REPORT TO THE BOARDS OF HEALTH

Jennifer Morse, MD, MPH, FAAFP, Medical Director

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Central Michigan District Health Department, Wednesday, January 27, 2021
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Variant Strains of SARS-CoV-2

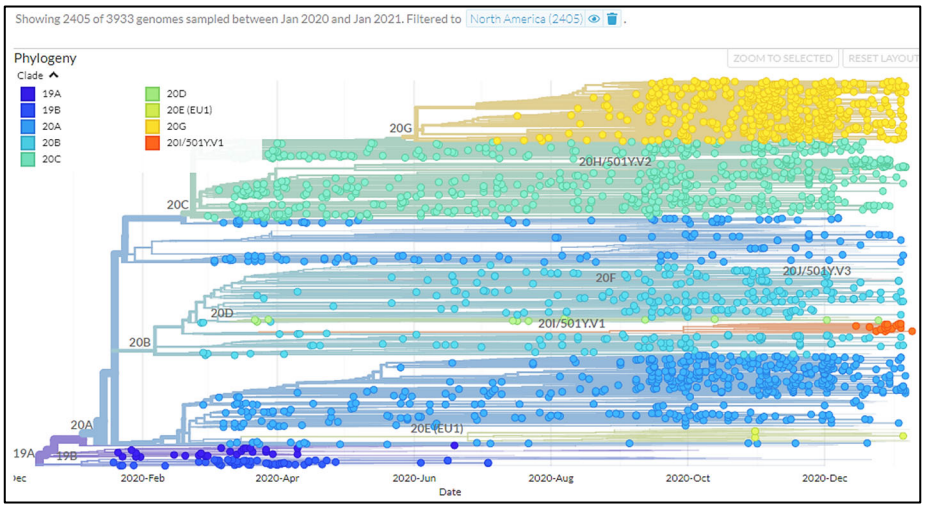
Mutations are changes in the genetic material, or genes, of cells and organisms. It is normal for all viruses to change through mutations, whether their genes are made of DNA or RNA. These changes are usually mistakes made as the virus reproduces or replicates itself in our cells. Some mutations will be very small and will make little, if any, difference in how the virus behaves. Some changes will have a bigger impact or there may be more changes at one time. They may affect how the virus spreads, how it causes sickness, whether our immune system can recognize it, or whether treatments still work. Some mutations can change a virus that infects animals so that it is able to infect humans.

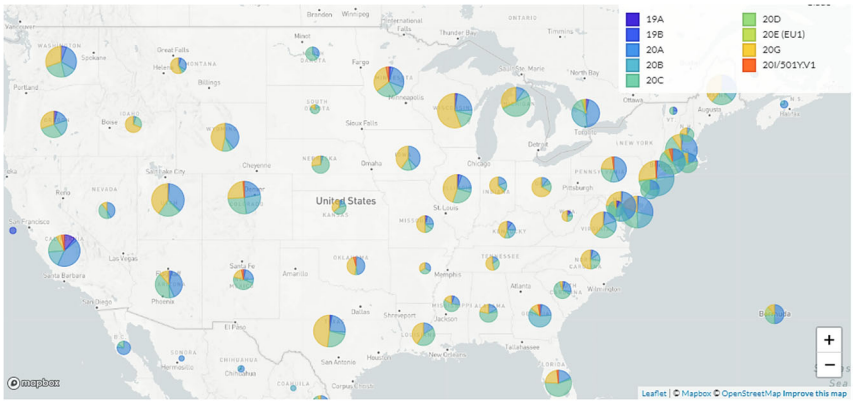
RNA viruses reproduce more quickly than DNA viruses, so they are more likely to make mistakes or have mutations. Influenza and coronaviruses are RNA viruses and are constantly changing. Influenza has eight RNA segments so there are a lot of possible mutations that can occur in and between these segments. Coronaviruses only have one RNA segment, so they mutate much more slowly. (*Great explanation of all of this is available at "Viruses Mutate. What does that mean for us?"* https://lifeology.us.lifeomic.com/static/ologies/virology/viruses-mutate/index.html#/)

SARS-CoV-2, the virus that causes COVID-19, gets about one new mutation every two weeks. If enough mutations occur at once or cause a large enough effect to the virus and continue to spread from person to person, it is called a variant.

