Update:
SARS-CoV-2 Variants of Concern

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Overview

• New scientific knowledge of variants
  • Variant classification scheme
  • Risks posed by variants of concern

• Update on variants in Virginia
A U.S. government interagency group developed a Variant Classification Scheme that defines three classes of SARS-CoV-2 variants:

- Variants of Interest
- Variants of Concern
- Variants of High Consequence
Variants of Interest

- A variant with genetic markers that have been associated with:
  - Changes to the way the virus attaches to host cells,
  - Reduced immune protection after vaccination or previous infection,
  - Reduced efficacy of antibody treatments,
  - Potential impact on the ability of diagnostic tests to detect the virus,
  - Predicted increase in transmissibility or disease severity.

- Four variants of interest: B.1.526, B.1.526.1, B.1.529, P.2
Variants of Concern

- A variant for which there is evidence of:
  - Increased transmissibility,
  - More severe disease,
  - Reduced immune protection after vaccination or previous infection,
  - Reduced efficacy of antibody treatments, or
  - Diagnostic detection failures.

- Five variants of concern: B.1.1.7, B.1.351, P.1, B.1.427/B.1.429
B.1.1.7

• First identified in the U.K. in November 2020

• This variant spreads more easily and quickly (about 50% more transmissible) than other variants

• Some evidence that B.1.1.7 is associated with an increased risk of hospitalization and death compared with previous variants
  • Absolute risk of death per infection remains low

• This has now become the dominant strain in the U.S.
B.1.351

• First identified in South Africa in October 2020

• This variant spreads more easily and quickly (about 50% more transmissible) than other variants

• Some studies suggest that antibodies generated through vaccination and natural infection might provide reduced protection against B.1.351

• To date, there is no evidence that this variant causes more serious illness
P.1

• First identified in travelers from Brazil who arrived in Japan in January 2021

• This variant spreads more easily and quickly than other variants (transmissibility rate not determined)

• Some studies suggest that antibodies generated through vaccination and natural infection might provide reduced protection against P.1

• To date, there is no evidence that this variant causes more serious illness
B.1.427 / B.1.429

- First identified in California and closely related to one another

- **Spread more easily and quickly (about 20% more transmissible)** than other variants

- Preliminary data show that these variants might be associated with an increased risk for serious illness

- Detected in nearly every state in the U.S. Given the national prevalence of these variants, B.1.427 and B.1.429 are **not** reportable to CDC
Variants of High Consequence

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

• Currently there are no SARS-CoV-2 variants that rise to the level of high consequence
Variants in Virginia

- New VDH Variant Dashboard available at:
- Updated weekly on Fridays
Based on representative CDC sequence data collected over a 4-week period ending 4/10/21

Proportions of variants do not represent the total number that may be circulating

- B.1.1.7 = 53.3%
- B.1.351 = 2.3%
- P.1 = 0.5%
- B.1.427/B.1.429 = 6.0%
- Other lineages = 37.9%
Variant Resources

- VDH: Variant Webpage (new)
- VDH: Variant Dashboard (new)
- CDC: SARS-CoV-2 Variant Classifications and Definitions (new)
- CDC: Variant Proportions in the U.S. (new)
Additional CDC Resources

• CDC Consumer web page: [About Variants of the Virus that Causes COVID-19](#)

• CDC Scientific brief: [Genomic Surveillance for SARS-CoV-2 Variants](#)

• CDC Scientific brief: [Emerging SARS-CoV-2 Variants](#)

• 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](#)
Questions?