Genome sequencing in Pandemic Response

What is the issue?

- Emerging variants, with evidence of higher transmissibility and immune escape, demand re-strategised responses to COVID-19 pandemic in India.
- Genomic sequencing becomes significant in this context.

How does genome sequencing help?

- [Genome sequencing refers to figuring out the order of DNA nucleotides, or bases, in a genome - the order of As, Cs, Gs, and Ts that make up an organism's DNA.]

- An effective COVID-19 pandemic response includes keeping track of emerging variants.
- There are a total of 10 variants till now including variants of interest and concern.
- Conducting further studies about their transmissibility, immune escape and potential to cause severe disease is essential now.
- Therefore, genomic sequencing becomes one of the first steps in this important process.
- Besides increasing vaccination coverage, the U.S. and UK have scaled up genomic sequencing which went a long way in containing the virus.

What is the case with India?

- India seems to be faltering on both expanding vaccination coverage and genomic sequencing.
- Procedural steps such as setting up the Indian SARS-CoV2 Genomic Consortia, or INSACOG have been taken.
- But the sequencing has remained at a very low level of a few thousand cases only.

What are the measures to be taken?

- **Genomic sequencing** - India needs to scale up genomic sequencing, across all States.
- There should be sufficient and representative samples collected for genomic sequencing.

- This will help track district-level trends in circulating variants.
- A national-level analysis of collated genomic sequencing data should be done on a regular basis.
- And the findings should be shared publicly.
- **Research** - The government must invest and support more scientific and operational research on vaccine effectiveness.
- The data should include various stratifiers such as age, gender and comorbid conditions, etc.
- **Vaccine policy** - There are early indications of immune escape and reduced vaccine effectiveness against the *Delta variant* (especially after one shot).
- So, the policy on population coverage with two shots of vaccine, gap between the doses, priority groups, etc should be reviewed scientifically.

What is the way forward?

- Scientific knowledge and understanding about emerging virus strains is going to be the key to deploy public health interventions.
- In this regard, data from genomic sequencing has both policy and operational implications.
- There is thus a need for -
    1. rapidly expanding genomic sequencing
    2. sharing related data in a timely and transparent manner
    3. understanding of the impact of new variants on transmissibility, severity and vaccine effectiveness
- An assured way to fight the pandemic is to use scientific evidence to decide policies, modify strategies and take corrective actions.

Source: The Hindu

Quick Fact

Delta variant

- The Delta variant was previously known as the “Indian variant”, as it was first found in India.
- It is one of three sub-lineages of the Indian variant, and is also known as B.1.617.2.
- Studies have shown that the Delta variant became the most circulating variant in Delhi.
- The Delta variant is likely to be associated with high viral load.
- It also resulted in a higher proportion of breakthrough infection (people already vaccinated getting infected).

- The Public Health England (PHE) also reported that the Delta variant has become the most common circulating strain in the U.K., replacing Alpha variant (B.1.1.7, first reported from Kent, England in September 2020).
- The PHE also reported that the effectiveness of a single dose of vaccine (amongst symptomatic patients) was lower against the Delta strain.