INSACOG: Indian SARS-CoV-2 Genomics Consortium

MINISTRY OF HEALTH AND FAMILY WELFARE
Government of India

DEPARTMENT OF BIOTECHNOLOGY
Government of India

INDIAN COUNCIL OF MEDICAL RESEARCH
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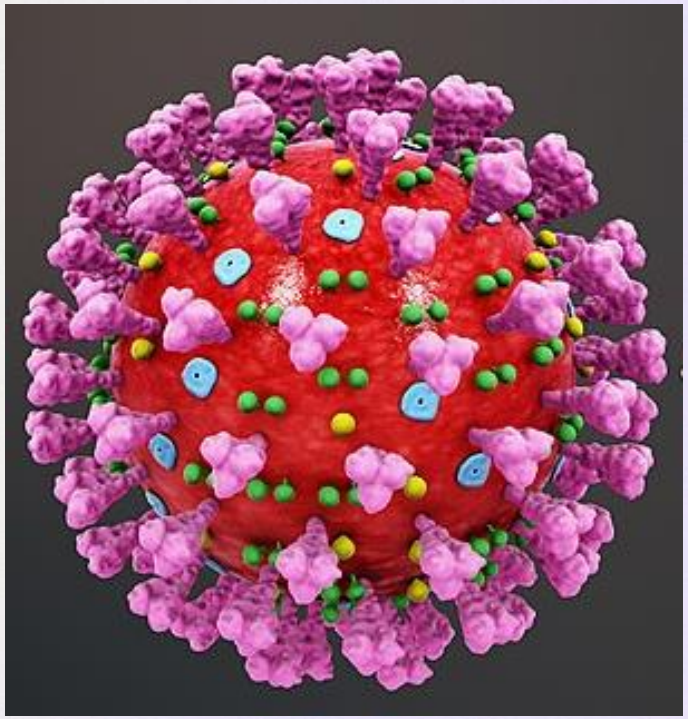
Inter-ministerial consortium of 28 Laboratories

Ascertain Status of new SARS-Cov-2 variants

B.1.1.7 (alpha), B.1.351 (beta), P2 (gamma) B.1.617.2 (delta) variants identified



Hospital Network for clinical correlation

Sequencing of infection breakthrough

Sewage surveillance

More than 45000 samples processed and 36,000 samples sequenced with approx. 50% variants of concern noted across the country

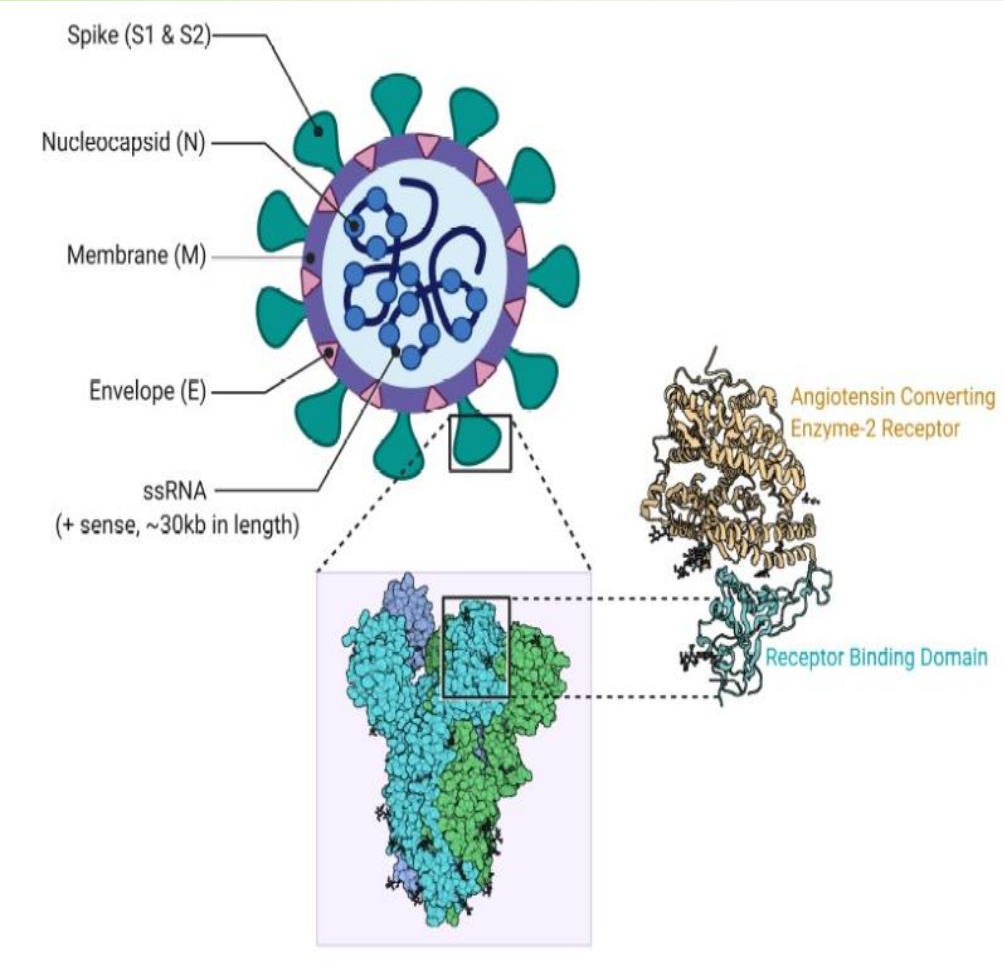
SARS-CoV-2 Variants of Concern (VoC)

