Study finds correlation between Long COVID and a particular human gene variant

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14 July 2023

A new pre-print study, coauthored by over 70 individuals and groups, provides significant insight into the relative susceptibility of COVID-19 patients to develop Long COVID based on their genetic makeup. The study is based on a review of data gathered from 24 previous studies in 16 countries, encompassing up to 6,450 Long COVID patients and nearly 1.1 million control individuals (i.e., with no known SARS-CoV-2 infection).

The study found a significant association between patients suffering from Long COVID and those possessing one of several particular variants of the *FOXP4* gene in their DNA. Importantly, the study also found that the genetic susceptibility to Long COVID was greater than that associated with the severity of the COVID-19 disease episode alone, meaning that the effects of the *FOXP4* variants could not be explained away by severity of COVID-19.

"Long COVID" refers to long-lasting, often debilitating symptoms which can persist for months or years after the acute phase of infection has passed. Estimates of Long COVID prevalence typically range from 10 to 30 percent of those who survive initial or repeated bouts of the disease. More than 200 symptoms, affecting nearly every organ in the body, including debilitating cognitive and lung impairments, chronic fatigue, thyroid dysfunction, kidney disease and more have been associated with COVID-19.

The newly reported study analyzed 24 genetic data sets from over 1 million individuals in North America, Europe and Japan. The data set included 6,450 individuals with Long COVID and over 1 million controls, who did not have Long COVID. The study identified a segment of the human genome near the gene known as *FOXP4*, which is active in the lungs and other organs, as being significant.

Individuals who possess any of several particular variants of the *FOXP4* gene were found to have 1.6 times the odds of developing Long COVID than those who do not.

Having a mutation in the *FOXP4* gene appears to increase one's chances of developing Long COVID, but not having the mutation does not mean that a patient will not develop Long COVID. As with any pathogen, COVID-19 is a very complex disease process, and the interaction between certain genetic mutations and the human body is complex. It is still critical to avoid infection to the greatest extent possible through the use of well-fitting N95 masks and other measures, as the risks of Long COVID remain high for the general population.

Previous research had identified an association between variants of the *FOXP4* gene and the likelihood of suffering a severe bout of COVID-19. However, the new research found that its association with Long COVID was even higher than its association with increased severity of the acute phase of SARS-CoV-2 infection. So, the severity of a COVID-19 attack does not account for all of the observed association between *FOXP4* variants and Long COVID.

Forkhead box protein P4 (*FOXP4*) is a gene in the subfamily P of transcription factors that regulate and direct tissue specific genes from embryonic development through adulthood, including the generation and regulation of T-cells. They also function in the development of tumors in the kidney or larynx. In particular, *FOXP4* is known to be expressed in the proximal and distal epithelium of the airway, as well as the cells in the gut. "Polymorphisms" seen in the gene correlate with lung disease like Long COVID as well as cancers and other diseases.

The authors noted that the frequency of the *FOXP4*

mutation varied in frequency based on the populations that were studied, with the lowest in non-Finnish Europeans at 1.6 percent to 7.1 percent in Finnish, 19 percent in "admixed" Americans and highest in East Asians at 36 percent.

Furthermore, they wrote, "We observed the highest expression of *FOXP4* in type 2 alveolar cells, a cell type that is capable of mounting robust innate immune responses, thus participating in the immune regulation of the lung."

They explained, "Type 2 alveolar secrete surfactant, keep the alveoli free from fluid, and serve as progenitor cells repopulating damaged epithelium after injury. In addition, we observed nearly equally high expression of *FOXP4* in granulocytes that similarly participate in regulation of innate immune responses."

They concluded that these findings could link the mutation in *FOXP4* to its "role of both immune and alveolar cells in lung in Long COVID."

Further analysis found that the particular *FOXP4* variants associated with Long COVID are also associated with the occurrence of lung cancer, at least in part by affecting the immune response of lung cells. Since it has previously been demonstrated that SARS-CoV-2 also impacts immune response by unleashing a cytokine storm, the effects of these two factors may compound each other.

Although the frequency of the gene variants in question varies somewhat between the six different genetic ancestries studied, the overall association remained consistent across all of them.

The findings of the new research point to the highly complex nature of the mechanisms whereby SARS-CoV-2 interacts with the human body and its genome, in particular. It is unlikely to be the only factor in producing Long COVID. Much more research will be needed to reveal the myriad effects of this deadly virus. It is a tragedy of immense proportions that the uncontrolled spread of COVID-19 being permitted and indeed encouraged by the ruling class's "profits before lives" policy will provide an ever larger body of data on which to base such studies.

The now more than three-year-long experience with the COVID-19 pandemic has thoroughly exposed as a crime against humanity the "herd immunity" strategy of the ruling class, which posited that allowing the SARS-CoV-2 virus to run rampant throughout the world's population would result in widespread acquired immunity that would end the pandemic. Instead, the virus continues to mutate and find new ways to evade the human immune system with deadly results.

This study adds to the evidence of the bourgeoisie's criminality in its propaganda campaign pushing the lie that COVID-19 has become "mild" and that the pandemic is "over" by shutting down virtually all testing and monitoring. Recent spikes in infections in such places as Okinawa and the rampage of the virus after the lifting of the Zero-COVID policy in China demonstrate clearly that the virus is not done with humanity.

The authors of the study predict that "Future studies and iterations of this work will likely grow the number of observed genetic variants and further clarify the biological mechanisms underlying Long COVID."

What this study already pointedly demonstrates is that when the scientific resources that are available are marshaled in a concentrated effort, valuable information necessary to confront this deadly disease can be obtained.

It also makes clear that while the information about the nature and consequences of COVID-19 is vital in educating the public and mobilizing a coordinated global effort to end the pandemic is available, the ruling class and its political lackeys will do everything in their power to block that effort.