Identifying a gene that could explain disparity in COVID-19 effects

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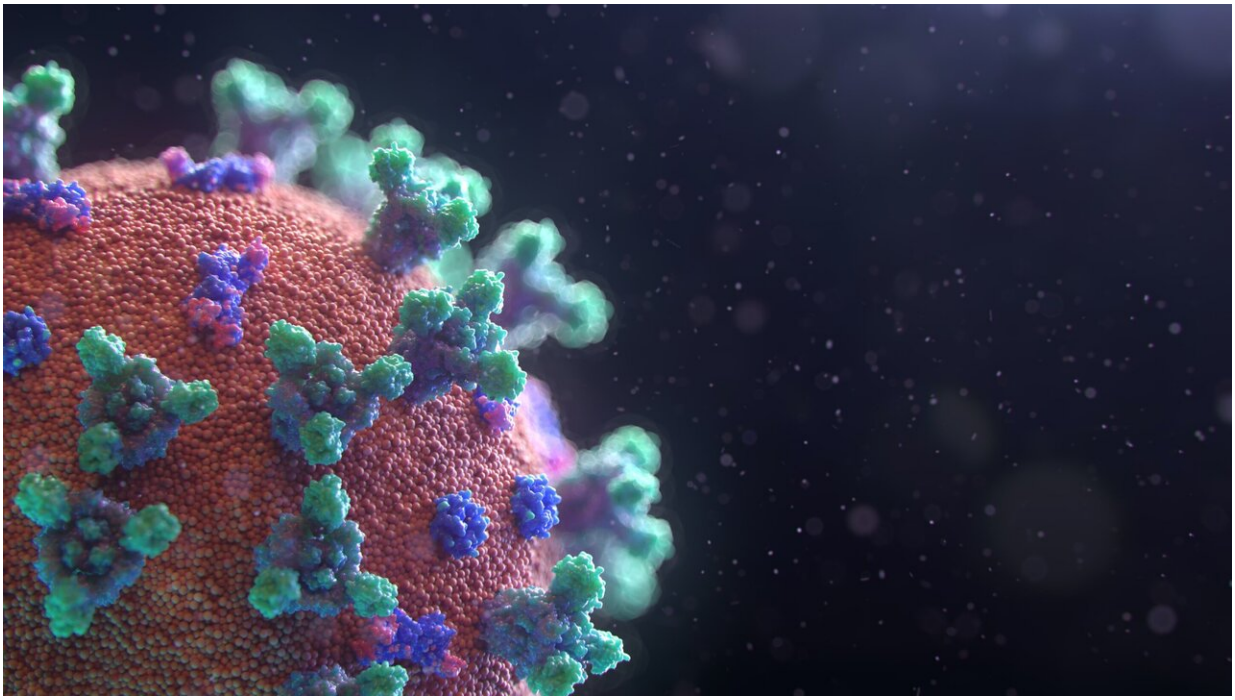

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The Translational Genomics Research Institute (TGen), an affiliate of City of Hope, has identified a specific genetic target that could help explain the tremendous variation in how sick those infected with COVID-19 become.

The study results, recently published in the journal *mSphere*, describe a

molecule made from DNA—miR1307—as a potential dimmer switch that may influence the severity of the disease; why some infected with SARS-CoV-2, the virus that causes COVID-19, have mild or even no symptoms, while others become seriously ill or die.

Led by Nicholas Schork, Ph.D., a Distinguished Professor and Director of TGen's Quantitative Medicine and Systems Biology Division, researchers identified miR1307 by comparing the genetic elements of SARS-Cov-2 with seven other human coronaviruses, some of which merely cause common colds. In addition, they examined the genomes of coronavirus strains known to infect bats, pigs, pangolins, ferrets, civets and chickens.

"We pursued a systematic gene-by-gene comparative analysis, investigating how and to what extent the SARS-CoV-2 genome sequence differs from other well-characterized human and animal coronavirus genomes," Dr. Schork said. "Our study results will allow the development of models of how the virus and its hosts interact, enhancing our understanding of the disease-causing mechanisms of SARS-CoV-2 and how to exploit both viral and host therapeutic targets."

Study results suggest that miR1307 serves as a switch that turns various genes within the virus on or off, potentially making the disease more or less harmful to patients by regulating, for example, how fast or slow the virus replicates. In past studies, miR1307 has been found to affect the severity of several types of cancer, lung disease and the flu, specifically the H1N1 influenza virus that caused a 2009 pandemic. It was first discovered as a key regulatory agent in the Epstein-Barr virus, best known as the cause of infectious mononucleosis.

According to Dr. Schork, the study results also provide the basis for additional investigations, such as designing vaccines based on proteins or RNA, developing specific genetic markers for community disease

monitoring, and tracing COVID-19 from one species to another.

More information: Agnes P. Chan et al, Conserved Genomic Terminals of SARS-CoV-2 as Coevolving Functional Elements and Potential Therapeutic Targets, *mSphere* (2020). DOI: 10.1128/mSphere.00754-20

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