



Short Communication

Importance Of Genomic Surveillance : Sars-Cov-2

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Viruses are constantly changing, and this includes SARS-CoV-2, the virus that causes COVID-19. These genetic variations occur over time and can lead to the emergence of new variants that may have different characteristics.

The SARS-CoV-2 genome encodes instructions organized into sections, called genes, to build the virus. Scientists use a process called genomic sequencing to decode the genes and learn more about the virus. Genomic sequencing allows scientists to identify SARS-CoV-2 and monitor how it changes over time into new variants, understand how these changes affect the characteristics of the virus, and use this information to better understand how it might impact health.

How do variants occur?

Mutations are changes in the genetic code of a virus that naturally occur over time when an animal or person is infected. While a certain amount of genetic variation is expected to occur as SARS-CoV-2 spreads, it's important to monitor circulating viruses for the key mutation(s) that happen in important regions of the genome. Many mutations do not affect the virus's ability to spread or cause disease because they do not alter the major proteins involved in infection; eventually, these are outcompeted by variants with mutations that are more beneficial for the virus.

Classification of Variants

1. Variant of Interest

A variant with specific genetic markers that have been associated with changes to receptor binding, reduced neutralization by antibodies generated against previous infection or vaccination, reduced efficacy of treatments, potential diagnostic impact, or predicted increase in transmissibility or disease severity.

Possible attributes of a variant of interest:



- Specific genetic markers that are predicted to affect the transmission, diagnostics, therapeutics, or immune escape
- Evidence that it is the cause of an increased proportion of cases or unique outbreak clusters
- Limited prevalence or expansion in India or other countries

A variant of interest might require one or more appropriate public health actions, including enhanced sequence surveillance, enhanced laboratory characterization, or epidemiological investigations to assess how easily the virus spreads to others, the severity of disease, the efficacy of therapeutics, and whether currently authorized vaccines to offer protection.

2. Variant of Concern

A variant for which there is evidence of an increase in transmissibility, more severe disease (e.g., increased hospitalizations or deaths), a significant reduction in neutralization by antibodies generated during previous infection or vaccination, reduced effectiveness of treatments or vaccines, or diagnostic detection failures.

Possible attributes of a variant of concern:

In addition to the possible attributes of a variant of interest

- Evidence of impact on diagnostics, treatments, or vaccines
 - Widespread interference with diagnostic test targets
 - Evidence of substantially decreased susceptibility to one or more class of therapies
 - Evidence of significantly decreased neutralization by antibodies generated during previous infection or vaccination
 - Evidence of reduced vaccine-induced protection from severe disease
- Evidence of increased transmissibility
- Evidence of increased disease severity

Variants of concern might require one or more appropriate public health actions, such as notification to WHO under the International Health Regulations, local or regional efforts to control spread,



increased testing, or research to determine the effectiveness of vaccines and treatments against the variant. Based on the characteristics of the variant, additional considerations may include the development of new diagnostics or the modification of vaccines or treatments.

3. Variant of High Consequence

A variant of high consequence has clear evidence that prevention measures or medical countermeasures (MCMs) have significantly reduced effectiveness relative to previously circulating variants.

Possible attributes of a variant of high consequence:

In addition to the possible attributes of a variant of concern

- Impact on Medical Countermeasures (MCM)
 - Demonstrated failure of diagnostics
 - Evidence to suggest a significant reduction in vaccine effectiveness, a disproportionately high number of vaccine breakthrough cases, or very low vaccine-induced protection against severe disease
 - Significantly reduced susceptibility to multiple Emergency Use Authorization (EUA) or approved therapeutics
 - More severe clinical disease and increased hospitalizations

A variant of high consequence would require notification to WHO under the International Health Regulations, an announcement of strategies to prevent or contain transmission, and recommendations to update treatments and vaccines.

Why is genomic surveillance important for public health?

Routine analysis of genetic sequence data enables to identify and characterize variant viruses—either new ones identified in the India or those already identified abroad—and to investigate how variants impact COVID-19 disease severity and the effectiveness of vaccines and treatment.



Surveillance of emerging variants can help detect variants with:

- Ability to spread more quickly in people
- Ability to cause either milder or more severe disease in people
- Ability to evade detection by specific diagnostic tests

Many commercial nucleic acid amplification tests (NAATs) that use reverse transcription polymerase chain reaction (RT-PCR) have multiple targets to detect the virus, such that even if a mutation impacts one of the targets, the other RT-PCR targets will still work. However, there are some tests that rely on only one target, and mutations may impact their ability to work. We are using public health sequencing data to monitor mutations and their impact on confidential/proprietary diagnostic test designs.

- Decreased susceptibility to medical therapies that employ monoclonal antibodies Such therapy involves specifically designed antibodies that target regions of the virus to block infection. Because these treatments are more specific than natural immune response-generated antibodies, they may be less effective against variants that emerge.
- Ability to evade natural or vaccine-induced immunity Both natural infection with and vaccination against SARS-CoV-2 produce a “polyclonal” antibody response that targets several parts of the spike protein. The virus would need to accumulate significant mutations in the spike protein to evade immunity induced by vaccines or by natural infection.

Among these possibilities, the ability to evade vaccine-induced immunity would be the most concerning. There is no definitive evidence yet that this is occurring, but scientists are closely evaluating this possibility.

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