

The new UK variant of coronavirus raises urgent questions about pandemic policy

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“The bottom line is that we need to suppress transmission of all SARS-CoV-2 viruses as quickly as we can. The more we allow it to spread, the more opportunity it has to change. I cannot stress enough to all governments and people how important it is to take the necessary precautions to limit transmission.” Director-General Tedros Adhanom Ghebreyesus

On December 14, Public Health England (PHE) informed the World Health Organization (WHO) of a new variant of the SARS-CoV-2 virus, designated VUI-202012/01, which stands for the first Variant Under Investigation in December 2020. By December 13, 1,108 cases of this specific variant had been identified, predominantly from south and east of England.

What concerned scientists were the high number of mutations it carried and the speed with which it was becoming the dominant strain. After first appearing in the county of Kent on September 20, it was responsible for 28 percent of infections in London in early November. By December 9, that figure had climbed to 62 percent.

Jeffrey Barrett, the director of the COVID Genomics Initiative at the Wellcome Sanger Institute, told the *Financial Times*, “This new variant is very concerning, and is unlike anything we have seen so far in the pandemic.” There have been 23 letters in its genetic code that have undergone a change, of which 17 could affect its behavior or improve its ability to adhere to human cells and propagate.

The UK is one of few countries, including the United States, Australia, Iceland, the Netherlands, South Africa and the Democratic Republic of the Congo, sequencing the SARS-CoV-2 virus. Since the pandemic began, close to 285,000 sequence submissions have been made to GISAID, a global science initiative and the primary source for open access to the coronavirus’s genomic data. The UK’s SARS-CoV-2 genomic sequencing consortium is the largest contributor to the GISAID database, with more than 120,000 sequences.

Dr. Susan Hopkins, PHE Joint Medical Advisor and epidemiologist for the Department of Infectious Disease at the Imperial College, London, added to the press release statement on December 14, “We are investigating a new strain of SARS-CoV-2, predominately in Kent and the surrounding areas. It is not unexpected that the virus should evolve, and it is important that we spot any changes quickly to understand the potential risk any variant may pose. There is currently no evidence that this strain causes more severe illness, although it is being detected in a wide geography especially where there are increased cases being detected.”

In a query from journalists at the WHO Press Brief on December 21, Dr. Mike Ryan explained that their colleagues at the PHE monitor complete sequences of a proportion of cases all the time. They became aware of increased transmissions in the population in the south and

east of England towards the end of November. When they began to look at the cases and the characteristics of the viral sequences, they identified the variance now under investigation. Their retrospective analysis determined that this variance had emerged in late September. Once they recognized the epidemic implications, they notified the WHO through their International Health Regulations reporting mechanisms.

The ability to trace in real time the changes in the genetic sequence of a virus around the world during a pandemic is unprecedented in human history. However, understanding how these mutations will affect the nature of the virus is a laborious and uncertain undertaking. It will require retrospective and prospective studies to appreciate scientifically how they will impact the population.

Kristian Andersen, director of infectious disease genomics at Scripps Research Institute in California, said, “I have seen many articles stating, ‘no effect on immunity or vaccines or clinical features.’ That is not correct. The fact is we don’t know but we will in coming weeks.” Given that the vaccines target multiple spike protein sites, many experts in the field have agreed that it is unlikely that these therapeutics would be ineffective.

Dr. Andersen added, “This spread is happening at a moment in time when there are already many lineages circulating, and despite that, it is displacing them all. We can’t say for sure, but to me, it looks like this very explosive growth is primarily because of the new mutation.” His report on the origin of the virus published in the journal *Nature Medicine* was critical in refuting the claim that the SARS-CoV-2 was produced in a laboratory.

However, this unknown factor in the change in the virus’s capabilities has created the present social consternation on the B.1.1.7 variant of the SARS-CoV-2 that makes the policy of herd immunity such a dangerous and demented proposal.

On December 18, the PHE notified the government after modeling analysis revealed the seriousness of its findings. The new strain is considered to be 70 percent more transmissible than the previous ones. According to Dr. Maria Kerkhove, technical lead for the WHO, the reproduction factor increased by 0.4. In other words, it climbed from 1.1 to 1.5 despite the measures that were already in place. This implies that before the emergence of this strain, the region’s epidemic’s growth factor with all its measures in place was only at a standstill. However, now the public health scientists see the epidemic grow despite these measures.

Regarding the term reproduction number (R0), it is a number that defines the number of expected secondary cases that are produced by a single infection in a completely susceptible population. In the above instance, ten people will go on to infect 15 others. The R0 is affected

by numerous biological (virus and host factors, duration of transmissibility, etc.), socio-behavioral (social distancing, lockdowns, mask usage), and environmental (season, population density, indoors versus outdoors) factors that govern the SARS-CoV-2's transmission. The R0 is not a constant number for the virus, and is estimated through complex mathematical models.

