The delta variant of SARS-CoV-2: What do we know about it?

Written by Maria Cohut, Ph.D. on June 16, 2021 — Fact checked by Yella Hewings-Martin, Ph.D.

The variant of the SARS-CoV-2 virus called delta continues to spread rapidly across many parts of the world. What do we know about this variant so far?

What do scientists know about the fast-spreading delta variant of SARS-CoV-2?
Image credit: Christopher Furlong/Getty Images

The delta variant of SARS-CoV-2 — scientifically known as the B.1.617.2 lineage — was first identified by scientists in December 2020 in India.

In April 2021, the delta variant became the most commonly spread variant that caused new COVID-19 cases in India. Since then, this variant has been reported in 80 countries, according to the World Health Organization (WHO).

Recently, there have been concerns — particularly in the United Kingdom and the United States — that the delta variant could give rise to another COVID-19 wave, thus setting back national and international efforts to

Stay informed with live updates on the current COVID-19 outbreak and visit our coronavirus hub for more advice on prevention and treatment.

According to the latest report from Public Health England (PHE), the delta variant may have become the dominant variant in the U.K., with "74% of sequenced cases [of SARS-CoV-2 infection] and 96% of sequenced and genotyped cases" being caused by this variant.

In the U.S., data from the Centers for Disease Control and Prevention (CDC) put the proportion of new COVID-19 cases attributed to the delta variant at 2.7%. This is the most recent genomic surveillance data dating to the 2 weeks ending on May 22, 2021.

More recently, former Food and Drug Administration (FDA) commissioner Dr. Scott Gottlieb has noted that around 10% of new COVID-19 cases are due to the delta variant.

Dr. Anthony S. Fauci, director of the National Institute of Allergy and Infectious Diseases, has reportedly warned that "any country that has the delta variant should be concerned that there will be a surge of infections, particularly if that particular country does not have a substantial proportion of their people vaccinated."

"We've seen that when delta variant spreads among non-vaccinated people, it can become dominant very, very quickly," he added.

Article highlights:

How infectious is the delta variant?

Based on the data from the U.K., the delta variant is about 60% more transmissible than the alpha variant, which was previously called B.1.1.7. Alpha, in turn, is more transmissible than the strain previously dominant in the country.

Prof. Wendy Barclay, professor of virology and head of the Department of Infectious Disease at Imperial College London in the U.K., explained that this variant is more transmissible than previous ones because of some key mutations in the spike protein, which allows the virus to penetrate and infect healthy cells.

“The delta variant has got two important mutations in its spike protein, or sets of mutations,” she noted. “One is at the furin cleavage site, which we think is quite important for the fitness of the virus in the airway.”

“The virus that emerged in Wuhan was suboptimal in that respect, so it transmitted but perhaps not as well as it might. The alpha variant took one step towards improving that with a certain mutation, and the delta variant has built on that and taken a second step now, a bigger step, towards improving that feature,” said Prof. Barclay.

Are infection symptoms different?

with those experienced upon infection with previous variants.

Thus, data from the ZOE Covid Symptom Study — whose scientific analysis is conducted by experts from King's College London — suggest that the main symptoms of infection with the delta variant are headaches, a sore throat, and a runny nose.

This is a change from official information on COVID-19 symptoms — such as that provided by the U.K.'s National Health Service (NHS) — that lists fever, continuous cough, and loss of smell or taste as the main symptoms of the condition.

Prof. Tim Spector, co-founder of ZOE, warns that SARS-CoV-2 infections are "acting differently now, [...] more like a bad cold," which may tempt people to dismiss the symptoms.

"It might just feel like a bad cold or some funny 'off' feeling — but do stay at home and do get a test," he urges.

What are the risks going forward?

variant.

Given the data on delta's increased transmissibility, some scientists have suggested that this may increase the risk of a further COVID-19 wave.

Modeling projections from Imperial College London indicate that the delta variant may significantly increase the risk of hospitalizations with COVID-19, exposing the U.K. to the possibility of a third wave, similar to the one the country experienced last winter.

Following concerning reports of the spread of this variant, the British government has already delayed the end of the pandemic restrictions in the country by 4 weeks.

Dr. Gottlieb also warned that the U.S. might experience further COVID-19 outbreaks because of this highly transmissible variant.

"I think in parts of the country where you have less vaccination, particularly in parts of the South, where you have some cities where vaccination rates are low, there's a risk that you could see outbreaks with this new variant," he suggested.

For this reason, he encouraged people to get fully vaccinated against COVID-19, noting that the vaccines currently authorized in the U.S. appear to hold up well against the emerging variant.

"The mRNA vaccine [Pfizer-BioNTech and Moderna] seems to be highly effective, two doses of that vaccine against this variant. The viral vector vaccines from [Johnson & Johnson] and AstraZeneca also appear to be effective, about 60% effective. The mRNA vaccines are about 88% effective. So we have the tools to control this and defeat it. We just need to use those tools," he commented.

For live updates on the latest developments regarding the novel coronavirus and COVID-19, click here.

Public Health Infectious Diseases / Bacteria / Viruses COVID-19

FEEDBACK:

New SARS-CoV-2 variants: How can vaccines be adapted?

Written by Yella Hewings-Martin, Ph.D. and Maria Cohut, Ph.D. on March 15, 2021

Design by Diego Sabogal

All data and statistics are based on publicly available data at the time of publication. Some information may be out of date. Visit our coronavirus hub and follow our live updates page for the most recent information on the COVID-19 pandemic.

As the SARS-CoV-2 virus continues to evolve, we explore what vaccine developers are doing to ensure their vaccines work against emerging variants and whether we need specifically adapted vaccines.