A SARS-CoV-2 VoC is associated with one or more of the following changes at a degree of global public health significance:

- Increase in transmissibility or detrimental change in COVID-19 epidemiology; or
- Increase in virulence or change in clinical disease presentation; or
- Decrease in effectiveness of public health and social measures or available diagnostics, vaccines, therapeutics

Alpha	B.1.1.7
Beta	B.1.351
Gamma	P.1
Delta	B.1.617.2

SARS-CoV-2 VoCs circulating globally :
SPIKE Gene Mutations



Alpha →

69-70 del | 69-70 del | N501Y | A570D | P681H | S982A | D614G | T716I | D1118H

Beta →

D80A | 242-245 del | K417N | D614G | R246I | E484K | A701V | N501Y

Gamma →

L18F | D138Y | K417T | D614G | T1027I | T20N | R190S | E484K | H655Y | V1176F | P26S | N501Y

Delta →

T19R | DEL 157-158 | R158G | L452R | T478K | D614G | P681R | D950N

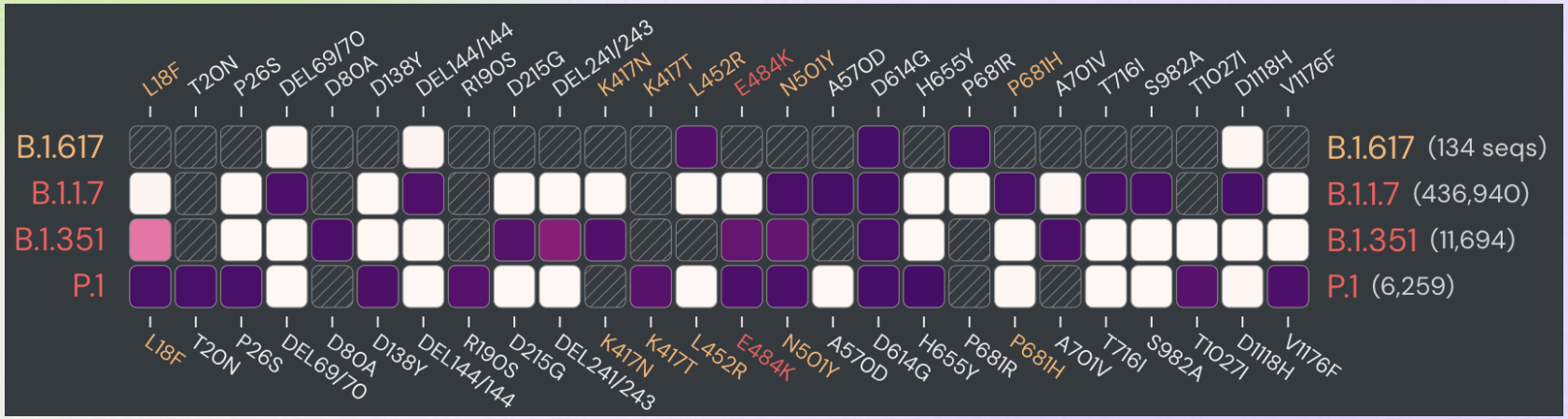
SARS-CoV-2 Variants of Interest (VoI)

A SARS-CoV-2 isolate is a Variant of Interest (VOI) if, compared to a reference isolate, its genome has mutations with established or suspected phenotypic implications, and either:

- It has been identified to cause community transmission/multiple COVID-19 cases/clusters, or has been detected in multiple countries; OR
- Assessed to be a VOI by WHO in consultation with the WHO SARS-CoV-2 Virus Evolution Working Group.

