Indian SARS-CoV-2 Genomics Consortium (INSACOG)

- Consortium of 10 National Laboratories
- Jointly established by the MoHFW and DBT in December 2020
- To monitor the genomic variations in the SARS-CoV-2 for genomic, epidemiological and clinical correlation to assist public health response to the pandemic

LIST OF PARTICIPATING INSTITUTIONS OF INSACOG :

1. DBT National Institute of Biomedical Genomics (**NIBMG**), Kalyani
2. National Centre for Disease Control (**NCDC**), **Delhi –**
3. CSIR Institute of Genomics and Integrative Biology (**IGIB**), **Delhi**
4. CSIR Centre for Cellular and Molecular Biology (**CCMB**), **Hyderabad**
5. DBT- Institute of Life Sciences (**ILS**), **Bhubaneshwar**
6. DBT **InSTEM**/**NCBS**, **Bengaluru**
7. DBT-Centre for DNA Fingerprinting and Diagnostics (**CDFD**), **Hyderabad**
8. DBT National Centre for Cell Science (**NCCS**), **Pune**
9. National Institute of Virology (**NIV**), **Pune**
10. National Institute of Mental Health and Neuro Sciences Hospital (**NIMHANS**), **Bengaluru**

STRATEGY

Target Samples

1. International arriving passengers: country scenario, duration stay, infection/ vaccination status, travel details etc.
2. Community samples:
   - States/districts with unusual scenarios: representative samples
   - Sentinel surveillance (as per WHO strategy) : identified sites – labs, hospitals, high transmission / low transmission areas.
3. Re-infection:
   - Repeat infection:
   - Infection post vaccination: single dose, full coverage etc.

SOP

- Sample transportation to RGSLs
- Genome sequencing and identification of
  - VOCs/VOI
  - Potential VOI
  - Other mutations
- Information on VOCs/VOI submission to CSU
- Expert discussion in SAG – on Potential VOI Other mutations and recommendations to CSU
- Sharing of information and clinico-Epidemiological correlation by IDSP (CSU/SSU/DSU)
- Regular sharing of information by IDSP
  - MOH&FW, ICMR, DBT & CSIR.
  - State authorities
- Virus culture, testing for efficacy

IMPLICATIONS OF GENOMIC SURVEILLANCE

Overall: better understanding of

1. Disease epidemiology: Time, place, person and transmission, Ds trends
2. Testingstrategies
3. Clinical:severity

State/district:

1. Understanding of epidemiological scenarios
2. Clinical picture of disease
3. Plan and strengthen preparedness

Others:

1. National and International travel
2. Monitoring of Re-infection:
   Repeat infection:
   Infection post vaccination: single dose, full coverage etc

Variants of Concern (VOCs)

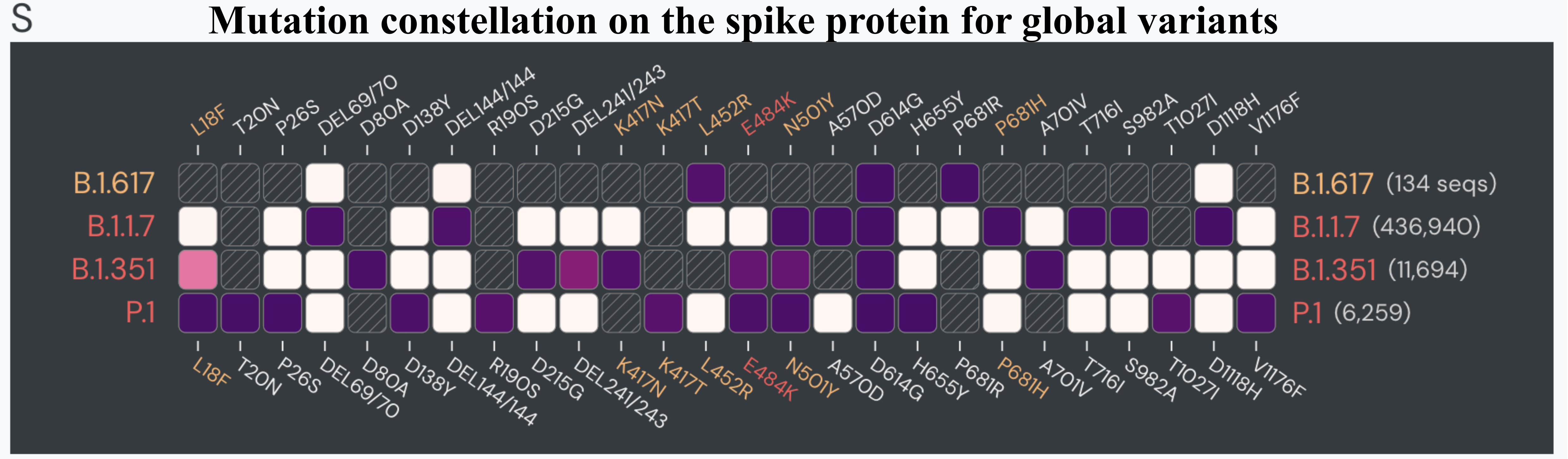
- **B.1.1.7**
  - 50% increased transmission
  - Increased severity
- **B.1.351**
  - 50% increased transmission
  - Reduced antibody neutralization
- **P.1**
  - Reduced neutralization by antibodies
  - Reduced neutralization after vaccination
- **B.1.617**[1,2]
  - Higher transmission rate[2]
  - Reduced susceptibility to neutralization antibodies[2]

