DEPARTMENT OF BIOTECHNOLOGY
MINISTRY OF SCIENCE & TECHNOLOGY, GOVERNMENT OF INDIA
वैज्ञानिक तथा औद्योगिक अनुसंधान परिषद
COUNCIL OF SCIENTIFIC & INDUSTRIAL RESEARCH
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Ministry of Health and Family Welfare
Government of India
INSACOG
THE INDIAN SARS-COV-2 GENOMIC CONSORTIA

INSACOG WEEKLY BULLETIN

No. 19| Nov 1, 2021

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 93,782
- Total number of samples sequenced is 93,782
- Total number of sequences analysed are 91,729

Samples from MoUs with state governments:

- Number of samples sequenced is 18,485

Total number of samples sequenced: 1,12,267

The number of samples with pangolin lineage assigned are 64,869

Table 1: Cumulative samples with Pangolin lineage assigned (as on 28-10-2021)

Community sample	Travelers sample	Total assigned	Total VOC/VOI	Proportion
59691	**5178**	**64869**	**44538**	**68.7**

Table 2: Distribution of VOC/VOI (as on 28-10-2021)

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	3655	4232	117	102	219	1	1	2	74	28115	28189	85	5365	5450	6446	44538

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

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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. The 29th Oct update from UK Health Security Agency (formerly Public Health England) states that the proportion of AY.4.2 continues to slowly grow (1). As per the update, vaccine effectiveness does not seem to be different for AY.4.2, when compared to other Delta. There is currently no biological basis for increased transmissibility of AY.4.2, as judged epidemiologically, and assays are in progress. Delta variants with immune escape mutations are also being tracked by UKHSA.

National

Delta (B.1.617.2 and AY.x) continues to be the main VOC in India. No new VOI or VOC are noted in India. With a new PANGO update (3.1.15) applied to all sequences in the INSACOG data portal, many issues noted with previous versions have been resolved. AY.4.2 frequency in Indian data varies based on the definition used (PHE vs PANGO), but is too low to be of concern at this time (less than 0.1 % of all VOC/VOI). Other than lineage-based tracking, Delta variants with immune escape mutations (e.g. S477I, E484K, E484Q, G446V, G446S, K417N, P26S, F490S, F490L) are also being tracked by INSACOG, some of which are also being seen by UKHSA.

1. UK Health Security Agency SARS CoV2 VOC Technical Briefing no. 27 https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/1029715/technical-briefing-27.pdf