

Anticipatory Talking Points

What to say when the US discovers the first domestic case of the new variant first identified in the UK

For reference, the new variant first identified in the UK is referred to using the following nomenclature:

- VOC 202012/01: Name assigned by Public Health England indicating the 1st “Variant of Concern” from December 2020.
- This variant also has been referred to as B.1.1.7 and as 20B/501Y.V1.

Framing Messages (should be stated upfront and frequently throughout when using these TPs)

- We are early in our efforts to understand this new variant and are sharing what we know at this time. What we know is based on the evidence we have now and may change as new data emerges. We will continue to provide updates as we learn more.
- Viruses constantly change through mutation, and new variants of a virus are expected to occur over time. Multiple variants of the virus that causes COVID-19 have been documented in the United States and globally during this pandemic.
 - Most variants do not change how the virus behaves and many disappear.
 - At this time, we have no evidence that infections by this variant cause more severe disease.
- CDC’s recommendations for slowing the spread—wearing masks, staying at least 6 feet apart from others, avoiding crowds, ventilating indoor spaces, and washing hands often—will also prevent the spread of this variant.

New Variant First Identified in UK

- Rapid spread of this new variant was recognized in the UK in mid-December 2020. At that time, public health experts cautioned that the virus was likely already in the United States.
 - This likelihood was due to the high prevalence of the variant in London and southeast England, the frequency of travel between the two countries, and the fact that the variant was already known to have been detected in other countries.
- In addition to the reported case in Colorado, it is likely that we will find additional cases in the United States in the coming days.
- Public health experts are working to better understand the potential impact of this variant, including how the variant spreads (the epidemiologic impact) and how it affects people who are infected with it (the clinical impact).
- We are early in our efforts to understand this new variant, but here is what we know at this time. What we know is based on the evidence we have now and may change as we learn more and new data emerges.
 - Based on analysis of the variant’s genome and the tracking of cases associated with it, the variant may spread more easily and quickly than previous strains. This could increase the overall spread of SARS-CoV-2.
 - The R_0 has been estimated at 1.4 to 1.7 times that of its predecessor.
 - The R_0 is the number of people, on average, that one infected person will infect. The estimate indicates a person infected with this variant could (on

average) infect more people than someone with other strains of SARS-CoV-2 that we've studied.

- The variant does not appear to cause more severe disease or death than the previous circulating strain. However, a higher rate of transmission could lead to more cases, which would increase the number of people overall who need clinical care.
- We are taking public health measures to prevent the spread of the new variant.
 - We continue to emphasize the importance of wearing a mask, staying at least 6 feet apart from others, avoiding crowds, ventilating indoor spaces, and washing hands frequently. These are our best tools for preventing the spread of this virus, no matter the strain.
 - If this variant is more easily spread, vigilance in following these prevention steps will be critical to slow its spread. We also may need to achieve higher vaccination coverage when vaccine is widely available.
- We are watching closely the impact of this variant on several dynamics of this pandemic.
 - *Impact on immunity:* Based on studies with other viruses containing similar mutations, experts believe that immunity to this virus from either natural infection or from vaccination will be effective against this strain. Studies are pending to assess whether the immune response to infection with other variants or current vaccines will work as effectively with this strain.
 - *Impact on diagnostic tests:* CDC, together with FDA, is evaluating diagnostic test performance against the variant. Diagnostic tests detect current infections with the virus. We expect that all currently available diagnostic tests will detect the variant.
 - One commonly used test (ThermoFisher TaqPath assay) gives a characteristic pattern (“S-target dropout”) when detecting this variant in a specimen. This result does not adversely affect the performance of the test.
 - *Impact on monoclonal antibody treatment:* In theory, mutations in this virus might render some monoclonal antibodies less effective. However, there is no evidence yet that this is the case.
 - *Impact on vaccines:* As noted above, experts anticipate little or no impact, although testing to confirm this is still pending.
- CDC continues to track the emergence of new variants and their potential impact on the pandemic.
 - CDC has been doing SARS-CoV-2 Strain Surveillance to build a collection of virus specimens and sequences to support public health response. Routine analysis of these available genetic sequence data enables a targeted approach to identify variant viruses for further characterization.
 - CDC, public health agencies, and researchers throughout the United States have already sequenced over 50,000 SARS-CoV-2 viruses in the United States.
 - CDC is working with public health agencies and industry partners to scale this effort up to further sequence thousands of viruses every week that are submitted to state public health laboratories and commercial diagnostic agencies, which represents a substantial increase over current efforts.
 - These data are anonymized and made publicly available to help public health agencies, researchers, and industry.

- CDC has also been leading a consortium (SPHERES) of over 160 public and private organizations that are sequencing SARS-CoV-2 or analyzing data from the US.

General information about viral mutation

- Virus mutation is common. Viruses mutate when small errors in the genetic code are introduced randomly as the virus multiplies.
- SARS-CoV-2 mutates regularly, acquiring about one new mutation in its genome every two weeks. Many mutations cause no change in the structure or function of the virus's proteins. Other mutations may change an amino acid that alters the structure or function of the protein.
- Mutations can emerge and disappear quickly. Some mutations can emerge that help a virus spread more easily, cause infection to be more or less severe, or lead to resistance to treatments or vaccines.
- CDC and other public health agencies monitor viruses that threaten human health to identify and understand mutations of concern.

Anticipatory Talking Points

What to say when the US discovers the first domestic case of the new variant that first emerged in South Africa

For reference, the South Africa variant is referred to using the following nomenclature:

- 20B/501Y.V2: Name assigned by the South African investigators.
- This variant also has been referred to as B.1.351.

Framing Messages (should be stated upfront and frequently throughout when using these TPs)

- We are early in our efforts to understand this new variant and are sharing what we know at this time. What we know is based on the evidence we have now and may change as new data emerges. We will continue to provide updates as we learn more.
- Viruses constantly change through mutation, and new variants of a virus are expected to occur over time. Multiple variants of the virus that causes COVID-19 have been documented in the United States and globally during this pandemic.
 - Most variants do not change how the virus behaves and many disappear.
 - At this time, we have no evidence that infections by this variant cause more severe disease.
- CDC's recommendations for slowing the spread—wearing masks, staying at least 6 feet apart from others, avoiding crowds, ventilating indoor spaces, and washing hands often—will also prevent the spread of this variant.

New Variant that First Emerged in South Africa

- Much less is known about the new variant that first emerged in South Africa (B.1.351) at this time.
- Like the new variant first identified in the UK, preliminary data suggests that it may spread more easily and quickly than other variants. It has quickly become the predominant variant in parts of South Africa.
- This new variant emerged in South Africa independently from the new variant first identified in the UK and is from a completely different lineage. Although both variants share the same mutation in the spike protein, the two variants also have several different mutations.
- We have much less data about how this variant is spreading. We do not yet know if the severity of disease this variant causes is clinically different from other SARS-CoV-2 strains. Most experts believe it is likely to cause similar disease, with severity not being much greater or much less than we are seeing now.
 - We will continue to provide updates as we learn more about this new variant and our guidance may change as we better understand it.
- We are taking public health measures to prevent the spread of the new variant.
 - We continue to emphasize the importance of wearing a mask, staying at least 6 feet apart from others, avoiding crowds, ventilating indoor spaces, and washing hands frequently. These are our best tools for preventing the spread of this virus, no matter the strain.
 - If this variant is more easily spread, vigilance in following these prevention steps will be critical to slow its spread. We also may need to achieve higher vaccination coverage when vaccine is widely available.

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