Epsilon	B.1.427/ B.1.429
Zeta	P.2
Eta	B.1.525
Theta	P.3
Iota	B.1.526
Kappa	B.1.617.1
Lambda	C.37

Mutation Constellation on the SPIKE protein for global Variants



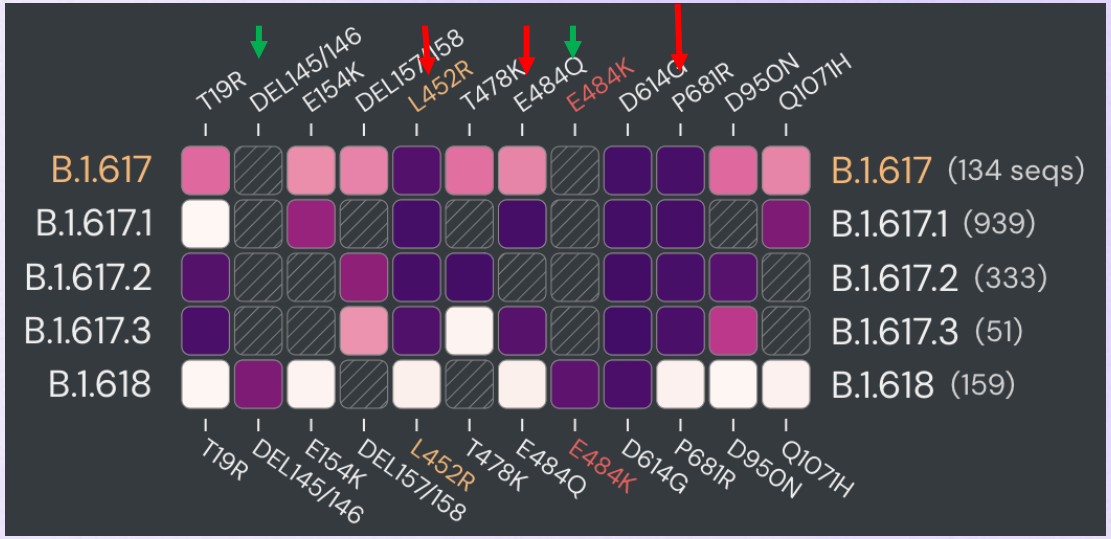
B.1.617 : High levels in Maharashtra, Bengal, Delhi, Karnataka /Appearing in multiple states

B.1.617 has E484Q (not R)/T478K, L452R and P681R in addition to D614G.

B.1.617.1 has both L452R and E484Q along with P681R

B.1.617.2 don't have E484Q, but T478K alongwith P681R

B.1.618 In addition to E484K, it has two deletions, Y145 and H146 in Spike. D614G is also present.

