









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 and district-wise analysis for some states under State MoUs (Maharashtra, Kerala and some others). A summary of the INSACOG information is at https://dbtindia.gov.in/insacog. All cumulative data of INSACOG and other state sequencing initiatives can be found at the INSACOG data portal link (http://clingen.igib.res.in/covid19genomes/). 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 62,755
- Total number of samples sequenced is 62,755
- Total number of sequences analysed are 48,478.

Samples from MoU with state government:

• Number of samples sequenced is 6,970

Total number of samples sequenced: 69,725

The number of samples with pangolin lineage assigned are

Table 1: C	Table 1: Cumulative samples with pangolin lineage assigned (as on 06.08.2021)											
Community sample	Tra	avelers sample	Total pangolin lineage assigned	Total VOC/VOI	Proportion							
42078		5178	47256	27825	58.9%							











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	Table 2: Distribution of VOCs (as on 06-08-2021) & 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/		
	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total	Tr&Co	Com	Total		VOI
	577	3626	4203	117	100	217	1	0	1	74	17896	17970	85	5304	5389	45	27825
Tr&Co-Travelers and contacts: * Com-Community samples																	

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











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Variants reported during the period

National

During the week no new Variant has been reported from within the country samples '

Delta continues to be the dominant lineage for new cases across all parts of India in samples collected in July

Breakthrough infections have also been reported from Kerala and other States. In view of large number of breakthrough infection State officials in Kerala have been requested for details regarding timeline of such infections in various districts in terms of vaccine type, duration, disease severity etc for better clarity on variant prevalence and vaccine efficacy. Current genomic analysis of around 200 samples of breakthrough infections indicate presence of Delta variant. At present, there is no evidence on any other VOC as the cause

Global

Globally also there is no new variant reported during the period. Delta remains the most rapidly rising lineage globally, with severe outbreaks being reported in many regions of United States.

Published reports

There are now published peer-reviewed reports from India documenting breakthrough infection and transmission between fully vaccinated people with Delta variant (1). CDC, USA has released a warning that fully vaccinated people with Delta variant breakthrough infections have viral loads comparable to unvaccinated people and can spread the virus to others (2).

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) JS Shastri et al, Front. Med. | doi: 10.3389/fmed.2021.737007, https://www.frontiersin.org/articles/10.3389/fmed.2021.737007/abstract
- 2) https://www.cdc.gov/coronavirus/2019-ncov/variants/delta-variant.html