

## VARIANTS OF COVID-19: WHAT DO WE NEED TO KNOW

О. М. Krekhovska-Lepiavko, В. А. Lokay, Л. М. Lykha

*I. Horbachevsky Ternopil National Medical University*

The article describes the variants of COVID-19 and their classification, which is very important for better understanding and prevention of COVID-19 pandemic. Some variants spread more easily and quickly than other variants, which may lead to more cases of COVID-19. An increase in the number of cases will put more strain on healthcare resources, lead to more hospitalizations, and potentially more deaths. These classifications are based on how easily the variant spreads, how severe the symptoms are, how the variant responds to treatments, and how well vaccines protect against the variant.

## ВАРИАНТИ COVID-19: ЩО НАМ НЕОВХІДНО ЗНАТИ

О. М. Креховська-Лепявко, Б. А. Локай, Л. М. Лиха

*Тернопільський національний медичний університет  
імені І. Я. Горбачевського МОЗ України*

У статті описано варіанти COVID-19 і наведено їх класифікацію, що дуже важливо для кращого розуміння та запобігання пандемії COVID-19. Деякі варіанти поширюються легше та швидше, ніж інші, що може привести до збільшення кількості випадків COVID-19, у результаті чого зросте навантаження на ресурси охорони здоров'я внаслідок підвищення кількості госпіталізацій і, потенційно, смертей. Наведену класифікацію розроблено з урахуванням особливостей поширення кожного з варіантів, ступенів тяжкості симптомів, ефективності лікування та ступенів захисту вакцинації від кожного з варіантів COVID-19.

**Introduction.** The virus that causes COVID-19 is constantly changing, and new variants of the virus are expected to occur. Sometimes new variants emerge and disappear. Other times, new variants persist. Numerous variants of the virus that causes COVID-19 are being tracked in the United States and globally during this pandemic.

### How Variants Work

If you think about a virus like a tree growing and branching out; each branch on the tree is slightly different than the others. By comparing the branches, scientists can label them according to the differences. These small differences, or variants, have been studied and identified since the beginning of the pandemic.

Some variations allow the virus to spread more easily or make it resistant to treatments or vaccines. Those variants must be monitored more carefully.

### How Variants Change

As the virus spreads, it has new opportunities to change and may become more difficult to stop. These changes can be monitored by comparing differences in physical traits (such as resistance to treatment) or changes in genetic code (mutations) from one variant to another.

### What We Are Doing

By studying each variant and understanding these differences, scientists can monitor, and often predict, whether a variant is more dangerous than others. Scientists can also use this information to track the spread of a variant [1].

**The main part.** Nowadays, scientists monitor all variants but may classify certain ones as

- variants being monitored,
- variants of interest,
- variants of concern and
- variants of high consequence.

Some variants spread more easily and quickly than other variants, which may lead to more cases of

COVID-19. An increase in the number of cases will put more strain on healthcare resources, lead to more hospitalizations, and potentially more deaths.

These classifications are based on how easily the variant spreads, how severe the symptoms are, how the variant responds to treatments, and how well vaccines protect against the variant.

Viruses like SARS-CoV-2 continuously evolve as changes in the genetic code (genetic mutations) occur during replication of the genome. A lineage is a genetically closely related group of virus variants derived from a common ancestor. A variant has one or more mutations that differentiate it from other variants of the SARS-CoV-2 viruses. As expected, multiple variants of SARS-CoV-2 have been documented in the United States and globally throughout this pandemic. To inform local outbreak investigations and understand national trends, scientists compare genetic differences between viruses to identify variants and how they are related to each other.

- Genetic lineages of SARS-CoV-2 have been emerging and circulating around the world since the beginning of the COVID-19 pandemic.

- SARS-CoV-2 genetic lineages in the United States are routinely monitored through epidemiological investigations, virus genetic sequence-based surveillance, and laboratory studies.

- On November 30, 2021, the U.S. government SARS-CoV-2 Interagency Group (SIG) classified Omicron as a Variant of Concern (VOC). This classification was based on the following:

- Detection of cases attributed to Omicron in multiple countries, including among those without travel history.

- Transmission and replacement of the Delta variant in South Africa.

- The number and locations of substitutions in the spike protein.

- Available data for other variants with fewer substitutions in the spike protein that indicate a reduction in neutralization by sera from vaccinated or convalescent individuals.

- Available data for other variants with fewer substitutions in the spike protein that indicate reduced susceptibility to certain monoclonal antibody treatments.