To date, 12 COVID-19 vaccines have received authorization for use in at least one country, and many more vaccine candidates are undergoing clinical trials to test their safety and efficacy.

Yet, like other viruses, SARS-CoV-2, the coronavirus that causes COVID-19, naturally undergoes mutations in time. These mutations can be negligible or affect how infectious or likely to cause severe disease a

With this in mind, and while the global vaccine rollout is currently underway, scientists and the public alike have raised a key concern: How will available vaccines and vaccine candidates hold up against emerging SARS-CoV-2 variants?

> *Stay informed with live updates on the current COVID-19 outbreak and visit our coronavirus hub for more advice on prevention and treatment.*

Do vaccines work against variants?

The answer to this question lies in the definition of the word "work." When vaccine developers set out the conditions of their clinical trials, they work closely with regulatory authorities, such as the Food and Drug Administration (FDA), to ensure they answer the most important questions.

For most experimental COVID-19 vaccines, the primary endpoints, or the main questions that a clinical trial asks, were the prevention of COVID-19. This meant that the developers would assess any case of COVID-19, including mild and moderate cases, when they were calculating how well their vaccine candidate performed.

In the case of the Pfizer-BioNTech vaccine, which was the first to receive emergency use authorization from the FDA, eight people who had received the vaccine and 162 people who had received the placebo developed COVID-19. This equates to a vaccine efficacy of 95%.

There were no deaths in either group in the clinical trial that the researchers could attribute to COVID-19 by the time the data became publicly available in the *New England Journal of Medicine* on December 31, 2020.

According to a recent study, real-world data from Israel suggest that this vaccine is highly effective in preventing COVID-19, including severe disease.

The authors of this paper could not provide a specific breakdown of how well the vaccine works at preventing COVID-19 in those who have the B.1.1.7 SARS-CoV-2 variant. However, they suggest that the vaccine is effective against the variant based on their overall data.

B.1.1.7 — a SARS-CoV-2 variant first identified in the United Kingdom — is one of a handful of emerging variants that have given rise to some concerns. Other variants that have caused some worry are B.1.351, first identified in South Africa, and P.1, which appears to originate in Brazil.

These variants are causing concern because they appear to be more transmissible than previous variants, and there is also some conjecture that some of them might give rise to more severe cases of COVID-19.

Given these concerns, two main questions have arisen: Will existing COVID-19 vaccines be able to match these emerging variants? And, how might vaccine producers modify their candidates to respond to new variants?

Adapting vaccines to match variants

While data suggest that most COVID-19 vaccines might hold up reasonably well against B.1.1.7, the B.1.351 variant is causing significant concern.

When it comes to this variant, vaccine efficacy is lower, in some instances quite dramatically so.

A sub-group analysis of data from the Oxford-AstraZeneca vaccine trial showed that the vaccine only had an efficacy of 10.4 % against COVID-19 in people who had an infection with B.1.351. However, it is worth noting that this study was small and has not been through peer review yet.

Nevertheless, in an interview for *the BMJ* from January 2021, Prof. Andrew Pollard, Director of the Oxford Vaccine Group and one of the leaders of the Oxford vaccine trials, explained that it would not be difficult to modify both mRNA and viral vector vaccines — of which the Oxford-AstraZeneca vaccine is one — to match emerging variants.

"For the RNA vaccines and the viral vectors, it's relatively straightforward because you just have to synthesize a new bit of DNA in our case — or RNA in [the Pfizer and Moderna] cases — and then insert that into the new vaccine. Then there's a bit of work to do to manufacture the new vaccine, which is a reasonably heavy lift. But the same processes would be used," he told *The BMJ*.

"The second component," he added, "is that there will almost certainly need to be some testing, whether it's in animals or humans, to show that you can still generate immune responses, and then the regulator would have to approve that new product."

Speaking to Reuters in February, the head of research and development at AstraZeneca, Sir Mene Pangalos, suggested that the company are already looking at a second-generation vaccine that would stand up to emerging variants.

This work could take at least until fall to complete. He declared: "We're working very hard, and we're already talking about not just the variants but also the clinical studies that we need to run, and we're very much aiming to try and have something ready by the [fall]."

*Medical News Today*contacted both AstraZeneca and the Oxford Vaccine Group for comment, asking them about addressing concerns as to whether their COVID-19 vaccine can provide immunity against emerging variants. However, the company and the research group did not reply to our queries.

More recently, Johnson & Johnson reported their phase 3 clinical trial results ahead of gaining emergency use authorization for their single-shot viral vector COVID-19 vaccine from the FDA.

This vaccine demonstrated an overall efficacy of 66% at preventing moderate to severe COVID-19 across all clinical study sites. Johnson & Johnson have taken a different approach and studied moderate to severe

When breaking down the data by region, the company reported efficacy against moderate to severe disease of 72% in the U.S., 66% in Latin America, and 57% in South Africa, indicating the drop in efficacy against COVID-19 caused by infection with B.1.351.

However, there were no cases of hospitalization or death in the group that had the vaccine from 4 weeks post-vaccination onward.

MNT contacted Johnson & Johnson for comment, but the company did not respond to our queries.

mRNA vaccines: Moderna and Pfizer BioNTech

Moderna are forging ahead with a variant-matched vaccine candidate. The company have already developed a new experimental vaccine specifically designed to match the B.1.351 variant.

In a press release from February 24, Moderna announced that they had shipped the first batch of this new vaccine candidate to the National Institutes of Health (NIH), who will be testing it in a new phase 1 trial.

The National Institute of Allergy and Infectious Diseases (NIAID) at the National Institutes of Health (NIH) told *MNT* that "NIAID plans to begin a phase 1 trial evaluating a vaccine against the B.1.351 variant developed by Moderna in (roughly) mid-March."

