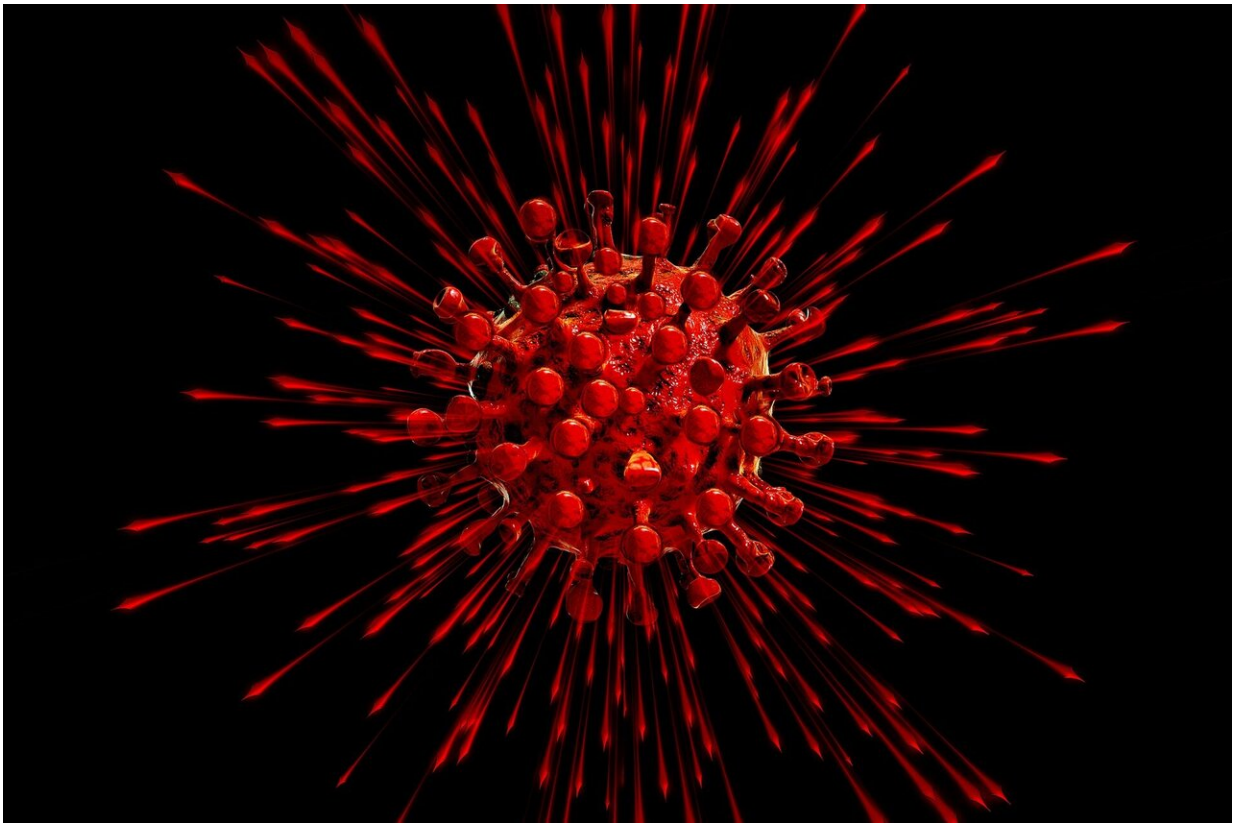


Expert discusses coronavirus 'variants of concern'

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As new coronavirus variants emerge, scientists are keeping a close eye on how the virus continues to evolve. Recent studies suggest some newer vaccines that are effective at preventing infection with the original virus

did not perform as well against the South African variant.

According to Art Poon, professor at Western University's Schulich School of Medicine & Dentistry, there is a greater chance it will continue to mutate and produce more "variants of concern" unless we can mitigate the spread of the [virus](#).

Poon uses computers to reconstruct the spread and adaptation of viruses by looking at their genetic sequence variation.

Why do virus variants occur?

Variants occur because like all other organisms, viruses evolve and accumulate mutations and some of those mutations persist.

The concern comes when these mutations cause something to change in the epidemiological or clinical characteristics of the virus. For example, the mutations may have changed the virus to enable it to better avoid our [immune system](#), or make it more successful at entering our cells.

So, while most variants are distinguished by mutations that have little effect, other variants carry mutations that can confer a selective advantage that cause it to rapidly increase in frequency in the population.

One hypothesis about why these "variants of concern" have appeared is that these are viruses that may have evolved within a chronically infected person—someone whose immune system had not been able to clear the virus in the usual amount of time and that favoured particular mutations to become established.

This hypothesis is receiving attention because scientists have found that the viruses from chronically infected patients had accumulated more mutations than usual and are the same that we've observed in these new

variants of concern.

Why is it that some of the newer vaccines appear to not be as effective against some variants?

The mutations that characterize the current variants of concern are often associated with parts of the virus that control how it enters the cell and determine whether that virus is going to be recognized by our immune system.

Those same mutations that influence how quickly the virus is transmitted through the population can potentially also affect the efficacy of a vaccine. For that reason, a very active area of research is evaluating how the mutations carried by variants of concern influence the effectiveness of vaccines.

Do we need to be worried about more variants of concern as the pandemic wears on?

The short answer is yes.

This is a new virus, so we don't know what paths it may take in its evolution. We have to limit the opportunities of the virus to explore the options available to it in its evolution. The best way to do that is to reduce the number of infections because the more people who become infected, the more viruses there are that are accumulating mutations and the more chances the virus as whole has to explore all of its evolutionary potential.

Everyone has a part to play. Wear a mask and follow public health guidelines so you don't catch the virus and don't pass it on.

If someone catches the virus—even if they are completely asymptomatic—they are still able to transmit that infection to multiple other people; and the more virus there is around, the more opportunities to mutate, and the greater likelihood we'll see more variants of concern.

That's an important aspect that still alludes some people, this isn't just about ourselves, it's that small part we can play to protect everyone else.

You are an expert in the genomic surveillance of infectious disease. What does that entail and why is it important?

What [genomic surveillance] means is that we are sampling infections from an epidemic and are sequencing viral genomes from those infections, and more importantly, comparing those sequences in order to reconstruct what's happening with that epidemic.

We look at how that infectious disease is spreading through the population, the rate at which it's spreading and whether that rate is associated with something in the population like recent travel.

Genomic surveillance provided some of our earliest evidence of human-to-human transmission for the COVID-19 pandemic, because when researchers obtained the first samples of the virus from people and sequenced those genomes, it was immediately clear the genomes were almost identical. The simplest explanation for that was that those infections had been transmitted from one person to another.

Genomic surveillance also allows us to track how the virus is moving from one country to another. That was important in the early days of the pandemic before it became established in all the different countries around the world.

Genomic surveillance also provides a way of detecting outbreaks, which may be associated with new [mutations](#). It enables us to prioritize our public health efforts to specific areas of the population.

Provided by University of Western Ontario

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