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 99,255
- Total number of samples sequenced is 99,255
- Total number of sequences analysed are 95,929

Samples from MoUs with state governments:

- Number of samples sequenced is 18,789

Total number of samples sequenced: 1,18,044

The number of samples with pangolin lineage assigned are 66,487

Table 1: Cumulative samples with pangolin lineage assigned (as on 11.11.2021)

Community sample	Travelers sample	Total assigned	Total VOC/VOI	Proportion
61309	5178	66487	46046	69.3

Table 2: Cummulative distribution of VOC/VOI (as on 11.11.2021)

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	29155	29229	85	5425	5510	6852	46046

Tr&Co= Travelers and contacts; Com= Communty 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. In addition to the well-described mutations in the spike protein, the greater infectiousness of Delta may additionally be due to R203M mutation in the nucleocapsid (N) protein (1).

National

Delta (B.1.617.2 and AY.x) continues to be the main VOC in India. No new VOI or VOC are noted. Analysis of Indian sequencing data for N mutations associated with greater infectivity shows that the N:R203M mutation was also present in the Kappa lineage (B.1.617.1 and B.1.617.3) that led to outbreaks in early 2021, especially in Maharashtra, before being displaced by Delta.

These mutations are not likely to have importance for cross-immunity. Both Covishield and Covaxin have already shown effectiveness against Delta (2,3).

1. Syed et al. Science Nov 2021 https://doi.org/10.1126/science.abl6184
2. Ella et al. Lancet Nov 2021 https://doi.org/10.1016/S0140-6736(21)02000-6
3. Bernal et al. NEJM Aug 2021 https://doi.org/10.1056/nejmoa2108891