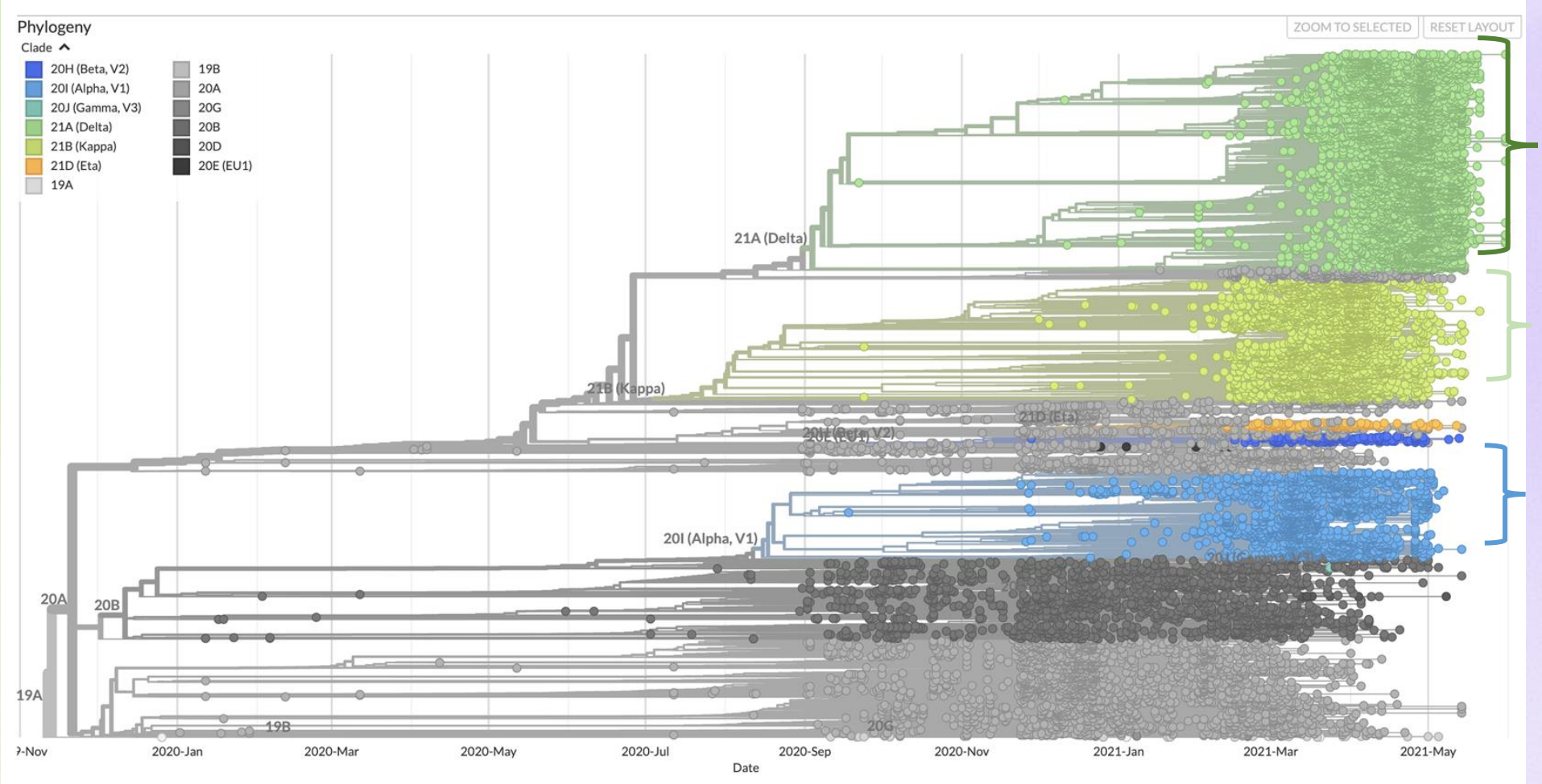


B.1.617 is evolving further into three sub-lineages as it accumulates new mutations in spike and other genes.

