, BA.2.75 is the most prevalent sub-lineage whereas in middle and southern part of India, XBB is the most prevalent sub-lineage of omicron variant. Although the detection of different sub-lineages in different parts of India was dependent on variable collection dates in respective regions. However, any increase in disease severity or hospitalization has not been observed over this period. Any up-surge of BF.7 or BQ.1 sub-lineage has not been seen in India over last few weeks. However, INSACOG is closely monitoring the current scenario regarding those sub-lineages.

Country wide analysis:

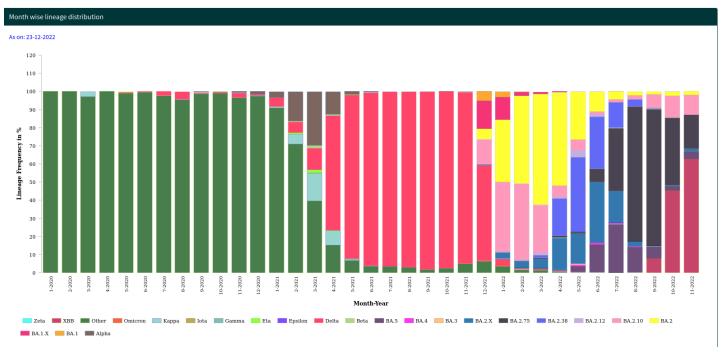






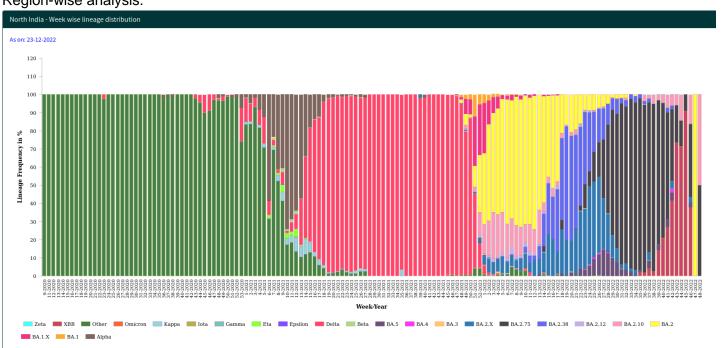




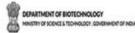


\*BA.5 in the graph includes its sub-lineages also.

### Region-wise analysis:



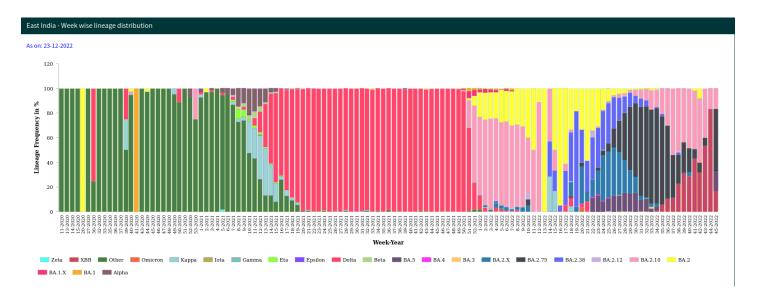


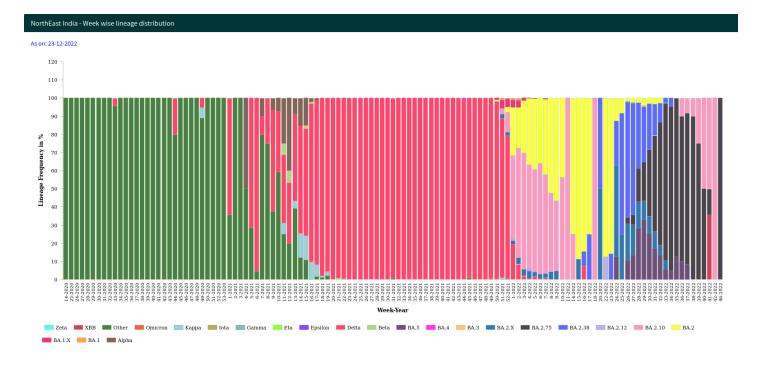












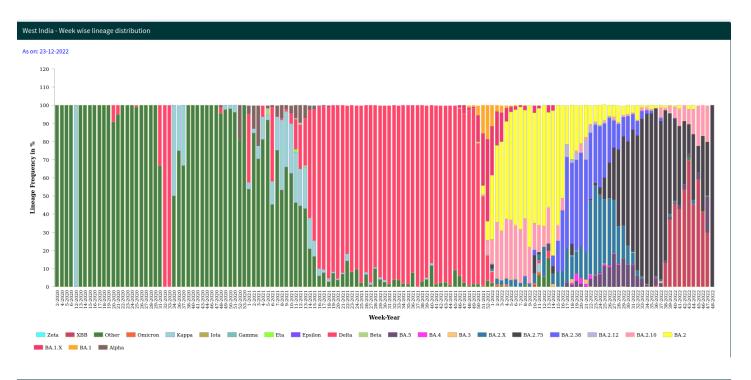




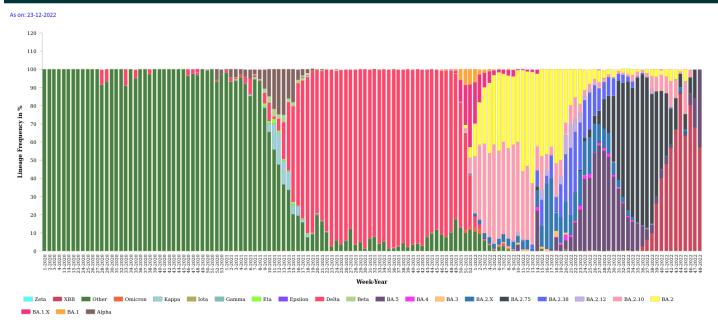












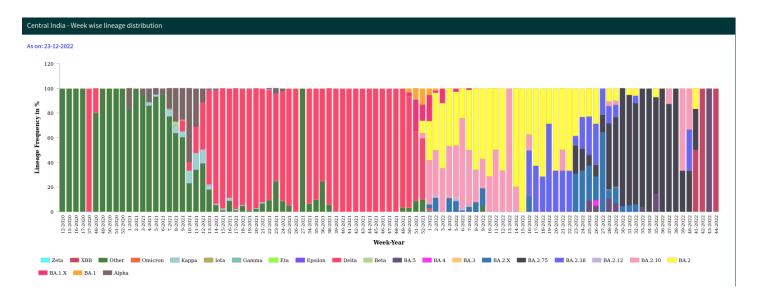












### Reference:

1. WHO weekly epidemiological report.