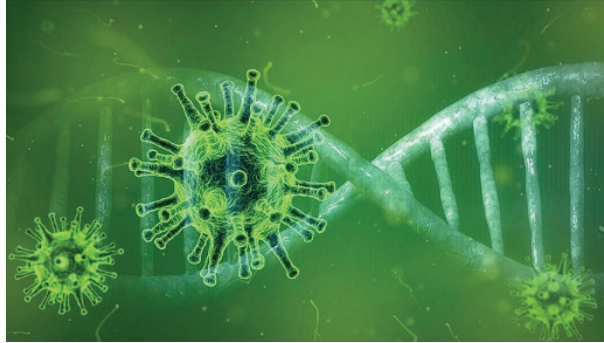


COVID-19 News: Scientists Warns That SARS-CoV-2 B.1.1.7 Variant Could Become Globally Dominant In Weeks As New Variant Replicates Twice Faster!

COVID-19 News: Polish researchers from the University of Warsaw and the Polish Academy of Sciences are warning based on a new study that the new variant of the SARS-CoV-2 detected in England replicates more than two times faster than the earlier strains. This replication advantage enhances its capability to become to a dominant global variant in a matter of a short time.



The novel SARS-CoV-2 Variant Under Investigation VUI-202012/01 (also known as B.1.1.7), first collected on September 20, 2020, in Kent, is a rapidly growing lineage that in the first half of December 2020 constitutes more than 1/3 of all SARS-CoV-2 genomes sequenced in England.

Based on GISAID data the study team have shown nearly exponential growth of the VUI- 202012/01 to non-VUI-202012/01 genomes ratio in the five-week period since October 19 till November 22, 2020, with weekly growth rate of 2.31 [95% CI: 2.08–2.57].

Assuming the serial interval of 6.73 days the study team estimated the replicative advantage of VUI-202012/01 lineage as $2.316.73/7 = 2.24$ [95% CI: 2.03–2.48].

Such significant replicative advantage and the fact that London serves as major international transportation hub suggest that the VUI-202012/01 strain will likely become globally dominant, hindering containment of the COVID- 19 epidemics prior to massive vaccinations.

Even then there are no real studies to actually prove that the new vaccines will work on these new strains with more than 23 mutations on them. All we have so far is mere hearsay from vaccine manufacturers who have trillions of dollars at stake.

The study findings were published on preprint server but are currently being peer reviewed. <https://www.medrxiv.org/content/10.1101/2020.12.28.20248906v1>

It was only in September 20, 2020, that researchers first detected the first two genomes that are now labeled as the novel SARS-CoV-2 Variant Under Investigation (VUI)-202012/01, also known as the B.1.1.7 lineage.

Alarmingly the next 30 days saw the exponential growth of the lineage, which comprised over 1/3 of all SARS-CoV-2 sequences in England in the first half of December.

The B1.1.7 variant has a total of 23 mutations with nine mutations in the spike protein, all of which are not unique to it. One of them is a deletion, del 6-70HV, which makes the spike gene invisible to the dPCR probe used in England. This is called spike gene target failure, SGTF.

<https://www.thailandmedical.news/news/emerging-sars-cov-2-variants-in-uk-like-the-b-1-1-7-strain-and-the-501-v2-strain-in-south-africa-and-elsewhere-will-change-course-of-covid-19-badlyected-super-strain>><https://www.thailandmedical.news/news/u-s-cdc-indicates-that-vaccines-might-not-protect-against-new-uk-variant-b-1-1-7-new-details-show-new-variant-could-be-the-expected-super-strain>

This new strain has become the most common strain to carry this deletion due to its high multiplication rate. It has been found, by scientists at Public Health England (PHE), to have a reproduction number that is almost 1.5 times higher than earlier strains, while others showed its estimated transmissibility to be 56% higher.

This Polish study uses a new approach. The study team gathered data from all over England, from the Global Initiative for Sharing All Influenza Data (GISAID) database, to find the ratio of genomes from VUI-202012/01 to non-VUI-202012/01. This data covers about 5% of genomes from England.

The study team tracked this ratio and calculated the growth rate of the number of sequenced genomes in these two categories from week to week, as over the five-week period of the whole study.

The study team found that the growth of VUI-202012/01 was virtually exponential over weeks 43-47 of 2020. The ratio of the replication numbers of the two types of genomes was estimated.

However over the four weeks from week 38 to week 42, the study team found that there were less than five genomes from the VUI-202012/01 being collected each week.

However, the number shot up to 28 in week 43 and continued to rise exponentially until week 47. In week 48, this growth seems to come to an end. This may be more apparent than real, perhaps because the data coming in was incomplete.

Interestingly in the five-week period, the growth rate fraction of VUI-202012/01 to non-VUI-202012/01 strains was at over 2 per week, in fact, it was 2.31. The ratio of reproduction numbers of these two types of variants was estimated on the assumption that both types of strain have the same serial interval (interval from symptom onset of the primary case to that of secondary cases), namely, 6.73 days. This ratio came to $2.316.73/7 = 2.24$.

However a smaller subset of sequenced variants was studied by using an earlier cut-off date for sequence submission. Setting the cut-off at December 16 rather than December 26 reduced the number of VUI-202012/01 genomes by 200.

Significantly, this work resulted in a calculated reproduction number advantage of 2.3 times in favor of VUI-202012/01 strains.

Also as there were only 19 cases of this lineage occurring outside England during weeks 43-48, the researchers used data from England rather than the UK.

Still, using whole-UK values instead still resulted in a ratio of 2.3.

In order to rule out the effect of a chance aggregation of cases caused by the new variant, the researchers looked at the confidence intervals again. They found that the confidence intervals calculated on the assumption that the genomes sequenced from the new variants were drawn at random from a binomial distribution were narrower than their own results, calculated from the standard error of the slope. This supports the accuracy of the data on which the current study is based.

However the serial interval was calculated as equal for both strains. However, this could be wrong, as the serial interval is not a number but has a sub-exponential distribution.

The study team commented, "Although no current data indicate this, it may happen that the faster spread of VUI-202012/01 strain partially results from the shorter generation time."

Most significantly and important, these study findings indicate that the reproduction number of VUI-202012/01 strains is 2.24 times higher than that of non-VUI-202012/01 strains of SARS-CoV-2.

Note that this difference in replication number is not the result of or affected by public health interventions such as protective measures because the growth rates were measured prospectively.

As London is a central hub connecting most of the transportation routes the world over, the new lineage may have already covered Europe and the USA to become globally dominant.

Importantly the day after the study ended, there were 12 of these genomes from Italy, nine from Denmark, 7 from Ireland, 6 from Japan, and several from other European and Asian countries.

The strain has also already been discovered in Thailand.

The study team said, "If confirmed, spread of the faster-replicating VUI-202012/01 strain may hinder the efforts to contain the COVID-19 epidemics prior to massive vaccinations."