

What the new COVID-19 variants mean and how to report on them

There is widespread concern that some new variants of SARS-CoV-2, the virus that causes COVID-19, appear to be more infectious than previous strains of the virus. Multiple variants of the virus have been documented globally during this pandemic, but scientists say that new variants identified in both the United Kingdom and South Africa appear to spread faster and are 40 to 70 percent more transmissible.

Since being identified in mid-December, 45 countries have detected the UK coronavirus variant, according to <https://cov-lineages.org> which, among other things, tracks the global spread of the new COVID-19 strains.

Although there's no evidence yet that the variants are more deadly, many countries closed their borders to travelers from UK as they worked on how to deal with the possible new threat. The US Centers for Disease Control and Prevention says the characteristics of these variants were rapidly emerging.

“Scientists are working to learn more about how easily they might spread, whether they could cause more severe illness, and whether currently authorized vaccines will protect people against them. At this time, there is no evidence that these variants cause more severe illness or increased risk of death,” adds the 3 January 2021 advisory.

If the variants spread much more easily, that means more people may become infected and there is the potential that more will be hospitalized. Once hospitals become overwhelmed, the quality of care may drop, which can lead to higher death rates than would otherwise be expected.

What do you need to know?

Question 1

What is the difference between a strain and a variant?

The media often uses the terms “strain” and “variant” interchangeably. But the distinctions are important.

In general, if a virus has enough mutations to make its biology significantly different it may be a considered new strain. This means that it may respond differently to vaccines or treatments, or it may infect a different species or transmit in a different way.

Broadly, a strain is a sub-type of a species of microorganisms. If you consider a family of viruses, like the coronavirus family, it is made up of several strains of the virus. So for example, Severe Acute Respiratory Syndrome (SARS) is one strain, SARS-CoV-2 is another. If a new strain had been discovered, hypothetically, it could be called SARS-CoV-3 for instance. These are all different strains belonging to the same virus family,

If the biology of the virus broadly remains the same, despite the mutations, the term “variant” may be more scientifically accurate. A variant of a virus means it has slight genetic changes — but not enough to be classified as a new strain. For example, B117 circulating in the UK (and not around the world) is a variant of COVID, meaning it is similar to the original virus. So, SARS-COV-2 is the strain, and these new mutations – like the UK case – are variants of that strain.

Question 2

What is a virus mutation?

Thanks to science fiction, the word “mutant” has become associated in popular culture with something that is abnormal and dangerous. Yet in reality, viruses like SARS-CoV-2, the virus that causes COVID-19, are mutating all the time and often this process does not have any impact on the risk the virus poses to humans. New variants of a virus are expected to occur over time. Sometimes new variants emerge and disappear. Other times, new variants emerge and persist.

A mutation is simply a change in the virus’ genome: the set of genetic instructions that contain all the information that the virus needs to function. These genome changes are detected by what is called genome sequencing.

When the virus replicates, this set of instructions needs to be copied, but errors can creep in during this process. It's just like copying a manuscript. Sometimes there are typos. The virus just makes random mistakes when it gets copied. Depending on where in the genome mistakes occur, they can have a negative or positive impact on the virus’ ability to survive and replicate.

In the majority of cases, these mistakes are harmless and hardly have any impact on the way the virus affects individuals. In fact, in many cases, the mutation could actually make a virus less potent. But in certain instances, a mutation could offer the virus an advantage – which may be what is happening in the UK and South Africa.

Question 3

What is genome sequencing?

A genome is an organism’s genetic material, and it contains all the instructions needed to build and develop that organism. Genomic sequencing is the process of figuring out the complete DNA sequence (in SARS-CoV-2 it is the RNA sequence) of an organism’s genome at a single time. It analyses the virus sample taken from a patient and compares it with other cases in order to understand if the virus has changed.

Recent technological advances have allowed SARS-CoV-2 genomes – the virus that causes COVID-19 – to be sequenced within several days of a case being identified. This is really significant, because it means that we can use these genomes to inform public health policy during an ongoing outbreak. For the first time, genomic sequencing can help to guide the public health response to a pandemic in near-real time.

Question 4

What are the new COVID-19 variants?

Scientists have tracked multiple mutations of SARS-CoV-2, since it appeared in China in late 2019. The vast majority of mutations did not materially alter either the virus's virulence (the virus strength, or likelihood you will get very sick) or transmissibility (how easily the virus spreads between people).

However, one mutation – variant B117, which likely emerged in southeastern England in September 2020, according to Imperial College London – has now been detected in countries across the world, including the US, France, and the Asia-Pacific.

On 12 January 2021, [Reuters](#) reported that the B117 variant accounted for almost half of the most recent sample of positive tests in Ireland. Another variant, 501.V2, was detected in South Africa in October, and has since spread to several nations, including the UK and France.

Question 5

What makes the new variants more transmissible?

A more transmissible strain, by definition, spreads more easily from person to person. The World Health Organization announced late December 2020 that the new variants have a reproductive, or R_0 , value of 1.5 rather than 1.1 (before the new variants were detected). The measure refers to the average number of people one sick person infects, so a difference of 0.4 means 100 sick people will infect another 150, not 110, on average, as understood previously.