"We will provide more information in an announcement once the trial has begun, per our usual process," they said.

There will be a three-pronged approach to addressing the specific challenges of the B.1.351 variant.

The first will involve testing the variant-matched vaccine candidate as a booster in its existing clinical trial cohort. The second will test the new experimental vaccine as a booster in combination with the authorized Moderna vaccine. Scientists refer to such a combination as a multivalent vaccine.

The third approach will be a booster with the original vaccine. According to the press release, Moderna has already started this third booster approach.

Separately, the company are also planning on testing the variant-matched or the multivalent vaccine in people who have not received a vaccination yet.

Moderna did not reply to *MNT*'s request for comments on their strategy

Pfizer and BioNTech are currently testing a third dose of their mRNA vaccine in their clinical trial cohort to assess how well this strategy will prevent COVID-19 in light of emerging variants.

"Separately, in order to be prepared for any potential future strain changes, Pfizer and BioNTech are in ongoing discussions with regulatory authorities, including the [FDA] and the European Medicines Agency (EMA), regarding a registration-enabling clinical study to evaluate a variant-specific vaccine having a modified mRNA sequence," the press release states.

"This study will evaluate the safety and immunogenicity of a third dose of the Pfizer-BioNTech COVID-19 vaccine (BNT162b2) to understand the safety and impact of a booster dose on immunity against COVID-19 caused by the circulating SARS-CoV-2 variants," a spokesperson from Pfizer told *MNT*.

They continued:

> "Based on in vitro studies conducted to date and observations from real-world evidence, we have not observed changes to neutralizing antibody levels that would predict a significant reduction in [the] protection provided by two doses of BNT162b2. [However], it is important to gather the clinical evidence to prepare in case an additional dose or an updated vaccine is needed."

The companies are looking to test both the booster and new variant-matched experimental vaccines. "We are doing this to be prepared in case immunity wanes or a variant were to emerge that escapes protection from the current vaccine," they explained.

They explained that a new vaccine with a modified mRNA sequence could facilitate a fast-paced updating process as new variants of concern emerge. Pfizer told us that they are already negotiating with the relevant authorities as to kickstarting a relevant evaluation study:

"Pfizer and BioNTech are in ongoing discussions with regulatory authorities regarding a potential registration-enabling study to evaluate an updated vaccine having a modified mRNA sequence. This could position us to update the current vaccine quickly if the need arises to

"Updated guidance issued by the FDA regarding emergency use of vaccines to prevent COVID-19 provides recommendations for evaluating a modified vaccine to address variants. By studying the effect of a booster vaccine now, the companies are hoping to inform the development of an efficient regulatory pathway for the validation of future modified mRNA vaccines, using the current pathways for influenza vaccines as models," they added.

Subunit vaccines: Novavax

American vaccine development company Novavax have also developed a vaccine candidate — a subunit vaccine — that has shown a lot of promise against SARS-CoV-2.

According to a press release from January 29, 2021, the vaccine candidate was 89.3% efficient against the original strain in the context of a phase 3 trial conducted in the United Kingdom.

"Importantly, the timing of the trial overlapped [with] the emergence of the 'U.K. variant,' and over half the U.K. cases had this strain: the vaccine showed 86% efficacy in these patients," Dr. Gillies O'Bryan-Tear, a fellow of the Faculty of Pharmaceutical Medicine in the U.K., who was not involved in the trial, explains.

In February, the EMA said they had started reviewing Novavax's vaccine candidate for rollout in the European Union (EU).

A month later, on March 11, 2021, Novavax announced that their candidate was effective in protecting against disease caused by two variants, B.1.1.7 and B.1.351, first identified in the U.K. and South Africa, respectively.

However, some experts caution that despite these promising results, the candidate is still not as effective against newer variants as it is against the original ones.

For example, Prof. Lawrence Young, from Warwick Medical School in Coventry, U.K., notes that: "The Novavax protein-based vaccine is very effective against infection with the original virus variant (96.4% against symptomatic disease) with slightly reduced efficacy against the U.K. variant (B.1.1.7). However, the overall efficacy of this vaccine against the B.1.351 South African variant is significantly reduced at 48.6% — increasing to 55.4% if HIV-positive participants are excluded."

"This study supports the need for modifying existing vaccines to provide better protection," he adds.

In a comment for *MNT*, Novavax said they "initiated the development of new vaccine constructs in January 2021 as soon as some of the emerging variants' (501Y.V1 and 501Y.V2) genetic sequences were available. [They] have begun the production process to make a purified variant recombinant spike protein for a bivalent vaccine."

Similarly to Pfizer, they added that: "Preclinical studies are underway, and we plan to begin clinical testing of these new vaccine candidates in the first half of this year. The FDA has issued preliminary guidance on a regulatory pathway that provides clarity on the path forward."

When asked how easy it would be to adapt their vaccine technology to match new variants, Novavax told *MNT*:

> "A hallmark of our technology platform is that our manufacturing processes are easily adaptable to producing other versions of the coronavirus spike protein that match the new strains. Additionally, our platform uses a very small amount of antigen, which provides the ability to create a bi- or multivalent vaccine and also the rapid creation and large-scale production of vaccine candidates that could potentially address multiple circulating strains of [the coronavirus that causes] COVID-19."

Do we really need second generation vaccines?

In light of both Moderna and Pfizer-BioNTech testing additional booster shots of their authorized vaccines, it stands to question whether variant-matched vaccines are necessary.

Prof. Jonathan Ball, a professor of molecular virology at the University of Nottingham in the U.K., recently made this argument on Twitter:

Tweet

"Our own (so far unpublished) work show[s] that repeat boosting can generate antibodies that potently knock out [SARS-CoV-1] — which is far more antigenically different than variants of [SARS-CoV-2]," he said on the social media platform.