Term	Description	Example
Strain	Virus with distinct properties that set it apart from other viruses	SARS-CoV-2
Variant	Still part of the same strain, but has collected enough mutations to be distinct	SARS-CoV-2 B.1.1.7
Mutation	Small changes in the genetic code of the virus	Mutation N501Y (mutation in the spike protein at position 501, where amino acid asparagine (N) has been replaced with tyrosine (Y)).

There have been several different variants of SARS-CoV-2 since December 2019 and new variants continue to be found. You can see the number of different variations in the United States below.





https://nextstrain.org/ncov/north-america?d=tree,map&f_region=North%20America&p=full

Concern over new variants is due in part to the following potential consequences:

- *Ability to spread more quickly in people:* the mutations can make the virus able to bind to cells better or change in other ways to spread faster.
- *Ability to cause more severe disease in people:* none of the new variants seem to cause more serious illness.
- *Ability to evade detection by specific diagnostic tests:* PCR tests detect the RNA of the virus so if the RNA changes, they may not work. However, most PCR tests are made to detect multiple different targets in the RNA of the virus, so even if several targets have mutated, the other PCR targets will still work.
- *Decreased susceptibility to therapeutic agents such as monoclonal antibodies:* a monoclonal antibody is one specific antibody against one target of the virus that has been reproduced in huge quantities and given as a treatment. If the target for that antibody on the virus changes, it will not work anymore.
- *Ability to avoid natural or vaccine-induced immunity*: Both vaccination and natural infection with COVID-19 produce an immune response to several targets on the virus. The virus would likely have to have several mutations to be able to avoid the immunity created by the vaccines or by natural infection.

In Denmark, a variant was found in late summer 2020 that was named Cluster 5. It was linked to farmed mink. And was later found in farmed mink in at least 5 other countries, including the United States. Only 12 human cases were proven to have been caused by this variant. In November, it was decided to cull all farmed mink, over 17 million animals, in Denmark.

Another variant was found in South Africa dating back to October 2020 and shares some similarities to B117. This variant is known as 0H/501Y.V2 or B.1.351 and also contains mutations in the spike protein. It has been found in other countries. It does not seem to cause any more serious illness. There is some evidence that one of the mutations might affect how well certain polyclonal and monoclonal antibody treatments would work.

A variant known as P.1 or 20J/501Y.V3 has been identified in Brazil that also involves mutations in the spike protein. There is some evidence that this strain may be more easily transmitted, and it is possible that the mutations may allow it to escape immunity from prior infection or vaccination.

In late 2020, variant B.1.1.7 (also called N501Y) was identified in the United Kingdom. It has now been found in several other countries around the world including the United States. It was announced Saturday, January 16 that the Michigan Department of Health and

