



## 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 64,460
- Total number of samples sequenced is 64,460
- Total number of sequences analysed are 49,867

### Samples from MoUs with state governments:

- Number of samples sequenced is 8,471

**Total number of samples sequenced: 72,931**

The number of samples with pangolin lineage assigned are

Table 1: Cumulative samples with pangolin lineage assigned (as on 13.08.2021)

	Community sample	Travelers sample	Total pangolin lineage assigned	Total VOC/VOI	Proportion
	44689	5178	49867	30230	60.6%

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Table 2: Distribution of VOCs (as on 16-08-2021) & B.1.617.1 and B.1.617.3

	Alpha variant			Beta Variant			Gamma Variant			Delta variant			B.1.1617.1 and B.1.617.3			Delta Plus	Total VOC/VOI
	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total		
	577	3641	4218	117	101	218	1	1	2	74	20250	20324	85	5322	5407	61	30230

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



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### Variants reported during the period

#### Global

Delta continues to expand around the world with China and Korea seeing new highs. Korea has reported that the new surge is with Delta + K417N mutation. As VoC Delta (B.1.617.2) has continued to evolve, a number of sub-lineages of delta with additional mutations in spike protein as well as other proteins have come up in different parts of the world. PANGO now classifies a total of 13 sublineages of delta with characteristic genetic mutations. AY.1, AY.2 and AY.3 are the predominant lineages globally and also found in India. AY.3.1 is a recently classified sublineage of AY.3 in the United States. AY.12 is a sublineage of delta recently classified from Israel. All these sublineages are being closely monitored from across the world and in India.

#### National

In India new cases of AY.1, AY.2, AY.3 are being seen in July samples from Maharashtra at a frequency of about 1%. This will continue to be monitored along with new AY sub-lineages. At this time none of these sub-lineages has been found to have a growth advantage over the Delta parent lineage.

There has been concern about whether increasing vaccination breakthroughs in India are because of a new variant. It is noted that UK, with a population of about 6.7 Crore, has reported about 18 lakh cases and 1.2 lakh vaccination breakthroughs with Delta, since April 2021 (1). Thus, vaccination breakthroughs are common during Delta outbreaks and are expected in India as well. Concern regarding appearance of new variants should be calibrated in the context of such data. As of now sequencing of vaccination breakthroughs in India is also showing a very high proportion of Delta variant. Investigations for any new variants are ongoing

In summary, Delta variant is the major VOC in India at this time. Continuing outbreaks across India are attributable to Delta, a susceptible population, reduced vaccine effectiveness in blocking transmission, and opportunities for transmission. Vaccination continues to be very effective in reducing severe disease and death. Public health measures to reduce transmission and vaccination remain critical.

- 1) Public Health England Briefing 20, accessed at <https://www.gov.uk/government/publications/investigation-of-novel-sars-cov-2-variant-variant-of-concern-20201201>