Both variants have multiple mutations, most importantly they have changes on its spike protein – the part of the virus that latches on to human cells and helps it spread.

The UK variant has 17 different mutations in its genetic code. And eight of those mutations occur in a critical part of the virus, called the spike protein, which reaches out and binds to human cells during the initial stages of infection. One mutation, called N501Y, makes the virus bind more tightly to human cells. The UK variant also contains a small deletion in the virus's genetic code, called 69-70del, and that deletion helps the new variant evade the body's immune system in some people.

Scientists believe the new variant may have gone through a rapid evolution in a chronically infected patient who then transmitted the virus. "We know this is rare but it can happen," said World Health Organization epidemiologist [Maria Van Kerkhove](#).

The variant might also be linked to higher loads of the virus in swab samples obtained from the nose and the back of the throat making it easier for the virus to spread to other people through coughing and sneezing. So if a person sneezes on a bus, the new variant is more likely to infect other people than the previous form of the virus.

On December 18, 2020, the South African government announced that it had also seen the emergence of a new variant in a scenario similar to that in the UK. The South African variant also has the N501Y mutation and several other mutations but emerged completely independently of the UK variant and is not related to it. The South African variant has two mutations – E484K and K417N – that are absent in the UK variant.

The E484K mutation has been shown to reduce antibody recognition. As such, it helps the virus SARS-CoV-2 to bypass immune protection provided by prior infection or vaccination. But even in the worst case scenario, vaccines can be redesigned and tweaked to be a better match in a matter of weeks or months, if necessary, say experts.

The variant 501.V2 now accounts for 90 percent of sequences analyzed in South Africa.

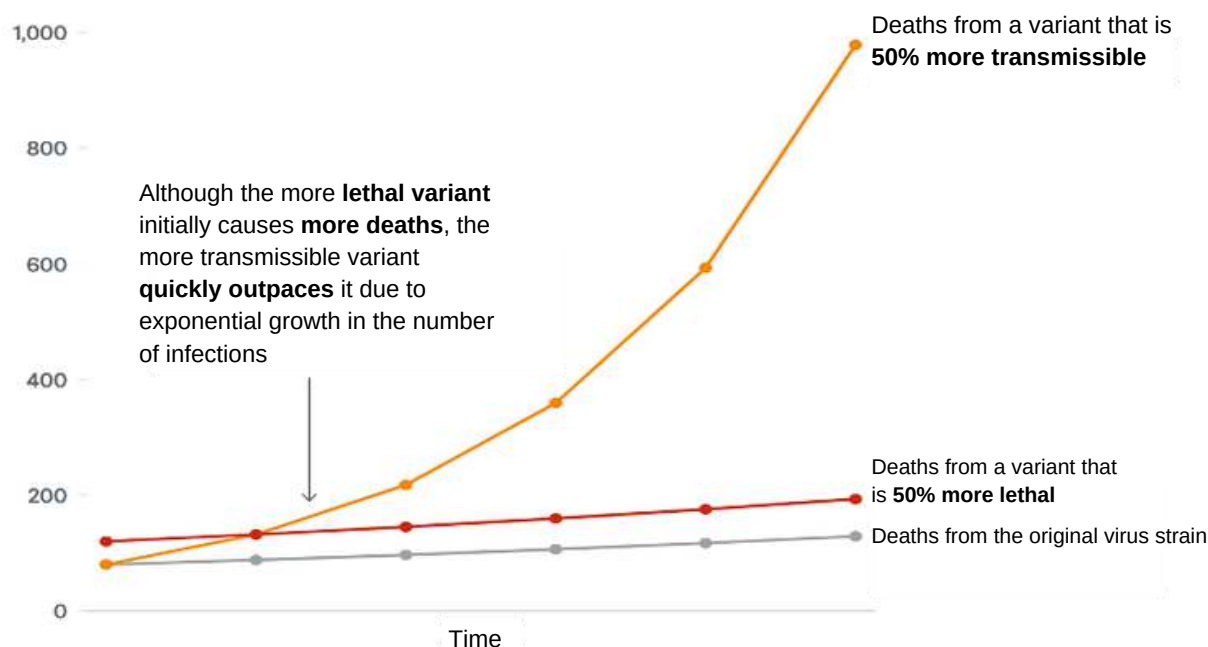
Question 6

Are the new COVID-19 variants more deadly?

Preliminary reports from scientists in the UK are that these variants are more transmissible than previous circulating viruses, with an estimated increase of between 40 percent and 70 percent in transmissibility. However, the US CDC notes that there is no evidence that they cause more severe illness or increased risk of death. Yet, the transmission of a more infectious variant could spur exponential growth in the number of COVID-19 cases. Such rapid growth in cases could, in turn, lead to more fatalities: with an increase in hospitalizations, health-care systems could become overwhelmed and consequently unable to care for large numbers of people with COVID-19 infections.

A More Infectious Virus Could Lead to Many More Deaths

Simplified, hypothetical scenario showing the number of new deaths every six days from three different virus variants, assuming each variant started from 10,000 infections



Adam Kucharski, Associate Professor, London School of Hygiene and Tropical Medicine.

