







09 January, 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 https://ibdc.rcb.res.in/

INSACOG:

Total number of samples sequenced is 271,003

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

Total number of samples sequenced: 305,766

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

Table 1: Cumulative	samples with p	angolin lineage	assigned (as	s on 05.01.2022)

Communit	y sample	Travelers sample	Total pangolin lineage assigned	Total VOC/VOI	Percentage
1876	328	12295	199923	165186	82.6

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	Distribution of VOC and B.1.617.1 & B.1.617.3 (as on 05.01.2023)																																								
Alp	ha Vari	ariant Beta Variant Gamma Variant					riant Delta Variant B.1.617			7.1 and	3.1.617.3	7.3 AY Series			Omicron*										Recombinant								XE	XM	XT	XU		Total			
Tr&Co	Com	Total	Tr&C	o Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com [‡]	Total	XAR	XAH XA	IB XA	G XBB	XBB.1	XBB.1.1	XBB.1.3	XBB.1.5	XBB.2	XBB.3	XBB.3.1	XBB.4	KBB.5)	BD OT	HERS Tota	Variant	Variant	t Varian	t Variar	t Variant	VOC/VOI
577	369	4267	1	17 109	222	1	2	3	387	43578	43969	84	5540	5624	227	20250	20477	5963	82544	88830	2	1	1	1 513	318	4	5	5	355	371	5	23	72	7	104 178	7	1	2	0	6	165186
Tr&Co=	Travele	rs and o	ontacts	:Com=	Commur	mity sam	oles																																		









Global Scenario

Globally, more than 3 million new cases and 10 000 deaths have been reported in the last week of December 2022. This represents a reduction in weekly cases and deaths of 22% and 12%, respectively [1]. During last week, BA.5 and its descendent lineages were still dominant globally, accounting for 63.7% of sequences submitted to GISAID even though their prevalence is decreasing. The prevalence of BA.2 and its descendent lineages is rising, mainly due to BA.2.75* (* indicates inclusion of descendent lineages); together they account for 15.2% of sequences submitted.

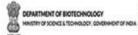
At the global level, six variants currently under monitoring account for 74.4% of prevalence as of week 50 and have replaced the former BA.5 descendent lineages. These six variants under monitoring (and the respective prevalence) are BQ.1* (44.9%), BA.5 with one or several of five mutations (S:R346X, S:K444X, S:V445X, S:N450D, S:N460X) (10.3%), BA.2.75* (11.8%), BA.4.6* (0.6%), and BA.2.3.20*. In week 50, the prevalence of XBB* was 6.8%, which includes XBB.1.5 which had an increase in sequences. 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 continue to be the dominant variants in India. Among the samples collected till the end of December 2022, XBB, BA.2.75 and BA.2.10 continued to be the most commonly circulating Omicron sub-lineages. Presence of BQ.1 sub-lineage has been seen in Eastern, Southern, Western and Northern parts of India. Overall, XBB is the most prevalent sub-lineage of omicron variant. Some occurrence of BF.7 sub-lineage has also been seen in Eastern and Northern part of India over last week. No increase in disease severity or hospitalization has been observed during this period.

Country wide analysis:

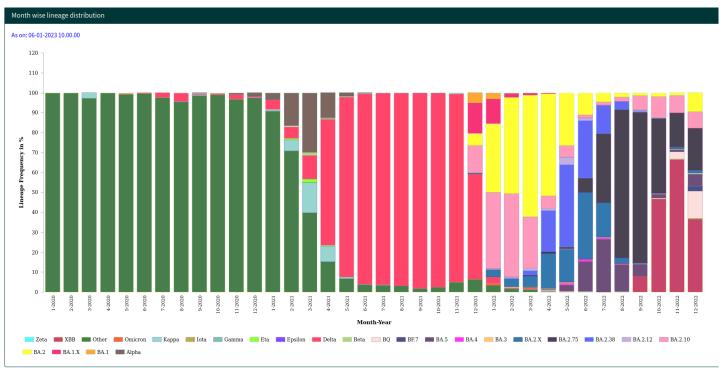










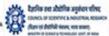


*BA.5 in the graph includes its sub-lineages also.

