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 1,02,880
- Total number of samples sequenced is 1,02,880
- Total number of sequences analysed are 99,832

Samples from MoUs with state governments:

- Number of samples sequenced is 18,789

**Total number of samples sequenced: 1,21,669**

The number of samples with pangolin lineage assigned are 69,586

### Table 1: Cumulative samples with Pangolin lineage assigned (as on 25.11.2021)

<table>
<thead>
<tr>
<th>Community sample</th>
<th>Travelers sample</th>
<th>Total assigned</th>
<th>Total VOC/VOI</th>
<th>Proportion</th>
</tr>
</thead>
<tbody>
<tr>
<td>64408</td>
<td>5178</td>
<td>69586</td>
<td>48708</td>
<td>70.0</td>
</tr>
</tbody>
</table>

### Table 2: Cumulative distribution of VOC/VOI (as on 25.11.2021)

<table>
<thead>
<tr>
<th>Alpha Variant</th>
<th>Beta Variant</th>
<th>Gamma Variant</th>
<th>Delta Variant</th>
<th>B.1.617.1 and B.1.617.3</th>
<th>AY series</th>
<th>Total VOC/VOI</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tr&amp;Co</td>
<td>Com</td>
<td>Total</td>
<td>Tr&amp;Co</td>
<td>Com</td>
<td>Total</td>
<td>Tr&amp;Co</td>
</tr>
<tr>
<td>577</td>
<td>3669</td>
<td>4246</td>
<td>117</td>
<td>102</td>
<td>219</td>
<td>1</td>
</tr>
</tbody>
</table>
Variants reported during the period

Global

Delta, including B.1.617.2 (AY) and AY.x sublineages, continues to be the main VOC globally. The SARS-CoV-2 variant, B.1.1.529, first found in Southern Africa, has been added to the WHO list of VOC and named ‘Omicron’ (1). Omicron is a heavily mutated variant that is predicted to be able to evade prior immunity from natural infections or from vaccines (2).

As per available sequence data, Omicron is characterised by 30 amino acid changes (15 in the receptor binding domain), three small deletions and one small insertion in the spike protein compared to the original virus (A67V, Δ69-70, T95I, G142D, Δ143-145, Δ211, L212I, ins214EPE, G339D, S371L, S373P, S375F, K417N, N440K, G446S, S477N, T478K, E484A, Q493K, G496S, Q498R, N501Y, Y505H, T547K, D614G, H655Y, N679K, P681H, N764K, D796Y, N856K, Q954H, N969K, L981F). This is the highest number of mutations yet seen, many of which are at antibody binding sites and may reduce the effectiveness of neutralizing antibodies. Some mutations have been associated with increased transmissibility in previous variants.

The variant also has changes in other genomic regions. The changes in Nucleocapsid (N) protein include the 203-204 site mutations recently reported to increase infectivity, as seen in Delta

NSP3: K38R, V1069I, Δ1265, L1266I, A1892T
NSP4 – T492I; NSP5 – P132H
NSP6 – Δ105-107, A189V
NSP12 – P323L
NSP14 – I42V
E – T9I
M – D3G, Q19E, A63T
N – P13L, Δ31- 33, R203K, G204R

Preliminary evidence suggests that Omicron may increase reinfection risk, which is expected from the structural changes due to the mutations, and the number of cases of this variant appears to be increasing in almost all provinces in South Africa. In some PCR tests, such as Thermo TaqPath, one of the three target genes is not detected (called S gene dropout or S gene target failure (SGTF)). Such a phenomenon was previously seen for Alpha, which is currently not in active circulation and thus SGTF can be used as marker for this variant, pending sequencing confirmation. The mutation spectrum of Omicron is predictive of high transmissibility, as noted. While there is initial suggestion that this variant may have a growth advantage over Delta, growth advantage is not the same as higher transmissibility, especially when there is prior immunity in the community. It is noted that after a
recent Delta surge, immunity to Delta has slowed down Delta propagation in Southern Africa and further studies are needed to quantify the immune escape and transmissibility aspects of Omicron. The clinical aspects such as severity of illness in naïve, previously infected, or vaccinated subjects are currently unknown.

National

Delta (B.1.617.2 and AY.x) continues to be the main VOC in India. No new VOI or VOC are noted, including Omicron. A fair and effective strategy for detecting and containing entry of Omicron into India is being implemented, since based on the preliminary data, it is likely that population immunity and vaccine-induced immunity may not sufficiently block its propagation.

Genomic surveillance will be critical for early detection of the presence of this variant, to enable necessary public health measures. Monitoring travel to and from the known affected areas, and contact tracing of COVID-19 cases with an epidemiological link to the affected areas has been implemented along with increased testing (with sequencing of confirmed cases and possible SGTF based rapid screening). Vaccination of all remaining unvaccinated at-risk people and consideration of a booster dose for those 40 years of age and over, first targeting the most high-risk / high-exposure may be considered, since low levels of neutralising antibodies from current vaccines are unlikely to be sufficient to neutralise Omicron, although risk of severe disease is still likely to be reduced.

Cluster outbreaks: Specific cluster outbreaks of COVID-19 in various parts of the country are also being investigated. This includes two reported outbreaks in Karnataka currently being investigated by the state surveillance programme of Karnataka.

1) WHO release (26th November) on Omicron: https://www.who.int/news/item/26-11-2021-classification-of-omicron-(b.1.1.529)-sars-cov-2-variant-of-concern