PHD COVID-19 Variant Information

July 2021

Background Information

- All viruses are unable to live on their own. They survive by infecting a new host that is able to be infected. After a new host is exposed to a virus, the virus infects the host's cells. Once inside the host cells, the virus hijacks the cell machinery to produce more copies of the virus. This process of making new copies of a virus within a host cell is called viral replication. o During replication, mistakes can be made that cause the new copies of the virus to not be exact copies of the "parent" virus. These mistakes are called mutations. Mutations happen all the time and usually don't result in big changes to the virus.
- Sometimes new variants emerge through mutation and then disappear. Other times, new variants can emerge and start infecting people.
- Genetic variants of SARS-CoV-2 have been emerging and circulating around the world throughout the COVID-19 pandemic.
- Scientists monitor for genetic changes in the virus, including changes that could alter the spike proteins on the surface of the virus. This helps us better understand how the virus is changing and if these changes might affect how the virus spreads, the degree of illness experienced by people infected with the virus, the ability of available diagnostic tests to detect the virus, and the effectiveness of available vaccines and therapies.

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Variant Labeling System

- On May 31, 2021, WHO assigned simple, easy to say and remember labels for key variants of SARS-CoV-2, the virus that causes COVID-19, using letters of the Greek alphabet (i.e., Alpha, Beta, Gamma, etc.).
  - These labels were chosen after wide consultation and a review of many potential naming systems. WHO will assign labels for those variants that are designated as Variants of Interest or Variants of Concern by WHO. These will be posted on the WHO website.
  - These labels do not replace existing scientific names which convey important scientific information and will continue to be used in research.
    - While they have their advantages, the scientific names can be difficult to say and recall, and are prone to misreporting. As a result, people often resort to calling variants by the places where they are detected, which is stigmatizing and discriminatory. To avoid this and to simplify public communications, WHO encourages national authorities, media outlets and others to adopt these new labels.
- In June 2021, WHO announced a new variant of interest called lambda (C.37). This is the newest variant that scientists are monitoring. The lambda variant was first detected in Peru in December 2020. As of this writing, CDC has not classified this variant as a variant of interest or a variant of concern for the U.S.

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Variant of Interest

Variants of interest show some evidence that they might be of concern.

A variant of interest is 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.

There are currently seven variants of interest in the United States that are being monitored. These are B.1.427 and B.1.429 (Epsilon), B.1.525 (Eta), B.1.526 (Iota), B.1.617.1 (Kappa), B.1.617.3 (no WHO label), and P.2 (Zeta).

Variant of Concern

Variants of concern show evidence of being concerning. These are being closely monitored and characterized by federal agencies and are discussed in more detail below.

A variant of concern is a variant for which there is evidence of an increase in transmissibility, more severe disease (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.

There are currently four variants of concern in the United States that are being closely monitored and characterized by federal agencies. These are B.1.1.7 (Alpha), B.1.351 (Beta), P.1 (Gamma), and B.1.617.2 (Delta).

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Variants of Concern

B.1.1.7 (Alpha)

First identified in the United Kingdom in the fall of 2020.

This variant spreads more easily and quickly than other variants. The transmissibility rate is estimated to be about 50% greater than the transmissibility rate of previous variants.

There is some evidence that B.1.1.7 (Alpha) might be associated with an increased risk of hospitalization and death compared with previous variants.

The absolute risk of death per infection remains low. This variant shows minimal impact on virus neutralization by available monoclonal antibody therapeutics with emergency use authorization (EUA).

Available diagnostic tests for COVID-19 will recognize this variant.

S-gene target failure, where one genetic target for SARS-CoV-2 reads negative but the other gene targets show a positive result, has been associated with B.1.1.7 (Alpha). As most diagnostic tests look for more than one genetic target, this is considered to have a minimal impact on the ability of available diagnostic tests to detect SARS-CoV-2.

This variant has since been detected in many countries around the world. B.1.1.7 (Alpha) was first announced in the United States at the end of December 2020 and in Virginia on January 25, 2021.

Between April-June 2021, B.1.1.7 (Alpha) was the most common variant circulating in the U.S.

B.1.351 (Beta)

First identified in South Africa in early October 2020.

B.1.351 (Beta) shares some of the same mutations with B.1.1.7 (Alpha), but emerged independently of B.1.1.7 (Alpha).

This variant spreads more easily and quickly than other variants. The transmissibility rate is estimated to be about 50% greater than the transmissibility rate of previous variants.

Currently, there is no evidence that B.1.351 (Beta) causes more serious illness, but this is something that is being closely monitored.

Some studies suggest that antibodies generated through vaccination with currently authorized vaccines and through natural infection might provide reduced protection against B.1.351 (Beta). This is something that is being closely monitored.

This variant shows a moderately decreased impact on virus neutralization by some, but not all, available monoclonal antibody therapeutics with EUA.

Available diagnostic tests for COVID-19 will recognize this variant.

Infections caused by this variant were reported in the United States at the end of January 2021. The first case of B.1.351 (Beta) in Virginia was announced on February 5, 2021.

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Variants of Concern

P.1 (Gamma)

In Brazil, a variant called P.1 (Gamma) emerged that was first identified in travelers from Brazil, who were tested during routine screening at an airport in Japan, in early January.

This variant might spread more easily and quickly than other variants. More studies are needed to determine the transmissibility rate.

Currently, there is no evidence that P.1 (Gamma) causes more serious illness, but this is something that is being closely monitored.

