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The dominant variant of the coronavirus in California has acquired dangerous mutations

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Scientists have recently reported that a new variant from California has become the dominant lineage in that state. In a review of their database, they had first identified it in the early part of last summer, laying dormant until the winter surge propelled it rapidly throughout the state. According to researchers at the University of California, San Francisco (UCSF), this particular variant grew from 0 percent in September to 50 percent in late January.

This new variant has also been detected in many other US states and has reached places as far as the UK, Singapore, and Australia. It possesses mutations in its spike protein that appear to make it not only more transmissible but also helps it to evade antibodies generated by the COVID-19 vaccines.

Scientists have designated the new mutation as the CAL.20C variant spanning the B.1.427 and B.1.429 lineages. It is associated with a mutation in its receptor-binding domain called L452R.

Dr. Charles Chiu is the senior author of a study documenting the rise of the CAL.20C variant among 8,000 residents of the Mission District in San Francisco, and first detected the variant on December 31. He told the press, “This variant is concerning because our data shows that it is more contagious, more likely to be associated with severe illness, and at least partially resistant to neutralizing antibodies. … The devil is already here. I wish it were different. But the science is the science.”

Speaking with the *Los Angeles Times*, Dr. Chiu indicated that it would be imperative to drive down infections as much as possible while rapidly moving to vaccinate the population. This assessment was echoed by Dr. Angela Rasmussen, a Georgetown University virologist, who stated, “The [UCSF] findings warrant taking a much closer look at this variant. … They underscore the importance of pulling out all the stops in terms of both exposure reduction and increased vaccine distribution and access.”

In a review of 324 people with COVID-19 treated at UCSF clinics or its medical centers, after adjusting for various confounding variables, such as age, gender, and race, those infected with the CAL.20C variant were almost five times more likely to need ICU admission and 11 times more likely to die. Analysis from nasal swabs also demonstrated that patients with CAL.20C carry twice the viral load. Additionally, during *in vivo* studies, the variant was four times less susceptible to antibodies from previously infected individuals and two times less susceptible to antibodies obtained from people vaccinated with the Pfizer and Moderna vaccines.

Infectious disease physician Dr. Robert “Chip” T. Schooley, who has been advocating for the Biden Administration to acknowledge the significant role that aerosol transmission plays in spreading SARS-CoV-2, affirmed these findings, stating, “The biology of having a higher level of virus … would certainly fit the thesis that people would not do well. We are seeing here in Southern California more people … for a longer period of time in our ICUs.”

The study results will undoubtedly need to be confirmed in more extensive epidemiological surveillance but they highlight the dangers these infections pose to communities. Critics had noted that the number of cases requiring admission to the ICU or leading to death, though statistically significant compared to the previous COVID infections, was small and occurred at the peak of the surge when health systems were inundated, which may have contributed to these findings.

The B.1.427 and B.1.429 variants share three identical mutations at their spike protein which appear to stabilize the interaction between the virus and the receptor on the human cell it binds to before gaining entry. Specifically, the L452R mutation, primarily circulating in California, has not been found in the other commonly discussed variants. But analysis from GISAID-deposited genomes of the virus has found several recent “independent L452R-carrying lineages that have emerged across the globe,” suggesting the mutation confers an adaptive advantage for the virus.

UCSF scientists conducting benchwork studies on this variant engineered a coronavirus with the L452R mutation. They found the mutated virus they created infected lung tissue 40 percent more readily than the common variants that had been circulating.

Given that the B.1.1.7 variant that first emerged in the UK along with the various homegrown variants have been quickly spreading throughout the United States, concerns are growing among scientists that if these variants manage to infect an individual simultaneously, the viruses could swap their mutations and produce a strain even more dangerous than the present versions of the SARS-CoV-2, a situation they describe as a “nightmare scenario.”

The multiplication of more infectious variants of the coronavirus is a direct result of the complete indifference that the ruling elite has shown to the dangers of herd immunity, which means establishing the contagion as endemic, so that everyone is exposed to it and those who survive return to work and producing profits.

Notwithstanding the unprecedented scale of death that the pandemic has caused in the United States since March 2020, the emergence of these new lineages that are more transmissible, lethal, and immune-evading, poses a calamitous dilemma for the working class, when coupled with the drive to open schools and resume in-class instruction at “warp speed.”

Just yesterday, Michigan reported that 81 students and staff at 18 school districts, including two colleges, were infected with COVID-19 in school-related outbreaks. Data from Quebec indicated that after January 18, children age nine or younger had the highest rate of relative increase in COVID-19 infections. Data is emerging that the attack rate of the B.1.1.7 variant has its highest propensity for younger people. Though these infections don’t appear to cause more severe illness in children, the data implies that not only are children critical in community transmission, but they may also be a necessary component in the selective advantages these variants enjoy.

With almost 30 million reported COVID-19 infections, the US has the largest outbreak of cases in any one nation globally. However, without a robust national genomic sequencing program to keep track of these evolving mutations, these variants will continue to spread largely undetected. Countries must develop the ability to systematically follow these developments in real time in order to make rational public-health decisions.

The genomic coverage in the US, however, is abysmal. According to *Nature*, the number of SARS-CoV-2 genomes that the United States has shared on GISAID is less than 0.3 percent of its total number of COVID-19 infections, or approximately 90,000. In comparison, the UK and Denmark have contributed 45 percent and 7 percent, respectively, of the 360,000 SARS-CoV-2 genomes sequenced and stored on GISAID.

The World Health Organization’s technical lead, Dr. Maria Van Kerkhove, warned, “We really need to expand this [genomic sequencing], so we have better eyes on the changes in this virus that are happening, especially in areas where transmission is most intense.”

Dr. Oliver Pybus, an infectious disease expert at the University of Oxford, told *Nature*, “Genomic epidemiology has come of age during this pandemic.” However, it isn’t the science that humanity has failed to master, but the understanding that the fruits of science belong to the entire human race to make this fragile world a more hospitable home for everyone. Without implementing an international global pandemic-prevention surveillance program, the potential for future outbreaks will haunt the world.

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