In his view, there is thus enough ground to test the potential of an additional booster dose in creating immunity against emerging SARS-CoV-2 variants, rather than developing second generation vaccines that match these variants.

Responding to *MNT*'s queries, Novavax told us that they did expect that matched, bivalent, or multivalent vaccines against COVID-19 will become necessary in the future.

Another company looking at specifically targeting emerging variants are CureVac. With their mRNA vaccine candidate currently in phase 3 clinical trials, CureVac are currently studying how well it will perform against SARS-CoV-2 variants in "targeted in vitro studies," Vice President of Communications Thorsten Schüller told *MNT*.

CureVac have teamed up with GSK and the U.K. government to develop second generation COVID-19 vaccines.

"Mutations are natural survival strategies of viruses, and SARS-CoV-2 variants are going to continue to occur throughout the world, and their number is likely to increase in the future," Mr. Schüller explained. "There will be an enormous need for vaccines in general and particularly for multivalent vaccines."

Vaccine developers are clearly taking the threat that new SARS-CoV-2 variants may pose risks seriously. Whether we face a future with variant-matched annual boosters akin to the flu shot remains to be seen.

For pharmaceutical companies, a steady demand for vaccines may also spell a guaranteed income.

Only as scientists continue to study how well the existing vaccines and those in development cope with SARS-CoV-2 variants will the full picture emerge.

For live updates on the latest developments regarding the novel coronavirus and COVID-19, click here.

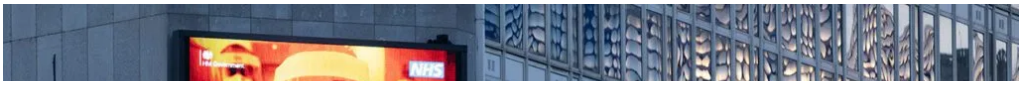
Public Health Immune System / Vaccines Infectious Diseases / Bacteria / Viruses COVID-19

FEEDBACK:

COVID-19: What do we know about the new coronavirus variant?

Written by Maria Cohut, Ph.D. and Yella Hewings-Martin, Ph.D. on January 28, 2021 — Fact checked by Gianna D'Emilio

First identified in the United Kingdom last year, a new variant of the virus that causes COVID-19 has increased concern throughout the world. In this Special Feature, Medical News Today look at what we do — and do not — know about this variant and what health experts have to say.



Mike Kemp/Getty Images

All data and statistics are based on publicly available data at the time of publication. Some information may be out of date. Visit our coronavirus hub *and follow our* live updates page *for the most recent information on the COVID-19 pandemic.*

Recently, global media has been abuzz with news and speculation about a new variant of SARS-CoV-2, the virus responsible for COVID-19.

The variant, which researchers first identified in the U.K., is called B.1.1.7, though as scientists began to express concern about it, initial U.K. government documents dubbed it VUI – 202012/01, standing for "the first variant under investigation in December 2020."

Later government documents from December designated it as a "variant of concern," and referred to it as VOC 202012/01.

B.1.1.7 was first spotted in the U.K. in September 2020. It began to draw attention from the scientific community and governmental authorities in early December, when the U.K. health secretary, Matt Hancock, suggested that it was spreading fast and likely contributing to the rising number of SARS-CoV-2 infections in the South of England.

Now, at the time of this article's publication, the new variant has been spotted in at least 60 countries.

But why is this variant of so much interest to scientists, public health organizations, and the public at large? In this Special Feature, we review what we know so far about B.1.1.7 and look into the questions that scientists are still trying to answer.

Below, we explore what viral mutations are, how they relate to the development of new viral strains, and whether the new SARS-CoV-2 variant identified in the U.K. is a cause for concern.

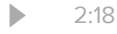
Also, *MNT* have been in touch with Pfizer and the National Institute of

vaccines currently available in the United States and Europe will be effective against B.1.1.7. Learn what they had to tell us.

Article summary:

WATCH VIDEO

MNT Spotlight January 12, 2021



2:18

MNT Spotlight January 12, 2021

1:54

MNT Spotlight January 8, 2021

2:13

MNT Spotlight Janua 2021

Why do viruses mutate?

Viruses are prone to mutations. Indeed, all genetic material, including that of humans, can mutate when mistakes occur during replication.

A mutation of a virus occurs when there is a change in its genetic sequence. This creates variation and drives virus evolution.

Mutations lead to changes in the proteins that are encoded in the viral genetic code. These changes can either be advantageous, harmful, or neutral.

How many mutations does it take to produce a new strain of the virus? This is not easy to answer, in part because scientists disagree about the definition of the word “strain.”

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.

But if the biology of the virus broadly remains the same, despite the mutations, the term “variant” may be more scientifically accurate.

Since the start of the pandemic, there has been much discussion about SARS-CoV-2 mutations and what implications they may have.

SARS-CoV-2, like many other coronaviruses, has an enzyme that proofreads its genetic code during replication, reducing the rate of mutations.

While the novel coronavirus has a relatively stable genome, compared with other types of virus, it does mutate sometimes, and scientists have closely monitored these changes.

One of the most widely talked about mutations has resulted in the D614G variant. This causes a change in the spike protein, which interacts with the ACE2 receptor on human cells to facilitate viral entry.

Specifically, an amino acid in the spike protein at position 614 is changed from aspartic acid to glycine.

Research by Dr. Bette Korber, from the Los Alamos National Laboratory, in New Mexico, and colleagues suggests that this change allows the variant to infect people more easily.

The D614G variant has become the predominant variant of SARS-CoV-2 worldwide, the research shows.

