

# S'pore scientists find milder variant of Covid-19 virus

## Patients infected with variant had better clinical outcomes; findings could influence treatment

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Researchers in Singapore have discovered a new variant of the Covid-19 virus that causes less severe infections.

They have observed that patients infected with the variant, which is missing a section in its genome, had better clinical outcomes relative to those infected by viruses without this deletion.

A lower proportion of them, for example, had low blood oxygen (hypoxia) or needed intensive care in hospital, compared with those infected by the wild-type virus.

These findings were announ-

ced by the National Centre for Infectious Diseases (NCID), the Agency for Science, Technology and Research's Singapore Immunology Network and Duke-NUS Medical School at a virtual press briefing yesterday.

They had just been published in the prestigious journal *The Lancet*.

Mutations occur as Sars-CoV-2, the virus which causes Covid-19, spreads.

The latest reported variant of the virus emerged in Wuhan, China, early in the pandemic and was exported to Singapore and Taiwan.

It was transmitted from person to person across several clusters here from January to March.

"One of the Covid-19 puzzles we have been trying to solve is why

some of our patients get sick, while some have only a mild illness," Dr Barnaby Young, an NCID consultant and clinical lead for the study behind the findings, said in a release.

"Most of our clinical research efforts have focused on the role of patient factors such as age and chronic medical conditions.

"Whether different virus types are also important has been much debated, but till now good evidence was lacking. Discovery of this deletion variant and that it had such a profound effect on the infection course is very exciting."

So far, a few different Sars-CoV-2 variants have been detected globally, including the D614G variant that is spreading widely now.

The new variant in the study, which has a large deletion that removes the ORF8 gene, has been contained and not detected since March. "It is gone, and it is not

likely to come back... but other viruses with deletions are appearing" and could become clinically significant, said Dr Young.

Similar deletions were also detected with the severe acute respiratory syndrome virus in 2003.

The researchers said the findings can have implications on the development of treatment and vaccines.

Dr Young said: "If we can give a treatment that inhibits ORF8, maybe we can help people recover faster from infection with the wild-type virus."

At the briefing, NCID executive director Leo Yee Sin said the discovery of the new variant generated a lot of excitement among researchers as it opens up many areas of investigation for a virus that is very new.

Weighing in, Professor Edison Liu, former founding head of the Genome Institute of Singapore and current president and chief execu-

tive 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."

Associate Professor Hsu Li Yang, an infectious diseases specialist at the National University of Singapore's Saw Swee Hock School of Public Health, said Sars-CoV-2 mutations are to be expected.

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 deletion resulted in a virus that is less deadly," he said.

If the deletion variant is still around and becomes very widespread, then the impact on health will become less, he said.

"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."

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OPENING UP NEW AREAS OF INQUIRY

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