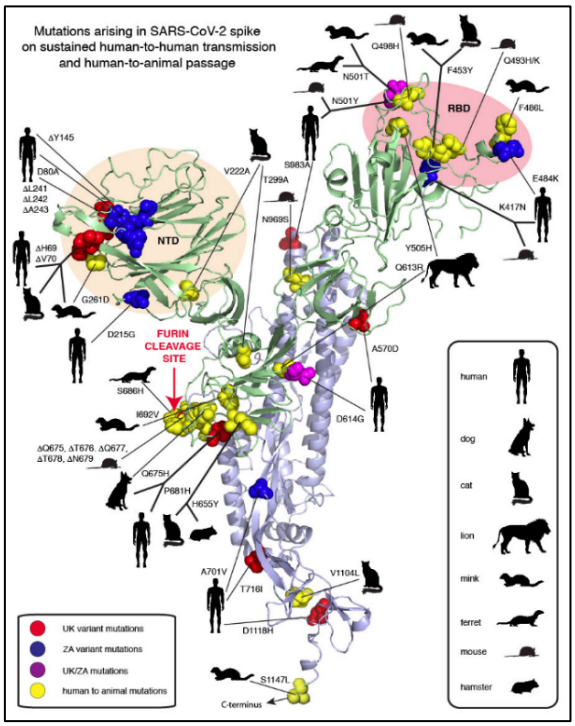
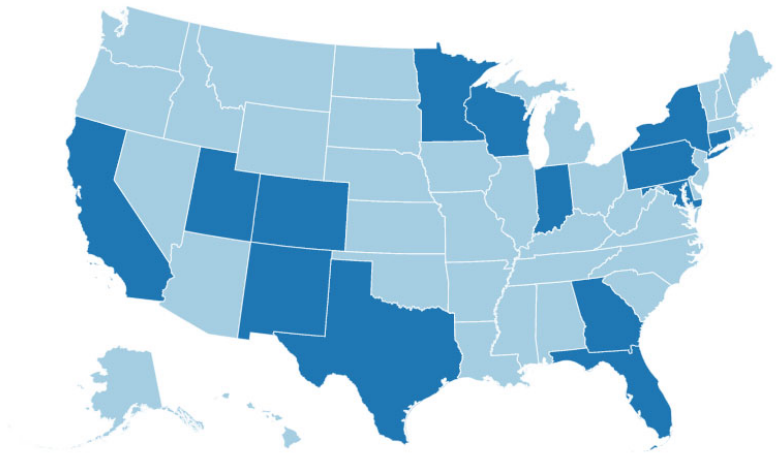


Figure 1. Compilation of SARS-CoV-2 spike mutations occurring in humans and animals. Red spheres: United Kingdom (UK) variant, Blue spheres: South African (ZA) variant, Magenta: both UK/ZA variants, Yellow spheres: animals as indicated in the inset. NTD: Amino-terminal domain. RBD: Receptor binding domain. Garry, R., 2021

Human Services (MDHHS) Bureau of Laboratories identified a case of SARS-CoV-2 B.1.1.7. in Washtenaw County in an adult that had recently traveled to the United Kingdom in early January. Two additional cases of COVID-19 have been identified among close contacts, but it is not known if the cases are infected with the variant. This variant has mutations in the spike protein and spreads more efficiently and quickly. It does not cause more serious illness or change the effectiveness of the current vaccines.

US COVID-19 Cases Caused by Variants as of January 15, 2021

State	Cases
CA	40
CO	5
CT	2
FL	22
GA	1
IN	1
MD	2
MN	5
NM	1
NY	4
PA	1
TX	2
UT	1
WI	1
Total	88



Source: https://www.cdc.gov/coronavirus/2019-ncov/transmission/variant-cases.html

The B117 variant is spreading more efficiently. A higher number of close contacts to people infected with B117 seems to become infected. Modeling estimates that this new variant will increase rapidly in the United States and take over as the dominant variant in March. Depending on how well the spread of virus is being controlled when this switch occurs, the change in variant to B117 will lead to a new phase of increased viral spread (figure 1A: poorly controlled with rates increasing; figure 1B: improving control with slow decrease, below). Vaccination is expected to improve, though not prevent, this situation (figure 2A and B, below).

For a high-level course on how public health uses genetics of viruses and bacteria to track disease, see the COVID-19 Genomic Epidemiology Toolkit https://www.cdc.gov/amd/training/covid-19-gen-epi-toolkit.html

