Reinfections of COVID-19 after natural infection or vaccination

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On April 5, Bridge Michigan reported that 246 fully vaccinated people in Michigan were later infected with the coronavirus, including 11 hospitalized and three who died. A spokesperson from the Michigan Department of Health and Human Services (MDHHS) was quoted by Bridge Michigan a week later that the deaths have since undergone a more "detailed review," and all three had histories of earlier infections before vaccination. Moreover, neither COVID-19 nor any "other acute respiratory infection" was identified on the trio's death certificates.

Vaccinations have shown to be safe and highly effective at reducing hospitalization and death. Recently the Centers for Disease Control and Prevention (CDC) reported that out of 75 million people that had been fully vaccinated, there had been 5,800 reported infections, of which 396 required hospitalization, of which 74 died. While the deaths might appear to be literally one in a million, many of the 75 million continued to quarantine and social distance, and so were protected by other means than just the vaccine.

An alarming study published by the CDC last week was based on an investigation conducted by the Kentucky Department for Public Health on a COVID-19 outbreak at a skilled nursing facility attributed to an unvaccinated symptomatic health care worker.

It was reported that 75 of the 83 residents (90.4 percent) had already received both doses of the Pfizer mRNA vaccine, while only 61 (53 percent) of the 116 health care personnel had completed their immunization. The investigation found that 26 residents and 20 workers were diagnosed with a COVID-19 infection. Eighteen of the infected residents and four infected workers were beyond the 14-day window of their second dose.

The CDC report mentioned that the genetic sequencing of the virus identified it as an R.1 lineage variant, characterized by the E484K and other mutations within the spike protein. Though this variant has not been classified as a variant of concern or interest, it possesses several mutations known to make it more transmissible and immune evading.

The report attempts to downplay concerns raised by the infection of fully vaccinated individuals arguing that the attack rate was four times higher among unvaccinated individuals. Those who were vaccinated were much less symptomatic and required fewer hospitalizations. However, one fully vaccinated resident did die. The infection rate among vaccinated residents was 24 percent. Among the health care workers, it was 6.6 percent. These findings raise serious and critical questions about the safety of a reopening campaign relying largely on vaccines to assure the public they are safe from catching and spreading the infection.

Though vaccinations have demonstrated their ability to reduce the chance of hospitalizations and death, vaccination alone is wholly inadequate to stop the pandemic. The quantitative assessment of viral transmission among vaccinated people is woefully lacking, and suppositions like those made by the CDC are premature and ill-conceived, motivated by pressures to reopen all aspects of commerce. There is also the issue that a significant number of the US population has yet to receive a vaccine dose.

Dr. Nick Gilpin, medical director of infection prevention and epidemiology at Beaumont Health in Michigan, recently referred to the crisis plaguing his state as "a runaway train." The slow rollout has meant that Michigan has vaccinated less than a third of its population and, without a massively expanded rollout, many more will suffer and die needlessly or suffer the consequences of its acute and chronic health complications, which are considerable. As evidenced by recent disturbing reports of younger people and children becoming infected and hospitalized, no one should assume they are impervious.

The politics of variants of concern and the COVID-19 vaccines

In January, a second wave of the virus devastated the Brazilian city of Manaus, capital of Amazonas state, with reinfections with a more virulent strain P.1 likely playing a part. A study led by Nuno Faria, a virologist at Imperial College London, titled "Genomics and epidemiology of a novel SARS-CoV-2 lineage in Manaus, Brazil" published in March, found that within seven weeks, starting from early November, the fraction of samples classified as P.1 increased from zero to 87 percent. By February, P.1 had taken over completely. Dr. Faria and his colleagues conducted an experiment that estimated that in 100 people infected with non-P.1 lineage in Manaus last year, somewhere between 25 and 61 could have been reinfected if they were exposed to P.1 in Manaus.

A recent study of 149 people in Israel who became infected after vaccination with the Pfizer/BioNTech vaccine (BNT162b2) found that the South African variant (B.1.351) was eight times more likely to cause breakthrough infections on infections that occurred at least a week after the second jab. The authors suggested that while this pointed to an increased breakthrough of B.1.351 occurring mainly in a limited time window post-vaccination, that further research with larger sample size is required to validate this hypothesis. This study suggests that B.1.351 has the ability to evade the vaccine.

William A. Haseltine, a world-renowned infectious disease expert, referring to the study by Dr. Nuno R. Faria of Sao Paulo's Institute of Tropical Medicine, wrote to Forbes in March: "Natural infections do

not seem to protect against reinfection, yet vaccines remain to be seen. While Faria found that antibodies derived from the CoronaVac vaccine [COVID-19 vaccine made by the Chinese company Sinovac Biotech] in Brazil were less effective at stopping the P.1 variant, little data is yet available on reinfections after vaccine administration. We know that antibodies fade over time, and data suggest that you lose tremendous antibody potency six to eight months after natural infections. It is possible that vaccine protection wanes six months to a year after administration, but that data will not be available for many months."