Some studies suggest that antibodies generated through vaccination with currently authorized vaccines and through natural infection might provide reduced protection against P.1 (Gamma). This is something that is being closely monitored.

This variant shows a moderately decreased impact on virus neutralization by some, but not all, available monoclonal antibody therapeutics with EUA.

Available diagnostic tests for COVID-19 will recognize this variant.

This variant was first detected in the United States at the end of January 2021. The first cases of P.1 (Gamma) in Virginia were announced on April 16, 2021.

B.1.617.2 (Delta)

First identified in India December 2020.

This variant spreads more easily and quickly than other variants. The transmissibility rate is thought to be about 40-60% greater than B.1.1.7 (Alpha). More studies are needed to determine the transmissibility rate.

Early evidence suggests that B.1.617.2 (Delta) might cause more serious illness; this is something that is being closely monitored.

There is a possibility that antibodies generated through vaccination with currently authorized vaccines and through natural infection might provide reduced protection against B.1.617.2 (Delta). This is something that is being closely monitored.

This variant could have a decreased impact on virus neutralization by some, but not all, available monoclonal antibody therapeutics with EUA.

Available diagnostic tests for COVID-19 will recognize this variant.

This variant was first detected in the United States in March 2021. The first cases of B.1.617.2 (Delta) in Virginia were announced on June 18, 2021. According to new estimates released by CDC on July 6, 2021, B.1.617.2 (Delta) became the most commonly sequenced variant of SARS-CoV-2 in the U.S. during June 20–July 3.

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Variants of Concern in Portsmouth

Health District	Alpha (B.1.1.7)	Beta (B.1.351)	Gamma (P.1)	Delta (B.1.617.2)
Portsmouth	47 (65.3%)	12 (16.7%)	5 (6.9%)	8 (11.1%)

This data is accurate as of 7/30/2021 and shows which VOCs have been identified in Portsmouth with percentage breakdown. Percentage is from the total of VOCs identified, not from total case count.

Data pulled from VDH's Variants of Concern dashboard

What is PHD's Process?

PHD specifically wants to look at variants when it comes to vaccine breakthrough cases

- When a breakthrough case is identified, the Epi team starts the process of genetic sequencing to determine if the case has been infected with a variant
- In order to verify breakthrough status, we must have proof of vaccination status (Either in VIIS or from the case's vaccine card)
- Specimens can either be sent from where the case was originally tested or new specimens can be collected at PHD to be sent to DCLS for sequencing
- Central Office then will send an email us with any variant results and it is uploaded into VEDSS under the investigation

Vaccine Breakthrough Cases

From June 1, 2021 through July 29, 2021 in Portsmouth we had 24 vaccine breakthrough cases identified

Percentage died from illness

Yes – 0.00%

No – 100%

Unk – 0.00%

Percentage hospitalized

Yes – 12.50%

No – 83.33%

Unk – 4.17%

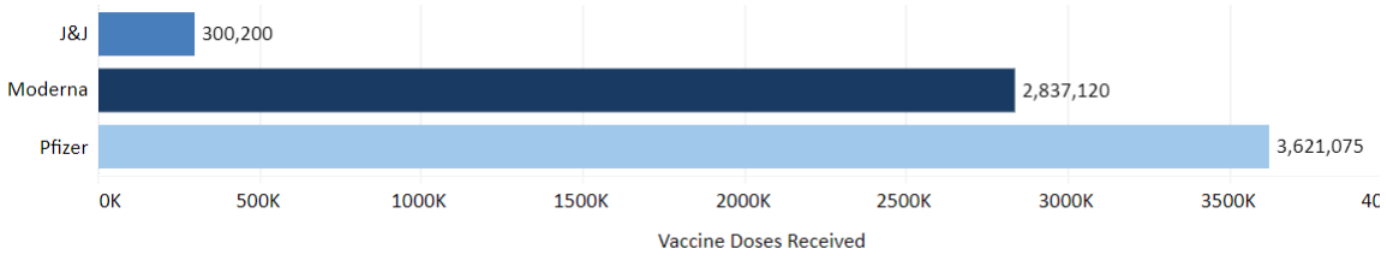
Vaccine receive

Pfizer – 66.66%

Moderna – 16.66%

J&J – 16.66%

Note: The vaccine percentage does not necessarily speak to each vaccine's effectiveness. To date, more Pfizer vaccines have been administered throughout Virginia than any other dose, giving it a higher chance of being associated with a breakthrough case.



For More Information

From the CDC:

-Scientific brief: SARS-CoV-2 Variant Classifications and Definitions
-Scientific brief: Genomic Surveillance for SARS-CoV-2 Variants
-Scientific brief: Emerging SARS-CoV-2 Variants
-Data: Variant Proportions in the U.S.
-Consumer web page: New Variant of Virus that Causes COVID-19 Detected
-Consumer web page: Requirement for Proof of Negative COVID-19 Test Required for Passengers Arriving from the UK
-Consumer web page: Requirement for Proof of Negative COVID-19 Test or Recovery from COVID-19 for All Air Passengers Arriving in the United States

From VDH:

-COVID-19 Variants webpage for the public
-COVID-19 Variants of Concern data dashboard
-COVID-19 Testing and Laboratory webpage for healthcare providers
-COVID-19 Therapeutics webpage for healthcare providers

For more information on DCLS and its use of next-generation sequencing, visit dgs.virginia.gov/dcls