







INSACOG BULLETIN

June 27, 2022

The INSACOG reports 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 sequenced is 223,954
- · Total number of sequences analyzed 222,659

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

Total number of samples sequenced: 258,717

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

Table 1: Cumulative samples with pangolin lineage assigned (as on 24.06. 2022)											
Community sample	Travelers sample	Total pangolin lineage assigned	Total VOC/VOI	Proportion							
151404	12285	163689	131461	80.3							

	Distribution of VOC & B.1.617.1 and B.1.617.3 (as on 24-06-2022)																							
Alpha Variant		Beta Variant		Gamma Variant		Delta Variant		B.1.617.1 and B.1.617.3			AY Series			Omicron			XE	XM Variant V	XJ Variant	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	Vallalit	Valiatio	Variatio	VOC/VOI
577	3690	4267	117	104	221	1	2	3	387	43566	43953	84	5540	5624	227	20235	20462	5895	50708	56926	1	2	2	131461
Tr&Co=	Travelers	and cont	r&Co= Travelers and contacts ; Com= Community samples																					









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Global Scenario

Globally, the number of new weekly cases has continued to decline since a peak in January 2022. At the regional level, the number of new weekly cases increased in the South-East Asia Region, the Eastern Mediterranean Region, and the European Region, while it decreased in the other regions. The Omicron VOC remains the dominant variant circulating globally, accounting for 97% of sequences reported. Among Omicron lineages, the proportions of BA.2 and its descendent lineages are declining but nonetheless remain dominant. Globally, BA.5 and BA.4 lineages continue to rise in prevalence and have been detected in 62 and 58 countries respectively. BA.4 and BA.5 have a constellation of genetic mutations that differ from BA.2, including a shared mutation at S:L452 which has been associated with higher transmissibility.

Indian Scenario

The Omicron sub-variants BA.2 and BA.2.38 seem to be the prevalent sub-lineages over the last few weeks in India. An increase in patients infected with the BA.5 variant has also been observed. However, this has not led to any increase in hospitalization or any report of increase in disease severity. COVID appropriate behavior is likely to reduce the spread of the infection and hence continues to be recommended.