The team’s data indicate that people with the D614G variant of the virus may have higher levels of viral RNA than people with the original variant. But no evidence indicates that this causes more severe COVID-19.

Still, not all scientists agree with this group’s interpretation. Referring to the paper, Dr. Nathan Grubaugh, from the Yale School of Public Health, in

While researchers continue to study the differences between the D and G variants, the world has turned its focus toward B.1.1.7 and how it may shape the course of the pandemic.

B.1.1.7 and the founder effect

The B.1.1.7 variant has 23 mutations. Six cause no change in the amino acid sequence of the virus. Of the remaining 17 mutations, eight affect the spike protein.

The N501Y change, which involves a switch from asparagine to tyrosine at position 501, is located in the receptor-binding domain of the spike protein. This is a crucial section, as it interacts directly with the ACE2 receptor.

Another mutation in the RNA that encodes the spike protein allows researchers to detect this variant in polymerase chain reaction (PCR) test samples. This is because the mutation lies in one of the targeted areas that many diagnostic PCR tests use.

These tests also use other targets, usually a combination of at least two. Scientists can look for PCR tests that are negative for the spike sequence but positive for the other targets. This would indicate that the person has the B.1.1.7 variant of the SARS-CoV-2 virus.

Researchers from Public Health England used this method to track the spread of the variant in the British population and estimate how its transmissibility compared with those of earlier variants.

But studying how easily a virus transmits from one person to another is technically challenging. Epidemiological data can provide models, and laboratory investigations into the dynamics of infection can uncover more detail. Such studies are ongoing.

Some scientists have called into question whether the B.1.1.7 variant has a higher rate of transmissibility, suggesting that the high numbers of these cases of infection may result from the founder effect.

The founder effect is a term used by scientists who study evolution. It stipulates that a small group of individuals can give rise to a new population.

In the context of viruses, the founder effect could explain how B.1.1.7 has spread so rapidly. Researchers have suggested that superspreading events and a rise in rates of infection throughout England may be the reason for such large numbers of infections with the B.1.1.7 variant.

"While this was initially thought possible when the variant was first identified in September, the evidence has increasingly shown this to be unlikely and has now been largely ruled out," Prof. Martin Hibberd, a professor of emerging infectious disease at the London School of Hygiene and Tropical Medicine (LSHTM), in the U.K., told us.

Prof. Jonathan Stoye, a group leader at The Francis Crick Institute, in London, whose lab studies virus-host interactions, echoed this sentiment. "Initially I thought this might be the case," he noted, adding:

> "Though it might make some contribution to the initial spread of the new variant, it seems unlikely to explain the greatly increased case incidence, given the simultaneous increase in the proportion of the variant in multiple settings. Rather, it would appear likely that higher levels of virus release, perhaps resulting from the infection of more cells, lead to higher rates of virus transmission."
>
> – Prof. Jonathan Stoye

Exactly how is B.1.1.7 different?

Many questions about B.1.1.7. remain. How does it compare with preexisting strains, in terms of transmissibility? Is it likely to cause more severe COVID-19? Are children more vulnerable to this variant?

Available research seems to indicate that the new variant has a higher degree of transmissibility.

One study, which has yet to be peer-reviewed but which became available on the preprint server *medRxiv* on December 26, 2020, used mathematical modeling to estimate the new variant's transmissibility, compared with that of "preexisting variants of SARS-CoV-2."

The team of researchers, from the LSHTM, concludes that the B.1.1.7 variant "is 56% more transmissible" than other SARS-CoV-2 variants.

Meanwhile, a report, also in preprint form, from Imperial College London, looks at currently available epidemiological and genetic data and likewise concludes that B.1.1.7 appears to have higher transmissibility than other variants of SARS-CoV-2.

The researchers estimate that B.1.1.7 is 50–75% more transmissible, and they consider the founder effect in their analysis. However, their data speaks in favor of a competitive advantage of this variant over previous variants based on increased transmissibility.

However, Dr. Julian W. Tang, a clinical virologist at the University of Leicester, in the U.K., has cautioned that "It is still difficult to separate out human behavioral versus viral genetic contributions as causes for enhanced transmissibility in all populations," adding that "In practice, we just have to deal with this."

Information from Public Health England last updated on December 29, 2020, notes that there is "currently [...] no evidence that the variant is more likely to cause severe disease or mortality," though further investigations are underway.

Prof. Hibberd told *MNT* that based on existing data from the U.K., the new variant does not appear to lead to more severe cases of COVID-19, compared with other variants or strains of SARS-CoV-2.

"The infection case fatality rate, [which is] based on community population-based estimates of the number of people [with an infection] and the number of deaths observed — estimated from the data in the U.K. — does not seem to have changed significantly, suggesting that the new

However, he warned that accurate comparative data may be hard to gather, explaining:

> "More accurate estimates of the disease severity are being built up over time, based on the observed data directly comparing the new and old variants. But as the old variant becomes rare in the U.K., this will become increasingly difficult. As the variant arrives in other countries, such as the U.S., further data will be [available]."

Impact on public health measures

The rapid spread of infections in the U.K. — largely blamed on the B.1.1.7 variant — throughout December 2020 led first to a local tightening of restrictions, then to the enforcement of strict lockdowns in England and Scotland. Ireland has prolonged its nationwide lockdown, with tighter rules in place.

In the preprint version of the LSHTM study, the researchers warn that given the new variant's apparently higher transmissibility, "Existing control measures [to contain the spread of the virus] are likely to be less effective, and countries may require stronger proactive interventions to achieve the same level of control."

In a statement published on December 31, 2020, the World Health Organization (WHO) noted that several countries are already taking what measures they can to stay ahead of the game.

