

# Experts dispute claim about ‘very infectious’ virus variant

D614G, which Malaysia says is 10 times more infectious, is already found in Singapore, they add

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Experts in Singapore say there is no basis for Malaysia’s claim that it has found a strain of the coronavirus that is 10 times more infectious.

They also say this strain – D614G – which is already found in Singapore, will have no impact on vaccine development. The variant has also been found in the Philippines.

Malaysia’s director-general of Health, Dr Noor Hisham Abdullah, had posted on his Facebook page on Sunday that this mutation, which he said had been “found by scientists in July 2020” and had now been identified in three patients in Malaysia, is “10 times more infectious”.

He added that vaccines being developed may be ineffective against this mutation.

He attributed the spread of two recent clusters to this mutation, which was first sequenced in Malaysia last month.

But Professor Wang Linfa, director of the emerging infectious diseases programme at Duke-NUS Medical School, told *The Straits Times* that there is “no real scientific data to make the claim that D614G is more transmissible, let alone the tenfold claim”.

His programme deputy, Professor Ooi Eng Eong, said: “This mutation would certainly not impact vaccine efficacy since vaccines would generate antibodies that bind to many different parts of the virus spike protein and not just be limited to the site of mutation.”

Associate Professor Hsu Liyang, an infectious diseases specialist and epidemiologist at the National University of Singapore’s Saw Swee Hock School of Public Health, said this mutation has been circulating here since February.

Singapore sequences a sampling of the virus from patients, and has found more than 100 infections with this mutation between February and last month.

Since only a fraction of virus samples are sequenced, Prof Hsu said it would likely mean that thousands of infections here are due to the D614G mutation.

In June, an article in the highly prestigious *Cell* journal said the D614G variant was rapidly becoming dominant in the world. It said this mutation is “unlikely to have a



Singapore sequences a sampling of the coronavirus from patients here, and has found more than 100 infections with the D614G mutation between February and last month. ST PHOTO: KEVIN LIM

**In June, an article in the highly prestigious *Cell* journal said the D614G variant was rapidly becoming dominant in the world. It said this mutation is “unlikely to have a major impact on the efficacy of vaccines currently in the pipeline”. Professor Wang Linfa said this variant is genetically more fit, but that does not mean it is more easily spread.**

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The Philippine Genome Centre disclosed that G614 was found in nine samples randomly collected in Quezon City.

It is the same as D614G – which indicates that D614 has become G614, due to a change in position 614 of the virus genome from D (aspartic acid) to G (glycine).

Philippines Health Undersecretary Maria Rosario Vergeire said the sample size was still too small to conclude that G614 had already spread in the Philippines.

She added that there is no definitive study showing that G614 was more transmissible than D614.

Prof Hsu said: “It is unsurprising to find the D614G in the Philippines, given how widely spread it is.”

Dr Sebastian Maurer-Stroh, deputy executive director for research at the Agency for Science, Technology and Research’s Bioinformatics Institute, said mutations are natural steps in the evolution of viruses.

He said there are now three “G” clades or mutations, including D614G, which have a “fitness advantage” that has seen them grow from 0 per cent of infections in January

to 95 per cent last month.

He told *The Straits Times*: “There is no need to panic.”

“Since this variant has been circulating globally, it can be expected to be seen in any country, and every country with active surveillance has seen it already, especially related to import from travellers.”

He expects the virus to continue mutating and, in fact, there are already six new groupings.

Dr Maurer-Stroh said: “So you can see that evolution is already beyond just clade G (D614G) and we have seen ‘daughters’ of the virus being formed with clade GR common in Europe and India and clade GH more common in the US.”

He said mutation “doesn’t necessarily mean increased virulence, but can have an opposite effect – milder or asymptomatic infection leading to longer undetected infection”.

Experts are still debating if D614G spreads more easily.

Dr Asok Kurup, who chairs the Academy of Medicine’s Chapter of Infectious Disease Physicians, said there has been no clinical impact from the mutation.

But he added that should any mutation prove more infectious, then current measures such as masking and social distancing become even more important.

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