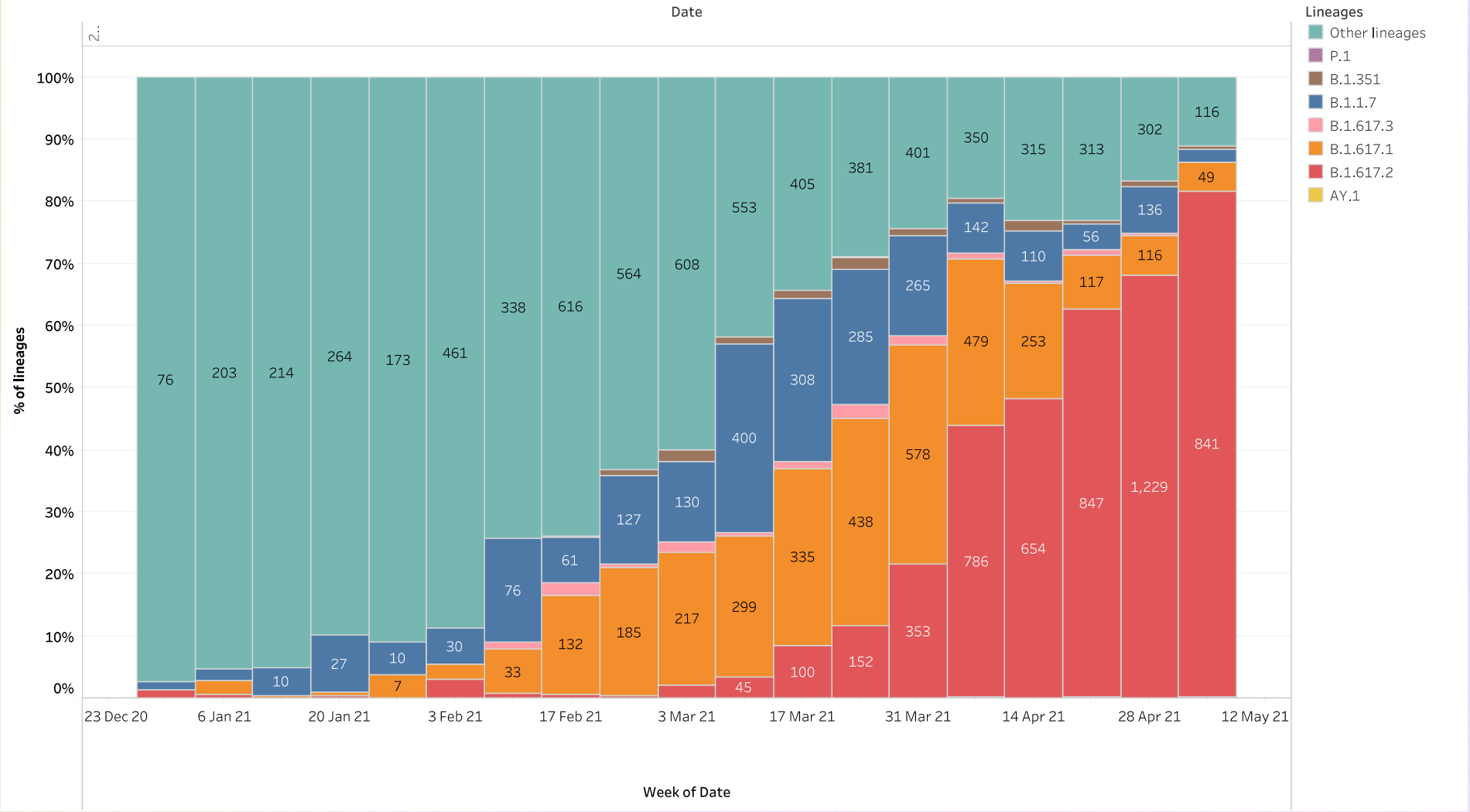
Distribution of major lineages in different states in India

(B.1.617.2 is over-enriched in Indian sequences)

B.1.617 lineage sequences were overrepresented March onwards



Sudden change in the landscape of VOCs in India from Feb-March onwards



Delta + K417N
AY.1 lineage (B.1.617.2.1)

- Characterized by the acquisition of **K417N** genetic variant in the background of Variant of Concern **Delta (B.1.617.2)**
- **Lysine(K) > Asparagine (N)** at 417th amino acid position in the **Spike protein**
- **K417N** is of note, and is also present in the Variant of Concern **Beta (B.1.351)**

B.1.617.2.1 (AY.1)
Spike Protein

Mutations
- D614G
- K417N
- P681R
- T19R
- D950N
- T478K
- L452R

Deletions
- del157/158

- Currently, the variant frequency is **low in India**
- Cases with Delta plus has been mostly reported from **Europe, Asia and America**
- **No functional evidence** of AY.1's role in immune escape, disease severity or increased transmissibility as yet
- Currently only 40 cases in India in 10 different states

Delta + K417N lineage of SARS-CoV-2 (called as AY.1)

- **Delta Plus** is a **variant of interest**, but not a variant of concern as on date
- Characterized by the **Spike K417N** mutation which is otherwise present in the Beta VoC
- K417N corresponds to change of amino acid **lysine (K) to asparagine (N)**
- Delta plus is **resistant to the COVID 19 monoclonal antibody** treatment (like Imdevimab, Casirivimab)[1]

[1] (Shang and Axelsen, Tegally et al. 2020, Wang et al. 2021, Hoffmann et al. 2021, Greaney et al. 2021)