Region-wise analysis:

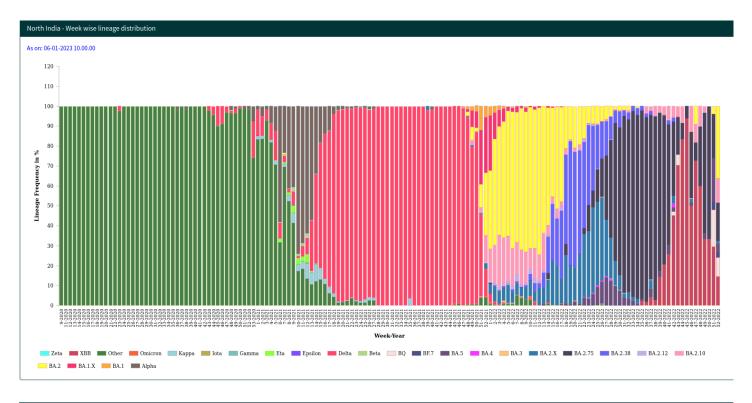


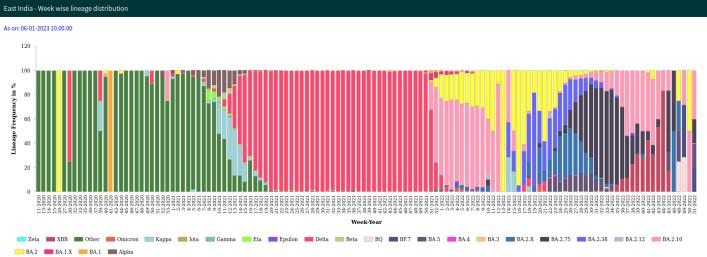




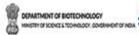








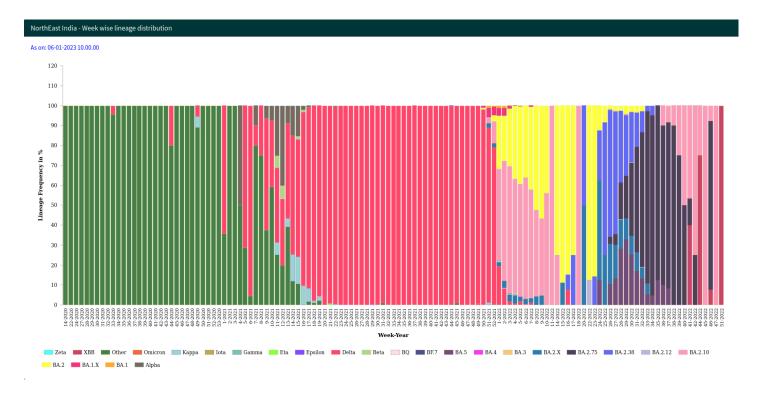




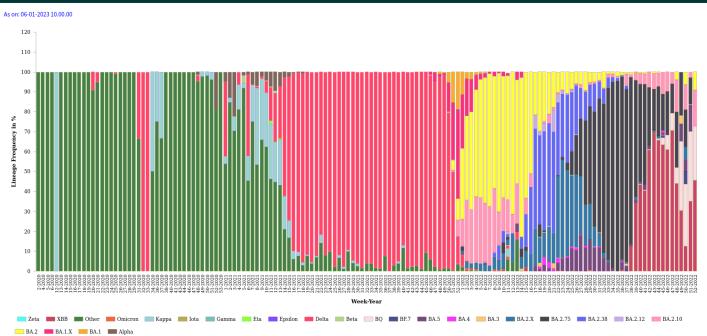












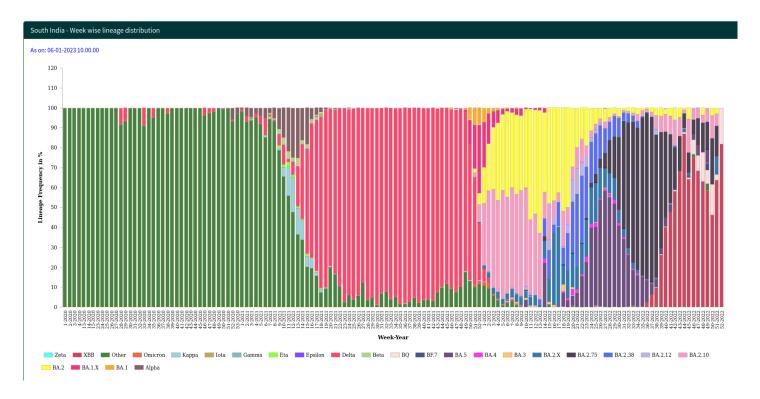


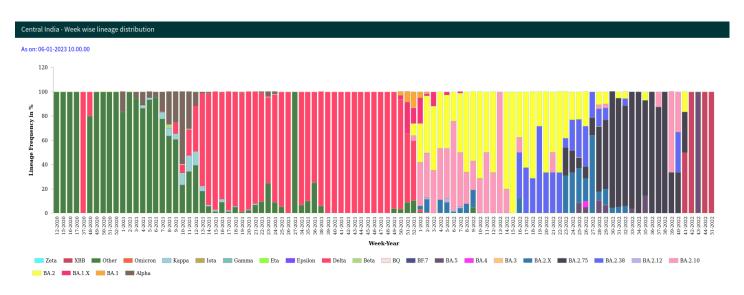












Reference:

1. WHO weekly epidemiological report.