Countries that have observed the spread of new virus variants have "intensified sampling to understand how widely these new variants are circulating," and scientists have ramped up efforts to understand whether or how new SARS-CoV-2 variants might affect transmission, disease severity, and vaccine effectiveness, according to the statement.

The WHO have also recommended that "Risk communication and community engagement activities [be] scaled up to explain the public health implications of SARS-CoV-2 variants to the public and emphasize the importance of maintaining ongoing preventive measures to reduce transmission."

One unanswered question about B.1.1.7 concerns the susceptibility of children to the new variant.

In the U.K., schools were largely open during the fall term but have recently closed for most children. Some scientists have suggested that children are more likely to develop an infection with B.1.1.7 than with previous variants of SARS-CoV-2.

However, there is no consensus among the scientific community.

“As children are frequently asymptomatic, it has been difficult to estimate their true population-based infection rates. The initial data seems to suggest that more teenagers are becoming positive, but the data is currently unclear,” Prof. Hibberd explained.

Prof. Stoye shared this view: “Given a more transmissible virus, it seems inevitable that more children will [have an infection with] the new variant and will then [pass this on] to their families. I cannot comment on the impact of infection on the health of individual children; more studies [...] will be required to resolve this question.”

COVID-19 vaccines and the new variant

According to Prof. Stoye, there are worries that currently authorized

they are against preexisting variants that were involved in testing during clinical trials.

“One area of concern relates to the possibility that new variants will show reduced sensitivity to immune responses to the recently introduced vaccines,” Prof. Stoye told *MNT*. “While it seems unlikely that the current variants will escape, future variants might do so.”

“It will be important to monitor new viruses for neutralization by sera [a blood component] from vaccinated individuals. In the future, it may be necessary to alter the vaccine composition in the way that we do with flu, but hopefully not as often,” he added.

MNT also contacted NIAID, an organization within the National Institutes of Health (NIH) that had collaborated with the biotechnology company Moderna to create a COVID-19 vaccine currently authorized for use in the U.S. and U.K. They explained:

> “NIAID scientists have communicated with counterparts at Public Health England, a part of the U.K. government, to closely track their understanding of SARS-CoV-2 VOC 202012/01, also known as the U.K. variant.
>
> At present, NIAID scientists believe that the SARS-CoV-2 vaccines supported by Operation Warp Speed [OWS] will provide protection against SARS-CoV-2 VOC 202012/01, including the OWS-supported Moderna and Pfizer-BioNTech COVID-19 vaccines authorized for emergency use by the U.S. Food and Drug Administration [FDA].”

“As part of a person’s immune response to the vaccine, they produce many antibodies that bind to different locations on the spike protein on the surface of the SARS-CoV-2 virus. Even if a SARS-CoV-2 variant has a few mutations that prevent binding of some antibodies, scientists expect that other antibodies with different binding properties will neutralize the virus,” NIAID also told *MNT*.

The pharmaceutical corporation Pfizer, whose COVID-19 vaccine — created in collaboration with the biotechnology company BioNTech — has gained authorization in the U.S., U.K., and the European Union, made a similar statement:

> "The identification of a new variant of the SARS-CoV-2 virus does not impact the rollout of the Pfizer and BioNTech COVID-19 mRNA Vaccine BNT162b2. Health professionals are advised to continue to follow the official guidance on [the] administration of the vaccine."

They added that "The companies [Pfizer and BioNTech] are monitoring SARS-CoV-2 sequence changes and working to generate data to evaluate how well serum from people immunized with BNT162b2 may be able to neutralize the new strain."

Hopeful findings and adaptable technology

In collaboration with scientists at the University of Texas Medical Branch at Galveston, Pfizer recently released a study, currently in preprint form, in which they looked at the N501Y mutation.

Using serum samples from volunteers who had received the Pfizer-BioNTech COVID-19 vaccine in a clinical trial, the researchers analyzed how well the antibodies in the samples could neutralize the SARS-CoV-2 virus.

They found that the sera had "equivalent neutralizing titers," which means that the same amount of serum was able to neutralize both the original virus and the mutant variant. This indicates that the vaccine will work just as well against the variant.

However, the team only studied the N501Y mutation in isolation, and B.1.1.7 has a number of mutations in its spike protein.

At a press conference on Dec 22, 2020, Dr. Uğur Şahin, the CEO of BioNTech, explained that the company had previously tested their vaccine in combination with a number of SARS-CoV-2 variants and found that it worked well against these. These findings are available in preprint form.

Dr. Şahin added that the company could easily adapt their vaccine platform to combat new variants.

The Pfizer-BioNTech COVID-19 vaccine is based on mRNA technology. This means that the vaccine contains a small amount of the genetic code of SARS-CoV-2 produced in a lab. Once injected as a vaccine, this code

Our immune system reacts to this manufactured spike protein and builds up immunity to the SARS-CoV-2 virus. At no point could the vaccine cause COVID-19 because it contains no live pathogens.

Technically, it would not be difficult to change the sequence of the genetic code in the vaccine so that it matches that of the new variant. Dr. Şahin estimates that this would take about 6 weeks.

He noted, however, that health authorities such as the FDA would need to approve any change in the vaccine before it could be administered.

On January 25, 2021, Moderna also published a press release announcing that their vaccine is effective against the B.1.1.7 variant. "The two-dose regimen of the Moderna COVID-19 vaccine at the 100 [microgram] dose is expected to be protective against emerging strains detected to date," they state.

The company have yet to publish data supporting these claims. Nevertheless, Moderna officials also said that "Out of an abundance of caution," they are launching a clinical program in which they will continue to test their vaccine's effectiveness against new SARS-CoV-2 variants and that the company aim to increase the vaccine's production of neutralizing titers against such variants.

