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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. 18| Oct 25, 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 90,301
- Total number of samples sequenced is 90,301
- Total number of sequences analysed are 88,802

Samples from MoUs with state governments:

- Number of samples sequenced is 17,520

Total number of samples sequenced: 1,07,520

The number of samples with pangolin lineage assigned are 63,764

Table 1: Cumulative samples with pangolin lineage assigned (21.10.2021)

Community sample	Travelers sample	Total assigned	Total VOC/VOI	Proportion
58586	**5178**	**63764**	**43542**	**68.3**

Table 2: Cummulative distribution of VOC/VOI (21-10-2021)

Alpha Variant			Beta Variant			Gamma Variant			Delta Variant			B.1.617.1 and B.1.617.3				Total VOC/VOI
Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	AY series	
577	3655	4232	117	102	219	1	1	2	74	27335	27409	85	5365	5450	6230	43542

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 recent rise in AY.4.2 in genomic surveillance needs to be interpreted with caution due to technical issues with detection of Y145H mutation. Using an optimized case surveillance definition (1), Public Health England has concluded that there is a modest growth advantage to AY.4.2 in recent surveillance data, but as of now there is no biological evidence of increased infectivity or severity. The case definition has not been validated on international data but provisionally AY.4.2 is seen mostly in Europe, North America and to a lower extent in Asia

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. Many cases earlier labelled as AY.4 are now reclassified at AY.33 in the new revised system. It has been noted that due to greater diversity of Delta in India, PANGO classifications may sometimes be inaccurate, especially for new sub-lineages. INSACOG is thus further examining the data on AY.33. Based on the case definition used by PHE, AY.4.2 is very infrequent (below 0.1%) in India. Most sequences from India that are being classified by PANGO as AY.4.2 have only either Y145H or A222V in Spike, not both mutations appearing together. For clarity, PANGO has classified 17 sequences from India as AY.4.2, which is also reflected in GISAID. Manual analysis of these 17 sequences has revealed that 8 sequences have only Spike_Y145H, 2 sequences have only Spike_A222V, whereas the remaining 4 sequences do not have either of the mutations. None of these sequences have both the mutations together.

1. PHE Technical Briefing 26 dt 22nd Oct 2021, https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/1028113/Technical_Briefing_26.pdf