

Letter to the Editor

SARS-CoV-2 Variants

All viruses constantly change through mutation and become more diverse over time; some variants persist and other disappear. Changes may affect the virus's properties, such as how easily it spreads, the severity of associated disease, or the performance of vaccines, therapeutic medicines, diagnostic tools, and other public health and social measures. The same development occurs with SARS-CoV-2, the coronavirus that causes COVID-19, which is producing genetic variants circulating around the world throughout the ongoing pandemic.

Currently there are six notable variants and six variants of interest of SARS-CoV-2 as follows:

- Alpha variant (B.1.1.7 strain) was initially detected in the United Kingdom in September 2020 and labeled by WHO on December 18, 2020.
- Beta variant (B.1.351 strain) was initially detected in South Africa in May 2020 and labeled by WHO on December 18, 2020.
- Delta variant (B.1.617.2 strain) was initially identified in India in October 2020.
- Gamma variant (P.1 strain) was initially identified in Brazil in November 2020, and in travelers from Brazil who were tested positive at an airport in Japan on January 11, 2021.
- Epsilon variant (B.1.427 and B.1.429 strains) were identified in the United States in March 2020.
- Zeta variant (P.2 strain) was detected in Brazil in April 2020.
- Eta variant (B.1.525 strain) was detected in multiple countries in December 2020.
- Theta variant (P.3 strain) was detected in the Philippines in January 2021.
- Iota variant (B.1.526 strain) was detected in the United States in November 2020.
- Kappa variant (B.1.617.1 strain) was detected in India in October 2020.
- Lambda variant (C.37 strain) was detected in Peru in August 2020.

Genesis of variations

Genetic variants of SARS-CoV-2 basically occur in the nucleobase form of the genetic alphabet, ATCG, which is conserved across all domains of life. Viral mutations and variants are monitored through sequence-based surveillance laboratory studies, and epidemiological investigations.

Laboratory studies revealed that cases of COVID-19 variants with the L452R or E484K substitution in the spike protein, the combination of K417N, E484K, and N501Y, or the combination of K417T, E484K, and N501Y substitutions in the spike protein may be less effectively treated with specific monoclonal antibodies.

- L452R is present in B.1.526.1 (Iota), B.1.427 (Epsilon), and B.1.429 (Epsilon) lineages, as well as the B.1.617 (Kappa, Delta) lineages and sub-lineages.
- E484K is present in B.1.525 (Eta), P.2 (Zeta), P.1 (Gamma), and B.1.351 (beta), but only some strains of B.1.526 (Iota) and B.1.1.7 (Alpha).
- The combination of K417N, E484K, and N501Y substitutions is present in B.1.351 (Beta).
- The combination of K417T, E484K, and N501Y substitutions is present in P.1 (Gamma).

Understanding is needed on whether the current and new variants:

- Spread more easily from person-to-person;
- Cause milder or more severe disease in people;
- Are detected by currently available viral tests;
- Respond to medicines currently being used to treat COVID-19;
- Change the effectiveness of COVID-19 vaccines.

Steps to protect oneself from the coronavirus include:

- Getting a COVID-19 vaccine when it is available;
- Wearing a mask that covers nose and mouth to help protect oneself and others;
- Staying 2 meters apart from others who don't live with you.
- Avoiding crowds and poorly ventilated indoor spaces;
- Wash hands often with soap and water. Use hand sanitizer if soap and water are not available.

Documents using for preparing this note:

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