In a phase 1 clinical trial, Moderna will thus test whether accounting for strain-specific spike proteins would improve the vaccine's effectiveness.

The pharmaceutical company AstraZeneca and the Oxford Vaccine Group did not reply to *MNT*'s request for comment regarding their vaccine's effectiveness against the B.1.1.7 variant.

Another new variant

While much of the news has focused on B.1.1.7, another new variant has

It also has two additional mutations in that region, prompting further concerns about how effective vaccination will be. A number of academic experts have told the Science Media Centre, in the U.K., that they believe that existing COVID-19 vaccines can combat this variant, however.

With increased travel restrictions and heightened lockdowns throughout much of the world, how likely is it that these variants will become dominant across wider areas?

"New variants with enhanced growth properties are a concern to everyone. The near-simultaneous appearance of two variants of concern in the U.K. and South Africa suggests that such events can occur in any setting," Prof. Stoye told *MNT*. "Short of total separation between different countries, spread will almost inevitably occur."

"From past experience, it is likely that this new variant will travel widely around the world and is likely to become the dominant strain worldwide," Prof. Hibberd commented. "This new variant is not likely to be the last and there will, no doubt, be further variants in the coming year or years."

Both experts stressed the importance of following public health guidelines, such as physical distancing, wearing face coverings, washing the hands frequently and thoroughly, and following all local lockdown rules.

Already last spring, scientists were cautioning the public that the new coronavirus may be here to stay, with waves of infections becoming a seasonal occurrence.

As more variants of SARS-CoV-2 begin to emerge around the world, adherence to these basic public health guidelines is becoming a "new normal," while national vaccination programs will help gradually build more widespread immunity to the virus.

Dr. Tedros Adhanom Ghebreyesus, director-general of the WHO, has pointed out that difficult experiences such as the ongoing pandemic help bring about much-needed change and improvements:

Tweet

For live updates on the latest developments regarding the novel coronavirus and COVID-19, click here.

Public Health Immune System / Vaccines Infectious Diseases / Bacteria / Viruses COVID-19

FEEDBACK:

Is there more than one strain of the new coronavirus?

Written by Yella Hewings-Martin, Ph.D. on May 22, 2020 — Fact checked by Jasmin Collier

Since the emergence of the new coronavirus, called SARS-CoV-2, several researchers have proposed that there is more than one strain, and that mutations have led to changes in how infectious and deadly it is. However, opinions are divided.

All data and statistics are based on publicly available data at the time of publication. Some information may be out of date. Visit our coronavirus hub *and follow our* live updates page *for the most recent information on the COVID-19 pandemic.*

Genetic mutations are a natural, everyday phenomenon. They can occur every time genetic material is copied.

When a virus replicates inside the cell it has infected, the myriad of new copies will have small differences. Why is this important?

When mutations lead to changes in how a virus behaves, it can have significant consequences. These do not necessarily have to be detrimental to the host, but in the case of vaccines or drugs that target specified viral proteins, mutations may weaken these interactions.

Since the emergence of SARS-CoV-2, several research studies have highlighted variations in the virus's genetic sequence. This has prompted discussion about whether or not there are several strains, if this has an impact on how easily the virus can infect a host, and whether or not this affects how many more people are likely to die.

Many scientists have called for caution. In this Special Feature, we summarize what researchers currently know about SARS-CoV-2 mutations and hear from experts about their views on what these mean for the pandemic.

> *Stay informed with live updates on the current COVID-19 outbreak and visit our coronavirus hub for more advice on prevention and treatment.*

SARS-CoV-2 is an enveloped RNA virus, which means that its genetic material is encoded in single-stranded RNA. Inside a host cell, it makes its own replication machinery.

RNA viruses have exceptionally high mutations rates because their replications enzymes are prone to errors when making new virus copies.

Virologist Prof. Jonathan Stoye, a senior group leader at the Francis Crick Institute in London in the United Kingdom, told *Medical News Today* what makes virus mutations significant.

“A mutation is a change in a genetic sequence,” he said. “The fact of a mutational change is not of primary importance, but the functional consequences are.”

If a particular genetic alteration changes the target of a drug or antibody that acts against the virus, those viral particles with the mutation will outgrow the ones that do not have it.

“A change in a protein to allow virus entry into a cell that carries very low amounts of receptor protein could also provide a growth advantage for the virus,” Prof. Stoye added.

“However, it should be stressed that only a fraction [of] all mutations will be advantageous; most will be neutral or harmful to the virus and will not persist.”

> “Mutations in viruses clearly do matter, as evidenced by the need to prepare new vaccines against [the] influenza virus every year for the effective prevention of seasonal flu and the need to treat HIV-1 simultaneously with several drugs to [prevent the] emergence of resistant virus.”
>
> – Prof. Jonathan Stoye

Researchers find mutations

MNT recently featured a research study by a team from Arizona State University in Tempe. The paper described a mutation that mimics a similar event that occurred during the SARS epidemic in 2003.

The team studied five nasal swab samples that had a positive SARS-CoV-2 test result. They found that one of these had a deletion, which means that a part of the viral genome was missing. To be precise, 81 nucleotides in the viral genetic code were gone.

Previous research indicated that similar mutations lowered the ability of the SARS virus to replicate.

Another study, this time in the *Journal of Translational Medicine*, proposed that SARS-CoV-2 had picked up specific mutation patterns in distinct geographical regions.

The researchers, from the University of Maryland in Baltimore and Italian biotech company Ulisse Biomed in Trieste, analyzed eight recurrent mutations in 220 COVID-19 patient samples.

They found three of these exclusively in European samples and another three exclusively in samples from North America.

