INSACOG
INDIAN SARS-COV-2 GENOMICS CONSORTIUM
DEPARTMENT OF BIOTECHNOLOGY
MINISTRY OF SCIENCE & TECHNOLOGY, GOVERNMENT OF INDIA

INSACOG BULLETIN

June 13, 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 219,780
- Total number of sequences analyzed 218,744

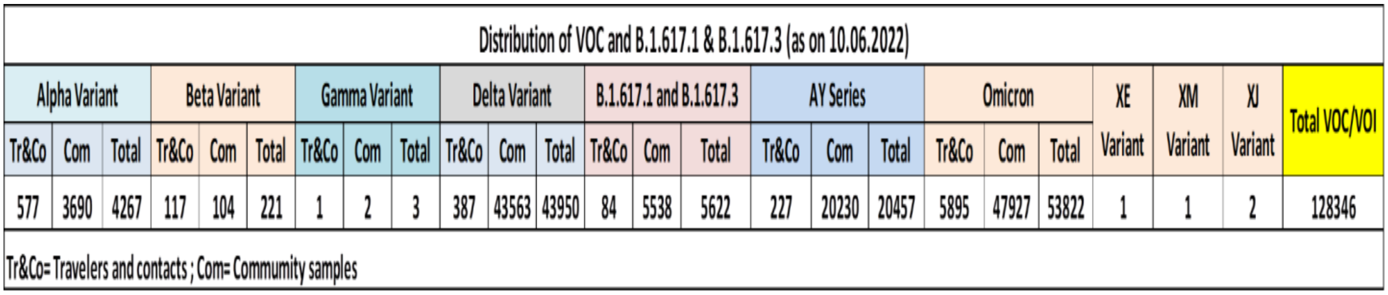
Samples sequenced by IGSLs under State government MoUs: 34,763

Total number of samples sequenced: 254,543

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

Table 1: Cumulative samples with pangolin lineage assigned (as on 10.06. 2022)

Community sample	Travelers sample	Total pangolin lineage assigned	Total VOC/VOI	Proportion
147981	**12285**	**160266**	**128344**	**80.1**



Distribution of VOC and B.1.617.1 & B.1.617.3 (as on 10.06.2022)

Alpha Variant			Beta Variant			Gamma Variant			Delta Variant			B.1.617.1 and B.1.617.3			AY Series			Omicron			XE Variant	XM Variant	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				
577	3690	4267	117	104	221	1	2	3	387	43563	43950	84	5538	5622	227	20230	20457	5895	47927	53822	1	1	2	128346

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

INSACOG BULLETIN

Global Scenario

Globally, the number of new weekly cases has continued the declining trend observed since a peak in January 2022.

The Omicron VOC continues to be the dominant variant circulating globally. Among Omicron lineages, BA.2 and its descendent lineages (pooled lineages named BA.2.X) are declining but remain dominant,. Several variants with preliminary evidence of a growth advantage over other Omicron lineages show a global prevalence of <1% and are no longer rising, namely BA.2.11, BA.2.13, and BA.2.9.1.

Globally, BA.2.12.1, BA.5, and BA.4 variants are rising in prevalence. As of now, BA.2.12.1 (detected in 53 countries) has reached a prevalence of 28%. BA.5 (detected in 47 countries) and BA.4 (detected in 42 countries) account for 4% and 2% of circulating variants, respectively. All three variants carry the signature mutation at locus S:L452 that is thought to confer greater transmissibility through higher cell fusogenicity and immune escape characteristics. However, there has been no observed increase in severity associated with BA.5 and BA.4.

Indian Scenario

Rise in infection has been observed in certain regions of India over the last week. BA.2 continues to be the dominant lineage in India. However, hospitalization due to severity of the disease has not been observed that much. INSACOG is closely monitoring the current situation.