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Singapore researchers discover new Covid-19 variant which causes milder infections



Patients infected with the latest variant of the coronavirus were observed to have had better clinical outcomes. ST PHOTO: LIM YAOHUI

🕒 PUBLISHED AUG 21, 2020, 10:45 AM SGT | UPDATED AUG 22, 2020, 12:29 AM

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SINGAPORE - Researchers in Singapore have discovered a new variant of Covid-19 that causes less severe infections, according to a new study in the prestigious medical journal The Lancet.

This could provide new avenues for vaccine and therapeutic development, experts say.

The latest reported variant of the Sars-CoV-2 virus which causes Covid-19 emerged in Wuhan, China early in the pandemic and was exported to Singapore and Taiwan, according to the study by researchers in various institutions, including the National Centre for Infectious Diseases (NCID) and the Duke-NUS Medical School.

It was detected in a cluster of cases here in January and February. The researchers said in the study that patients infected with the variant, which has a 382 nucleotide deletion, were observed to have had better clinical outcomes relative to those infected by viruses without this deletion.

A lower proportion of them, for example, had hypoxia (where the body is short of oxygen) requiring supplemental oxygen, when compared with those infected with the wild-type virus.

A pre-print publication in March said that the same variant was found in eight hospitalised patients in Singapore and that viruses with the mutation or deletion in a region known as ORF8 had been circulating for at least four weeks. Similar variants were also observed in the Sars virus.

According to the Lancet study, the 382 variant was not detected after March. The researchers said in the paper that further study of variants that have deletions in the same region could have implications for the development of treatments and vaccines.

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Weighing in, Professor Edison Liu, the former founding head of the Genome Institute of Singapore, and currently, the president and chief executive of The Jackson laboratory in the United States, said: "This is the first study to show a clinical difference based on the genetic differences between strains.

"This suggests that gene variations may have an important role in defining the disease outcome."

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Associate Professor Hsu Li Yang, an infectious diseases specialist from the NUS Saw Swee Hock School of Public Health, said mutations will occur as Sars-CoV-2 continues to spread, and most of the time, these mutations will have little discernible impact on the transmissibility or virulence of the virus.

In rare cases, though, they may enable the virus to spread more easily, or become more or less deadly, he said.

"In this particular case, the large (382 base pair) deletion resulted in a virus that is less deadly," he said.

"If this mutant clade becomes very widespread, then the impact on health will become less."

However, he added, "the actual impact will depend on how easily this particular mutant spreads, which we do not know well at present, because more than 99 per cent of the virus found in patients worldwide (or even in Singapore) will not have their full genomes sequenced".

Experts note that viruses mutate constantly. It is a natural and mundane part of life for a virus. While mutations can make a virus more virulent, or it can make it less so, the changes are rarely significant.

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