Question 7

Are current vaccines affected by the new COVID-19 variants?

Scientists are racing to understand why variants B117 and 501.V2 seem to spread so quickly and whether they might diminish the potency of first generation COVID-19 vaccines currently being rolled out.

The first lab results are trickling in and many more are expected in the coming days, as researchers rush to probe the viral variants and their constituent mutations in cell and animal models of SARS-CoV-2, and test them against antibodies produced by vaccines and natural infections.

A [publicly shared preprint study](#) published on 8 January found that the N501Y mutation shared by both variants did not alter the activity of antibodies produced by people who received a vaccine developed by Pfizer and BioNTech. More data, however, is expected soon.

Other mutations, however, might affect immunity. Chief among those is another receptor-binding-domain mutation, called E484K identified in the 501Y.V2 variant. The Africa Health Research Institute in Durban is testing the variant against convalescent serum and serum from people who have been vaccinated in trials and first results from these studies should be publicly available soon. The [E484 mutations are worrying](#) because they can 'fool' or escape three antibodies that the body's immune system makes.

[AstraZeneca](#) announced that its coronavirus vaccine is currently expected to be effective against the new COVID-19 variants, but more tests were necessary in the UK and South Africa. But scientists are hopeful that the mutations in the variants won't substantially weaken the performance of vaccines.

Our immune response depends on how many soldiers the vaccine brings to the battlefield. If plenty are at the ready, then a mutation that reduces the overall general firepower will be less of an issue. And there are other components of our immune response – T cells, or other antibodies not affected by the mutations – that likely play an important role in our protection against COVID-19.

If the vaccines are rendered significantly less effective or ineffective by the mutations, some of them could be easily adapted by replacing the current genetic material in vaccines with the variant sort of genome that codes for the spike proteins. [Vaccinologists](#) point out it would take just five to six weeks to do this, although research would still be needed to demonstrate safety and efficacy.



How can I report on this issue?

1. Deal carefully with uncertainty when reporting on research findings

Translating the results of SARS-CoV-2 genome sequences published in research papers into informative stories can be challenging, especially when there is uncertainty over the behaviour of the virus caused by the new mutations. A misleading interpretation could cause public panic.

It is important to decide which information you must include to give credibility to your article and what findings you can summarize without losing their accuracy. Always to explain percentage increases in real world terms, like what does it mean to be 40 percent more transmissible?

When you come across research findings, ask yourself these 3 questions:

- How much certainty is there over the results?
- How does it compare to the wider body of evidence?
- To what degree are scientists sure about the findings?

2. Bring the story to life after you've extracted key information from the research papers

- Ask someone working in the same field to comment on the findings. This is especially important for papers that are making big claims. Remember that you can get ideas for commenters in the introduction and discussion of the paper.
- Is it clear who the beneficiaries of this work would be?
- Are there people who could be negatively affected? Considering this will allow you to connect more effectively with your audience.
- Remember to consider your audience and outlet. How can you tailor the story to them?

3. Encourage dialogue between researchers/scientists

Bringing out the personal side of research can make your story more interesting. Ask the scientists about their own experience of doing the research. Perhaps they were frustrated for years before making this discovery, or have tales to tell of being filled with wonder when they looked at their results.

4. Remind your audiences that preventive measures still apply

Because the virus keeps changing continuously, the greater will the number of infected people and the more chances the virus gets to infecting more. For these reasons WHO has the following [basic protective measures](#):

Wash your hands frequently

Regularly and thoroughly clean your hands with an alcohol-based hand rub or wash them with soap and water.

Why?

Washing your hands with soap and water or using alcohol-based hand rub kills viruses that may be on your hands.

Maintain social distancing

Maintain at least 2 meters (6 feet) distance between yourself and anyone who is coughing or sneezing.

Why?

When someone coughs or sneezes, they spray small liquid droplets from their nose or mouth which may contain virus. If you are too close, you can breathe in the droplets, including the COVID-19 virus if the person coughing has the disease.

Avoid touching eyes, nose and mouth

Why?

Hands touch many surfaces and can pick up viruses. Once contaminated, hands can transfer the virus to your eyes, nose or mouth. From there, the virus can enter your body and can make you sick.

Practice respiratory hygiene

Make sure you, and the people around you, follow good respiratory hygiene. This means covering your mouth and nose with your bent elbow or tissue when you cough or sneeze. Then dispose of the used tissue immediately.

Why?

Droplets spread the virus. By following good respiratory hygiene, you protect the people around you from COVID-19.

Avoid the 3Cs: spaces that are closed, crowded or involve close contact

Outbreaks have been reported in restaurants, choir practices, fitness classes, nightclubs, offices and places of worship where people have gathered, often in crowded indoor settings where they talk loudly, shout, breathe heavily or sing.

Why?

The risks of getting COVID-19 are higher in crowded and inadequately ventilated spaces where infected people spend long periods of time together in close proximity. These environments are where the virus appears to spread by respiratory droplets or aerosols more efficiently, so taking precautions is even more important.