Key mutations

- **L452R** increases receptor binding and decreased sensitivity to some neutralizing antibodies
- **E484K/Q** increases receptor binding and may reduce efficacy of vaccinated sera and antibodies
- **L452R+E484Q** unique combination in India
- **N501Y** increases receptor binding and alters antibody recognition
- **N440K** immune evasion; loss of binding to one neutralizing antibody

1. Public Health England, 2021. SARS-CoV-2 variants of concern and variants under investigation in England. (Technical Briefing No. 10). https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/984274/Variants_of_Concern_VOC_Technical_Briefing_10_England.pdf
2. WHO Novel coronavirus Epidemiological Reports. https://www.who.int/publications/m/item/weekly-epidemiological-update-on-covid-19---11-may-2021

Mutation constellation on the spike protein for global variants



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

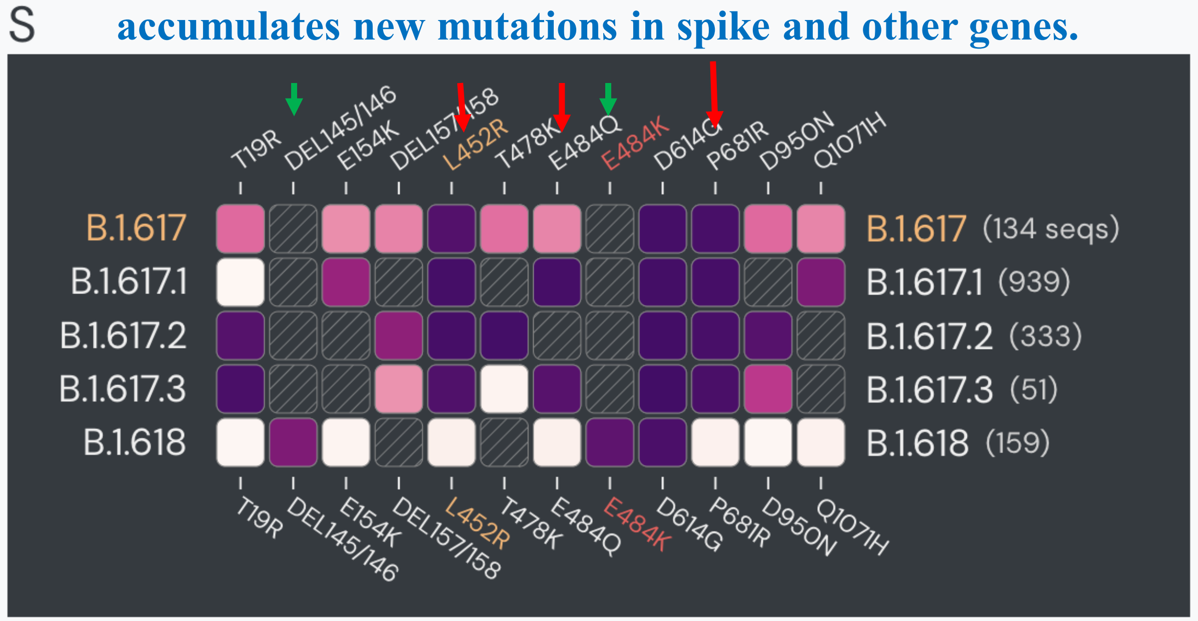
B.1.617 has E484Q (not R)/T478K, L452R and P681R in addition to D614G.

B.1.617.1 has both L452R and E484Q alongwith **P681R**

B.1.617.2 doesn't have E484Q, but T478K along with **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.