Another study, which has not yet been through the peer review process, suggests that SARS-CoV-2 mutations have made the virus more transmissible in some cases.

In the paper, Bette Korber — from the Los Alamos National Laboratory in New Mexico — and collaborators describe 13 mutations in the region of the viral genome that encodes the spike protein.

This protein is crucial for infection, as it helps the virus bind to the host cell.

The researchers note that one particular mutation, which changes an amino acid in the spike protein, “may have originated either in China or Europe, but [began] to spread rapidly first in Europe, and then in other parts of the world, and which is now the dominant pandemic form in many countries.”

Prof. Stoye commented that the results of this study are, in some ways,

“Viruses are typically finely tuned to their host species. If they jump species, e.g., from bat to human, a degree of retuning is inevitable both to avoid natural host defenses and for optimum interaction with the cells of the new host,” he said.

“Random mutations will occur, and the most fit viruses will come to predominate,” he added. “Therefore, it does not seem surprising that SARS-CoV-2 is evolving following its jump to, and spread through, the human population. Clearly, such changes are currently taking place, as evidenced by the apparent spread of the [mutation] observed by Korber [and colleagues].”

However, Prof. Stoye does not think that it is clear at this point how mutations will drive the behavior of SARS-CoV-2 in the long term.

“Fears about SARS-CoV-2 evolution to resist still-to-be-developed vaccines and drugs are not unreasonable,” he explained. “Nevertheless, it is also possible that we will see evolution to a less harmful version of the virus, as may well have occurred following initial human colonization by the so-called seasonal coronaviruses.”

Earlier this year, researchers from Peking University in Beijing, China, published a paper in *National Science Review* describing two distinct lineages of SARS-CoV-2, which they termed "S" and "L."

They analyzed 103 virus sequence samples and wrote that around 70% were of the L lineage.

However, a team at the Center for Virus Research at the University of Glasgow in the U.K. disagreed with the findings and published their critique of the data in the journal *Virus Evolution*.

"Given the repercussions of these claims and the intense media coverage of these types of articles, we have examined in detail the data presented [...] and show that the major conclusions of that paper cannot be substantiated," the authors write.

Prof. David Robertson, head of Viral Genomics and Bioinformatics at the Centre for Virus Research, was part of the team. *MNT* asked his views on the possibility of there being more than one strain of SARS-CoV-2.

"Until there is some evidence of a change in virus biology, we cannot say that there are new strains of the virus. It's important to appreciate that mutations are a normal byproduct of virus replication and that most mutations we observe won't have any impact on virus biology or function," he said.

"Some of the reports of, for example, amino acid changes in the spike protein are interesting, but at the moment, these are at best a hypothesis. Their potential impact is currently being tested in a number of labs."

Prof. Stoye thinks that it is "more a case of semantics rather than anything else" at the moment.

"If we have different sequences, we have different strains. Only when we have a greater understanding of the functional consequences of the evolutionary changes observed does it make sense to reclassify the different isolates," he said.

"At that point, we can seek to correlate sequence variation with prognostic or therapeutic implications. This may take a number of years."

Serotypes and future research

So, what kind of evidence are skeptical scientists looking for in the debate around multiple SARS-CoV-2 strains?

“For virologists, ‘strain’ is rather a subjective word that does not always have a clear specific meaning,” he commented.

“More useful in the SARS-CoV-2 situation would be the idea of ‘serotype,’ which is used to describe strains that can be distinguished by the human immune response — an immune response to one serotype will not usually protect against a different serotype. For SARS-CoV-2, there is no conclusive evidence that this has happened yet.”

“To show that the virus has genetically changed sufficiently to create a different immune response, we would need to characterize the immune protection and show that it worked for one serotype and not for another,” he continued.

Prof. Hibberd, who has been researching SARS-CoV-2 mutations, explained that scientists are studying neutralizing antibodies to help them define a serotype for SARS-CoV-2. These antibodies can prevent the virus from infecting a host cell, but they may not be effective against a new strain.

> “Several groups around the world have identified a specific mutation in the SARS-CoV-2 spike protein, and they are concerned that this mutation might alter this type of binding, but we cannot be sure it does that at the moment. More likely, this mutation will likely affect the virus binding to its receptor [...], which might affect transmissibility.”
>
> – Prof. Martin Hibberd

“We ideally need experimental evidence, [such as a] demonstration of a mutation leading to a functional change in the virus in the first instance, and secondly a demonstration that this change will have an impact in [people with the infection],” Prof. Robertson suggested.

He pointed to lessons that experts learned during the 2014–2018 Ebola outbreak in West Africa, where several research groups had suggested that a mutation had resulted in the virus becoming more easily passed between people and more deadly.

Cell culture experiments showed that the mutated virus was able to replicate more rapidly. However, when scientists subsequently studied this in animal models, they found that it did not behave any differently

Scientists around the world continue to search for answers to the many outstanding questions around SARS-CoV-2. No doubt, we will see more research emerge in the coming months and years that will assess the impact of SARS-CoV-2 mutations on the COVID-19 pandemic and the future of this new coronavirus.

For live updates on the latest developments regarding the novel coronavirus and COVID-19, click here.

Genetics Public Health Flu / Cold / SARS
Infectious Diseases / Bacteria / Viruses COVID-19

RELATED COVERAGE

Global COVID-19 vaccine summary: Side effects

In this feature, we look at the side effects of each of the 13 COVID-19 vaccines that have been authorized for use in at least one country.

How did we develop a COVID-19 vaccine so quickly?

safety.

READ MORE

Get our newsletter

Keep up with the ever-changing world of medical science with new and emerging developments in health.

Enter your email SUBSCRIBE

Your privacy is important to us