- The SIG Variant classification scheme defines four classes of SARS-CoV-2 variants:

- Variant Being Monitored (VBM)

- Alpha (B.1.1.7 and Q lineages)
- Beta (B.1.351 and descendant lineages)
- Gamma (P.1 and descendant lineages)
- Epsilon (B.1.427 and B.1.429)
- Eta (B.1.525)
- Iota (B.1.526)
- Kappa (B.1.617.1)
- 1.617.3
- Mu (B.1.621, B.1.621.1)
- Zeta (P.2)
- Variant of Interest (VOI)
- Variant of Concern (VOC)
- Delta (B.1.617.2 and AY lineages)
- Omicron (B.1.1.529 and BA lineages)
- Variant of High Consequence (VOHC)
- To date, no variants of high consequence have been identified.

Vaccines approved and authorized for use in the United States are effective against the predominant variant circulating in the United States and effective therapeutics are available. CDC continues to monitor all variants circulating within the United States [2].

The U.S. Department of Health and Human Services (HHS) established a SARS-CoV-2 Interagency Group (SIG) to enhance coordination among CDC, National Institutes of Health (NIH), Food and Drug Administration (FDA), Biomedical Advanced Research and Development Authority (BARDA), and Department of Defense (DoD). This interagency group is focused on the rapid characterization of emerging variants and actively monitors their potential impact on critical SARS-CoV-2 countermeasures, including vaccines, therapeutics, and diagnostics.

The SIG meets regularly to evaluate the risk posed by SARS-CoV-2 variants circulating in the United States and to make recommendations about the classification of variants. This evaluation is undertaken by a group of subject matter experts who assess available data, including variant proportions at the national and regional levels and the potential or known impact of the constellation of mutations on the effectiveness of medical countermeasures, severity of disease, and ability to spread from person to person. Given the continuous evolution of SARS-CoV-2 and our understanding of the impact of variants on public health, variants may be reclassified based on their attributes and prevalence in the United States.

- Variants being monitored (VBM)- View current VBM in the United States that continue to be monitored and characterized by federal agencies

- Variant of interest (VOI)– Currently, no SARS-CoV-2 variants are designated as VOI
- Variant of Concern (VOC)– View current VOC in the United States that are being closely monitored and characterized by federal agencies
- Variant of high consequence (VOHC)– Currently, no SARS-CoV-2 variants are designated as VOHC [3].

**Notes:** Each variant classification includes the possible attributes of lower classes (for example, VOC includes the possible attributes of VOI); variant status might escalate or deescalate based on emerging scientific evidence. This page will be updated as needed to show the variants that belong to each class. The World Health Organization (WHO) external icon also classifies variant viruses as variants of concern and variants of interest; U.S. classifications may differ from those of WHO because the impact of variants may differ by location. To assist with public discussions of variants, WHO proposed using labels consisting of the Greek alphabet (for example, alpha, beta, gamma) as a practical way to discuss variants for non-scientific audiences. The labels assigned to each variant are provided in the tables below.

#### *Variants Being Monitored (VBM)*

CDC monitors all variants circulating in the United States. Variants designated as VBM include those where data indicates there is a potential or clear impact on approved or authorized medical countermeasures or that have been associated with more severe disease or increased transmission but are no longer detected, or are circulating at very low levels, in the United States. These variants do not pose a significant and imminent risk to public health in the United States.

A Variant of Interest or a Variant of Concern may be downgraded to this list after a significant and sustained reduction in its national and regional proportions over time, or other evidence indicates that a variant does not pose significant risk to public health in the United States [4].

These variants continue to be closely monitored to identify changes in their proportions and new data are continually being analyzed. If the data indicate that a VBM warrants more concern, the classification will be changed based on the SIG assessment of the attributes of the variant and the risk to public health in the United States.

**Table. Variants Being Monitored**

WHO Label	Pango Lineage	Date of Designation		
Alpha	B.1.1.7 and Q lineages	VOC: December 29, 2020		VBM: September 21, 2021
Beta	B.1.351 and descendant lineages	VOC: December 29, 2020		VBM: September 21, 2021
Gamma	P.1 and descendant lineages	VOC: December 29, 2020		VBM: September 21, 2021
Epsilon	B.1.427 B.1.429	VOC: March 19, 2021	VOI: February 26, 2021 VOI: June 29, 2021	VBM: September 21, 2021
Eta	B.1.525		VOI: February 26, 2021	VBM: September 21, 2021
Iota	B.1.526		VOI: February 26, 2021	VBM: September 21, 2021
Kappa	B.1.617.1		VOI: May 7, 2021	VBM: September 21, 2021
N/A	B.1.617.3		VOI: May 7, 2021	VBM: September 21, 2021
Zeta	P.2		VOI: February 26, 2021	VBM: September 21, 2021
Mu	B.1.621, B.1.621.1			VBM: September 21, 2021

#### *Variant of Interest (VOI)*

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 [5].