A strategy of relying solely on vaccines is dangerous. As effective as the vaccines may have shown to be, it does not guarantee that the vaccines will continue to be effective on all possible variants. The SARS-CoV-2 has shown to evolve under pressures of mass community transmission into more virulent strains. That the coronaviruses from different regions of the globe have found common strategies to evade and become more transmissible speaks to the dangers raised by these measures to allow the world to "live with it."

The danger of mutations

Viruses independently acquire these mutations, which then gives them an advantage in disease spread, which scientists refer to as "convergent evolution." Stephen Goldstein, an evolutionary virologist who studies coronaviruses at the University of Utah, was quoted in *Wired* magazine that "These different lineages are essentially arriving at the same solution for how to interact more efficiently with the human receptor, ACE2." ACE2 is a protein molecule that sits on the outside of some human cells. The "spike" of the coronavirus latches onto ACE2, enters the cell, and starts replicating. All the mutations of concern have evolved at the virus' receptor binding domain, a region of its RNA that carries the blueprint for the spike protein.

The currently known mutations of concern to the receptor-binding domain include:

• N501Y, a mutation in the South Africa, U.K, and Brazil variants, replaces the coronavirus's 501st amino acid, asparagine, with tyrosine. Studies in cells and animal models suggest that the change makes it easier for SARS-CoV-2 to grab onto ACE2.

• The Brazilian and the South African variant also have a second and third mutation in common: K417T and E484K. E484K (also referred to as "eek") changes an amino acid that was negatively charged to one that's positively charged. This causes the negatively charged ACE2 to snap with the tip of the spike, known as the receptor-binding domain (RBD). It is known to assist with evading the infected host's immune system.

• The B.1.617 variant identified in India carries a double mutation. One named L452R is also present in the dominant strain current in California. The other is called E484Q, which is like the E484K mutation.

In early March, Brian O'Roak, a geneticist at Oregon Health and Science University, reported a new variant that surfaced in Oregon with the E484K mutation. The B.1.526 variant, which incorporates E484K, remains the most prevalent variant in New York City, comprising, as of April 13, about 45 percent of cases sequenced from the fourth week of March.

Dr. William Haseltine reported in *Forbes* on April 13 on yet another variant discovered in Oregon, which he dubbed B.1.1.7-O, which adds to the UK variant both the E484K and N501Y mutations: "The combination of these two mutations in the receptor-binding domain of the spike protein is the principal cause of vaccine resistance of the Brazilian isolate B.1.1.28.1 and the South African variant B.1.351. Together these two mutations are associated with an increased transmission and vaccine resistance." Dr. Haseltine concluded his article with a warning that without effective public health mitigation measures, the evolution of the virus could become a severe threat to vaccine effectiveness.

The American ruling class has pushed the mismanaged and entirely inadequate nationalist program of vaccination as a sufficient response to a pandemic that is causing 60,000 new infections and 700 deaths every day, as computed by a seven-day moving average.

The US has done a poor job in genome sequencing, an absolute prerequisite to get a sense of how widespread the variants are. GSAID Initiative, a global genome sequencing database project, notes that only 1.04 percent of samples are being sequenced in the United States to date, which ranks 43rd in the world. Scientists at Illumina—a lab that conducts genome sequencing for the US—estimate that 5 percent of new coronavirus cases would need sequencing to detect a new variant before it grows to more than 1 percent of total cases.

In February, scientists predicted that the $200 million infusion by the Biden administration would be sufficient to ramp up the nation's sequencing capacity from 7,000 to 25,000 samples per week, putting the US on track to capture about 5 percent of new coronavirus cases. This estimate was predicated upon the downward trend of new COVID cases seen in the winter, which now has somewhat reversed under the administration's disastrous policies. Under such conditions, while the American Rescue Act that became law on March 11 provides for $1.75 billion for genomic surveillance, the US is still woefully behind in its gene sequencing initiative.

The ruling elites are pushing to exit the pandemic and return to normalcy using mass vaccination in the United States alone, and perhaps a few other advanced industrialized countries, as a strategy to put their plans into action. However, the pandemic remains far from over as a significant portion of the globe's population has neither been infected nor received a vaccine. Little is known or clarified on the nature of the pressures the vaccine will impose on mutations nor how reinfections in the vaccinated population will promote the continued transmission of the disease. Vaccinated individuals will function as new vectors and weapons to promote the "policy of herd immunity" and ensure the virus becomes endemic throughout the world.