

INSACOG BULLETIN

April 11, 2022

The INSACOG conducts genomic surveillance of SARS-CoV-2 across the country through sequencing of samples from Sentinel sites and International passengers arriving in India. A summary of the cumulative data of INSACOG and other state sequencing initiatives can be found at the INSACOG data portal link along with other INSACOG information at <https://research.nibmg.ac.in/insacog/>.

INSACOG:

Total number of samples sequences as on 08.04.2022 by INSACOG is 2,05,807

Total number of sequences analysed is 2,04,697

Samples sequenced by IGSIs under state governments MoU is 34,763

Total number of samples sequenced: 2,40,570

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

Table 1: Cumulative samples with pangolin lineage assigned (as on 08.04.2022)				
Community sample	Travelers sample	Total pangolin lineage assigned	Total VOC/VOI	Proportion
138025	12263	150288	118569	78.9

Distribution of VOC and B.1.617.1 & B.1.617.3 (as on 08.04.2022)

Alpha Variant			Beta Variant			Gamma Variant			Delta Variant			B.1.617.1 and B.1.617.3			AY Series			Omicron			Total VOC/VOI
Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	
577	3689	4266	117	103	220	1	2	3	387	43538	43925	84	5523	5607	227	20221	20448	5877	38223	44100	118569

Tr&Co= Travelers and contacts; Com= Community samples

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Global Scenario

The number of new COVID-19 cases has decreased for a second consecutive week, with a 16% decline during the week. The number of new deaths also decreased as compared to the previous week.

Two recombinant variants XD and XE are being closely monitored worldwide. XD, which has an Omicron S gene incorporated into a Delta genome, is found primarily in France. XE is a BA.1/BA.2 recombinant, with the majority of the genome including the S gene belonging to BA.2. XE shows slightly higher transmission rate. XE also shows a higher growth rate above that of BA.2; however, this finding requires further confirmation.

Indian Scenario

Based on genome sequencing analysis, very few recombinant variants have been discovered in India. So far, none showed either increased transmission (locally or otherwise) or associated with severe disease or hospitalization. Incidences of suspected recombinants and the possible public health relevance are being closely monitored.