Sources

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- World Health Organization (WHO). (2020). SARS-CoV-2 Variants. https://www.who.int/csr/don/31-december-2020-sars-cov2-variants/en/
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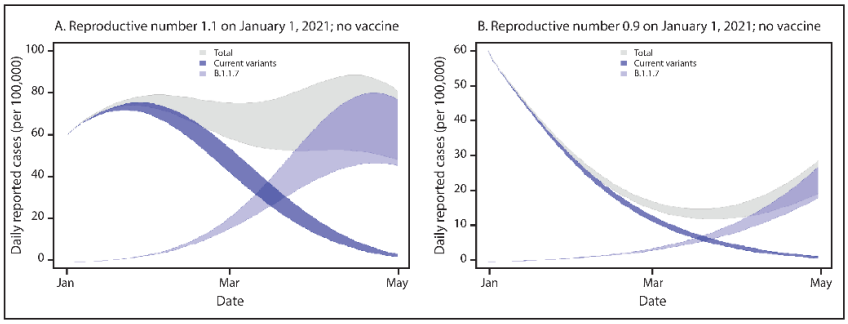
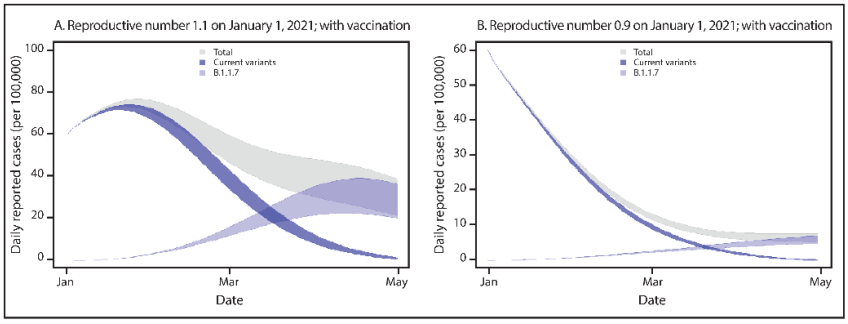
- Galloway SE, Paul P, MacCannell DR, et al. Emergence of SARS-CoV-2 B.1.1.7 Lineage — United States, December 29, 2020–January 12, 2021. MMWR Morbididy Mortality Weekly Rep. ePub: 15 January 2021. DOI: http://dx.doi.org/10.15585/mmwr.mm7003e2
- Hadfield et al., Nextstrain. https://nextstrain.org

FIGURE 1. Simulated case incidence trajectories* of current SARS-CoV-2 variants and the B.1.1.7 variant,† assuming no community vaccination and either initial R_t = 1.1 (A) or initial R_t = 0.9 (B) for current variants — United States, January–April 2021



Abbreviation: R_t = time-varying reproductive number.
* For all simulations, it was assumed that the reporting rate was 25% and that persons who were seropositive or infected within the simulation became immune. The simulation was initialized with 60 reported cases of SARS-CoV-2 infection per 100,000 persons (approximately 200,000 cases per day in the U.S. population) on January 1, 2021. Bands represent simulations with 10%–30% population-level immunity as of January 1, 2021.
† Initial B.1.1.7 prevalence is assumed to be 0.5% among all infections and B.1.1.7 is assumed to be 50% more transmissible than current variants.

FIGURE 2. Simulated case incidence trajectories* of current SARS-CoV-2 variants and the B.1.1.7 variant,† assuming community vaccination§ and initial R_t = 1.1 (A) or initial R_t = 0.9 (B) for current variants — United States, January–April 2021



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§ For vaccination, it was assumed that 300 doses were administered per 100,000 persons per day (approximately 1 million doses per day in the U.S. population) beginning January 1, 2021, that 2 doses achieved 95% immunity against infection, and that there was a 14-day delay between vaccination and protection.

Healthy Living Recommendations

1. Be aware of new travel requirements.
   a. Effective January 26, 2021 all air passengers arriving to the US from a foreign country to get tested for COVID-19 infection no more than 3 days before their flight departs and to provide proof of the negative result or documentation of having recovered from COVID-19 to the airline before boarding the flight.
   b. For more information on this testing requirement, see the Frequently Asked Questions.
   c. Get tested 3-5 days after travel AND stay home for 7 days after travel.
   d. Even if you test negative, stay home for the full 7 days.
   e. If you don't get tested, it's safest to stay home for 10 days after travel.
   f. Always follow state and local recommendations or requirements related to travel.
   g. Delay your travel if you are waiting for test results.
2. Continue to do all you can to prevent COVID-19 transmission.
   a. Get vaccinated for COVID-19.
   b. Wear a mask around others.
   c. Stay 6 feet apart from others.
   d. Wash hands often.
   e. Ventilate indoor spaces.