Prime Minister Boris Johnson, who has frequently downplayed the pandemic's health risks and called it "inhuman" to cancel Christmas, issued a sudden about-face on Saturday, placing London and most of England's Southeast into lockdown and banning Christmas-season gatherings beyond single households. The measures imposed were even more severe than those issued in March, reflecting the fear that has taken hold within the political establishment of this variant of the virus.

On Saturday, speaking to a live audience on camera, he said, "When the virus changes its method of attack, we must change our method of defense. We have to act on information as we have it because this is now spreading very fast." According to the *New York Times*, the pace of new infections has almost doubled over the last two weeks. Faster spread due to higher transmissibility implies more hospitalizations, which will lead to more fatalities, even if the mutated virus is no more deadly.

Viruses are constantly changing through random mutations, and monitoring these changes is useful in phylogenetic studies and contact tracing. In most cases, the mutations are benign and do not contribute any particular characteristics to the variant. They rarely impact clinical outcomes in the population. In the present case, however, the B.1.1.7 variant has demonstrated multiple mutations in the spike protein, which could aid the virus in binding to human cells more efficiently and entering them. In a particular comment regarding B.1.1.7 variant, the GISAID website notes, "Mutations in the spike protein have relevance for potential effects on both host receptor as well as antibody binding with possible consequences for infectivity, transmission potential, and antibody escape and vaccine escape. Actual effects need to be measured and verified experimentally."

These include mutation N501Y, in one of six key amino-acid residues in the receptor-binding domain (RBD) of the spike protein, critical for binding to the ACE2 receptor on human cells. Other notable mutations include the spike deletion 69-70 del, which has been described in the context of evasion of the human immune response, and mutation P681H, which plays an essential role in viral infectivity. It has been hypothesized that these changes are providing the virus with a selective advantage over other variants.

In a December 20 threat assessment brief, the European Center for Disease Prevention and Control writes, "The unusually high number of spike protein mutations, other genomic properties of the variant, and the high sequencing coverage in the UK suggests that the variant has not emerged through gradual accumulations of mutations in the UK. It is also unlikely that the variant could have arisen through selection pressure from ongoing vaccination programmes as the observed increase does not match the timing of such activities."

The last observation is important, since it means that the vaccination drive which began in Britain three weeks ago is not the cause of the mutations, and the mutated viruses are thus unlikely to be more resistant to the vaccination. But the very fact that there is as yet no convincing scientific explanation of how so many mutations could take place without being detected at an earlier stage appears to have shaken the British authorities.

South Africa has also reported a similar mutation in the virus that

has become the dominant form in more than 90 percent of cases. The new variant, known as 501.V2, is dominating the second wave of their battle with the pandemic, leading to sterner lockdown measures. Though this South African variant shares with the UK variant mutations in the N501Y region of the spike protein, they have no close evolutionary relationship. It does suggest "that the emergence of successful variants with similar properties may not be rare."

Since the announcement on Saturday of the UK lockdown, one country after another in Europe, Asia, South America, and the Middle East, now totaling at least 38 countries, is imposing restrictions on travel from the UK or other countries with documented cases of the variant. The US has avoided imposing such bans yet. Most experts believe these bans will not prevent the spread of the variant across their borders.

Dr. Ravindra Gupta, a virologist at the University of Cambridge, who detailed the recurrent emergence and significance of onward transmission of the deletion 69-70del in a publication dated December 15, noted that "this thing's transmitting, it's acquiring, it's adapting all the time. But people don't want to hear what we say, which is: this virus will mutate."

In the concluding remarks of the bioRxiv preprint, he writes, "Given the emergence of multiple clusters of variants carrying RBD mutations and the deletion 69/70del, limitation of transmission takes on a renewed urgency. Concerted global vaccination efforts with wide coverage should be accelerated. Continued emphasis on testing/tracing, social distancing, and mask-wearing is essential, with investment in other novel methods to limit transmission. Detection of the deletion by rapid diagnostics should be a research priority as such tests could be used as a proxy for antibody escape mutations to inform surveillance at a global scale."

In layman's terms, this means that it is essential for the struggle against COVID-19 to monitor in particular any mutations that would make it better able to evade the body's own immune systems. COVID-19 is not merely a moving target. It is constantly mutating in ways that, through natural selection, tend to make it more efficient. The longer the virus is allowed free rein, and the greater the number of people it is allowed to infect—through the criminal policy of "herd immunity"—the more likely it is to become more infective and, potentially, more lethal. That is why the only rational, scientific response to the pandemic is to shut it down as quickly as possible, through a lockdown of all non-essential businesses and schools until mass vaccination brings it under control.



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