INSACOG
INDIAN SARS-COV-2 GENOMICS SEQUENCING CONSORTIUM
DEPARTMENT OF BIOTECHNOLOGY
MINISTRY OF SCIENCE & TECHNOLOGY, GOVERNMENT OF INDIA
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icmr
Ministry of Health and Family Welfare
Government of India

INSACOG WEEKLY BULLETIN

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The INSACOG reports genomic surveillance of SARS CoV -2 across the country through sequencing of samples from Sentinel sites and also detailed State wise district analysis for some states under State MoUs (Maharashtra, Kerala and some others) A summary of the cumulative data of INSACOG and other state sequencing initiatives can be found at the INSACOG data portal link (http://clingen.igib.res.in/covid19genomes/) along with other INSACOG information at https://dbtindia.gov.in/insacog. New web-based query tool is now available on the data portal. All data presented on the portal is organized by date of sample collection, state, assigned lineage and mutations found on analysis.

INSACOG:

- Total number of samples processed so far is 1,00,744
- Total number of samples sequenced is 100, 744
- Total number of sequences analysed are 97,898

Samples from MoUs with state governments:

- Number of samples sequenced is 18, 789

Total number of samples sequenced: 1,19,533

The number of samples with pangolin lineage assigned are

Table 1: Cumulative samples with pangolin lineage assigned (as on 17.11.2021)

Community sample	Travelers sample	Total assigned	Total VOC/VOI	Proportion
63223	5178	68401	47719	69.8

Table 2: Cumulative distribution of VOC/VOI (17.11.2021)

Alpha Variant			Beta Variant			Gamma Variant			Delta Variant			B.1.617.1 and B.1.617.3			AY series	Total VOC/VOI
Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total		
577	3657	4234	117	102	219	1	1	2	74	30149	30223	85	5438	5523	7518	47719

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Variants reported during the period

Global

There is no change to the global scenario. Delta, including B.1.617.2 (AY) and AY.x sublineages, continues to be the main VOC globally. Sequencing data from European nations, such as France and Germany that are facing large outbreaks, shows Delta sub-lineages, e.g. AY.43, that have been in circulation for many months without any transmission advantage over other lineages. Increased indoor air-borne transmission in winter may be an important factor for the recent surge in Europe (1). Incomplete vaccination of at-risk population and declining neutralization activity in previously vaccinated people may be important additional factors (2).

National

Delta (B.1.617.2 and AY.x) continues to be the main VOC in India. No new VOI or VOC are noted. The most frequent Delta sub-lineage in India after B.1.617.2 ancestral lineage is AY.102 and AY.39. Based on uniform lineage assignment across all available sequencing data, there does not appear to be any transmission advantage to either AY.102 or AY.39 at this time. Other than lineage-based tracking, Delta variants with potentially clinically important mutations are being tracked by INSACOG, as mentioned in Nov 1 update. Some of these, such as E484Q, were previously seen in the Kappa variant, and have independently appeared on the Delta background in different geographies. These are still at low levels (~6%) but will continue to be monitored.

1. https://www.euro.who.int/en/about-us/regional-director/statements-and-speeches/2021/statement-update-on-covid-19-europe-and-central-asia-again-at-the-epicentre-of-the-pandemic
2. Kromer et al. Lancet Nov 2021 https://doi.org/10.1016/S2666-5247(21)00267-6