State-wise VOCs (28.05.21)

Table 2: Proportion of samples processed positive for VOC in community samples

B.1.617 and sub-lineages

	Community sample sequenced	**Community Sample +ve for B.1.1.7**	**Proportion of Community sample +ve for B.1.1.7**	**Community Sample +ve for B.1.351**	**Proportion of Community Sample +ve for B.1.351**	**Community sample +ve for B.1.617 + sub-lineages**	**Proportion of Community sample +ve for B.1.617+ sub lineages**
ANDAMAN AND NICOBAR ISLAND	0	0	0.0		0.0		0.0
ANDHRA PRADESH	855	42	4.9	4	0.5	404	47.3
ARUNACHAL PRADESH	0	0	0.0		0.0		0.0
ASSAM	0	0	0.0		0.0		0.0
BIHAR	33	5	15.2		0.0	5	15.2
CHANDIGARH UT	124	82	0.0		0.0	11	0.0
CHHATISGARH	562	23	4.1		0.0	114	20.3
DADRA AND NAGAR HAVELI	0	0	0.0		0.0		0.0
DAMAN AND DIU	0	0	0.0		0.0		0.0
DELHI	4201	564	13.4	23	0.5	1458	34.7
GOA	49	2	4.1		0.0	12	24.5
GUJARAT	438	119	27.2	1	0.2	339	77.4
HARYANA	470	14	3.0		0.0	1	0.2
HIMACHAL PRADESH	553	49	8.9	1	0.2	21	3.8
JAMMU AND KASHMIR	689	125	18.1		0.0	52	7.5
JHARKHAND	363	29	8.0		0.0	244	67.2
KARNATAKA	670	69	10.3		0.0	225	33.6
KERALA	21	5	23.8		0.0		0.0
LADAKH	43	5	11.6		0.0	17	39.5
LAKSHADWEEP	0	0	0.0		0.0		0.0
MADHYA PRADESH	846	55	6.5		0.0	109	12.9
MAHARASHTRA	4407	104	2.4	4	0.1	2077	47.1
MANIPUR	0	0	0.0		0.0		0.0
MEGHALAYA	0	0	0.0		0.0		0.0
MIZORAM	69	0	0.0		0.0		0.0
NAGALAND	0	0	0.0		0.0		0.0
ODISHA	903	30	3.3		0.0	251	27.8
PUDUCHERRY	60	0	0.0		0.0	23	38.3
PUNJAB	1189	815	68.5	1	0.1	124	10.4
RAJASTHAN	1010	19	1.9		0.0		0.0
SIKKIM	103	11	10.7		0.0	11	10.7
TAMIL NADU	5	1	20.0		0.0		0.0
TELANGANA	969	69	7.1	11	1.1	453	46.7
TRIPURA	18	5	27.8	1	5.6	9	50.0
UTTAR PRADESH	22	1	4.5		0.0	18	81.8
UTTARAKHAND	469	62	13.2		0.0	249	53.1
WEST BENGAL	2330	86	3.7	14	0.6	630	27.0
INDIA	**21471**	**2391**	**11.1**	**60**	**0.3**	**6857**	**31.9**

SHARING OF PUBLIC HEALTH INFORMATION WITH STATES

- Frequent written communications by Union Health Ministry and NCDC to all States/Uts (Not just to the high burden states) stressing the need for more stringent measures, have been sent at regular intervals.
- States/Uts advised to keep strict surveillance in the districts reporting new Variants of concern and take up stringent public health measures including contact tracing, genome sequencing of positive samples of persons having history of international travel.
- Information on genome sequencing is shared with the States twice in month.
- In VCs with States, Union Health Ministry also informed about the current status of Variants of Concern and new mutants and stressed on increased and stringent public health interventions.

CONCLUSIONS

- The B1.1.7 lineage of SARS CoV-2 is declining in proportion across the Country in the last 1½ months
- The B.1.617 lineage of SARS CoV-2 has been first reported from Maharashtra but now seen in other states like West Bengal, Andhra Pradesh, Delhi, Gujarat, Telangana
- The current surge in cases seen over the last 2 month in some states shows a correlation with the rise in the B1.617 lineage of SARS CoV-2
- B.1.617 lineage is further evolved into three sublineages – B.1.617.1, B.1.617.2 and B.1.617.3
- Early data shows B.1.617.2 has higher transmission advantages over the other two sub-lineages.

Key action being advised to be adopted by States to strengthen public health response in those regions where presence of B.1.617 has been noted

(increased testing, quick isolation, prevent crowds/inter-mingling of people, wearing of masks and vaccinations)