Possible attributes of a Variant of Interest:

- Specific genetic markers that are predicted to affect 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 the US or in 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 approved or authorized vaccines offer protection.

Currently, no SARS-CoV-2 variants are designated as VOI.

#### *Variant of Concern (VOC)*

A variant for which there is evidence of an increase in transmissibility, more severe disease (for example, increased hospitalizations or deaths), significant reduction in neutralization by antibodies generated during previous infection or vaccination, reduced effectiveness of treatments or vaccines, or diagnostic detection failures [6].

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, reporting to CDC, 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.

Current variants of concern in the United States that are being closely monitored and characterized are listed below. This table will be updated when a new variant of concern is identified.

#### *Variants of Concern*

##### **Omicron - B.1.1.529**

**First identified:** South Africa

**Spread:** May spread more easily than other variants, including Delta.

**Severe illness and death:** Due to the small number of cases, the current severity of illness and death associated with this variant is unclear.

**Vaccine:** Breakthrough infections in people who are fully vaccinated are expected, but vaccines are effective at preventing severe illness, hospitalizations, and death. Early evidence suggests that fully vaccinated people who become infected with the Omicron variant can spread the virus to others. All FDA-approved or authorized vaccines are expected to be effective against severe illness, hospitalizations, and deaths. The recent emergence of the Omicron variant further emphasizes the importance of vaccination and boosters.

**Treatments:** Some monoclonal antibody treatments may not be as effective against infection with Omicron.

##### **Delta - B.1.617.2**

**First identified:** India

**Spread:** Spreads more easily than other variants.

**Severe illness and death:** May cause more severe cases than the other variants

**Vaccine:** Breakthrough infections in people who are fully vaccinated are expected, but vaccines are effective at preventing severe illness, hospitalizations, and death. Early evidence suggests that fully vaccinated people who become infected with the Delta variant can spread the virus to others. All FDA-approved or authorized vaccines are effective against severe illness, hospitalization, and death.

**Treatments:** Nearly all variants circulating in the United States respond to treatment with FDA-authorized monoclonal antibody treatments [7].

**Conclusions.** There are many variants of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the virus that causes coronavirus disease 2019 (COVID-19). Some are believed, or have been stated, to be of particular importance due to their potential for increased transmissibility, increased virulence, or reduced effectiveness of vaccines against them. These variants contribute to the continuation of the COVID-19 pandemic.

**Recommendations.** Important Ways to Slow the Spread of COVID-19

Get a COVID-19 vaccine as soon as you can. Find a vaccine.

Wear a mask that covers your nose and mouth to help protect yourself and others.

Stay 6 feet apart from others who don't live with you.

Avoid crowds and poorly ventilated indoor spaces.

Test to prevent spread to others.

Wash your hands often with soap and water. Use hand sanitizer if soap and water aren't available.

## LIST OF LITERATURE

1. <https://www.cdc.gov/coronavirus/2019-ncov/variants/understanding-variants.html>
2. <https://www.cdc.gov/coronavirus/2019-ncov/variants/about-variants.html>
3. [https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-classifications.html#anchor\\_1632150752495](https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-classifications.html#anchor_1632150752495)
4. Mutation Signatures and In Silico Docking of Novel SARS-CoV-2 Variants of Concern / N. Shahhosseini, G. G. Babuadze, G. Wong, G. P. Kobinger // Microorganisms. – 2021. – Vol. 9, No. 5. – P. 926. doi:10.3390/microorganisms9050926. PMC 8146828. PMID 33925854. S2CID 233460887.
5. Coronavirus variants and mutations: The science explained. BBC News. 6 January 2021. Archived from the original on 22 February 2021. Retrieved 2 February 2021.
6. Kupferschmidt K. New coronavirus variants could cause more reinfections, require updated vaccines / K. Kupferschmidt // Science. – 2021. doi:10.1126/science. abg6028. S2CID 234141081. Archived from the original on 22 February 2021. Retrieved 2 February 2021.
7. SARS-CoV-2 spillover transmission due to recombination event / N. Shahhosseini, G. Wong, G. P. Kobinger, S. Chinikar // Gene Reports. –2021.– No. 23. – P. 101045. doi:10.1016/j.genrep.2021.101045. PMC 7884226. PMID 33615041.

Received 07.02.22