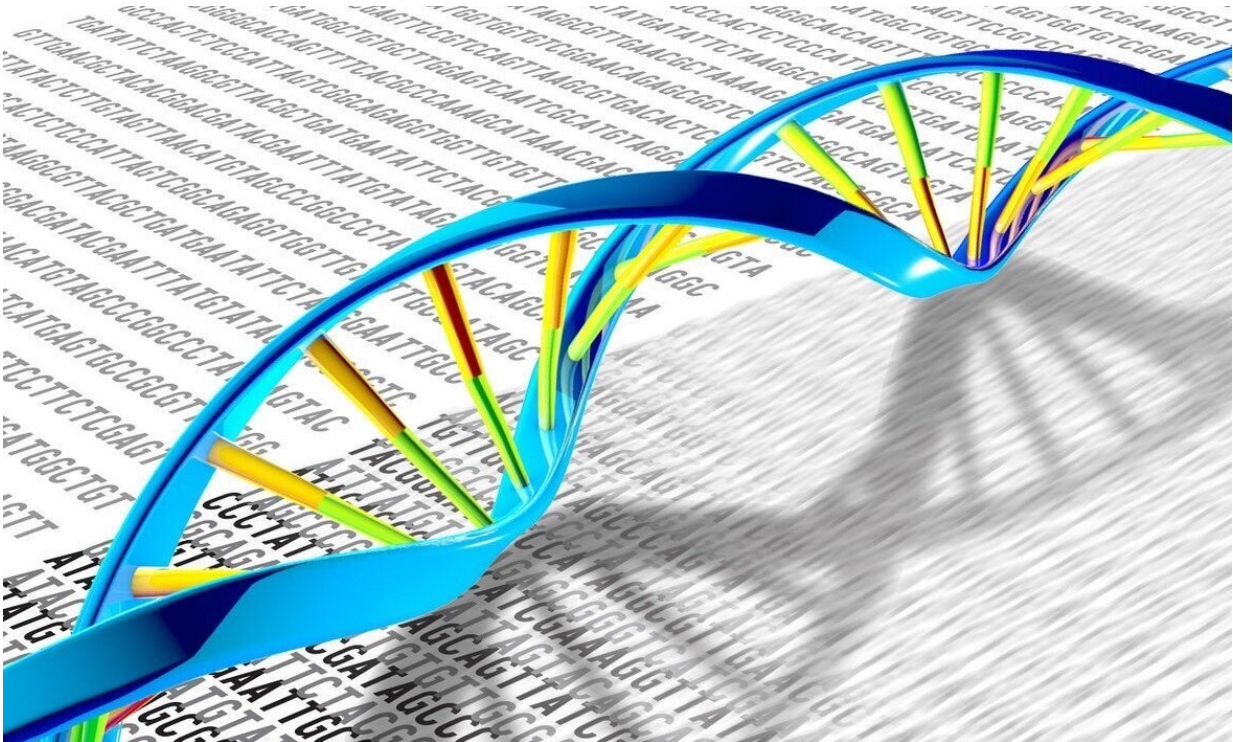


Study finds genetic risk of COVID-19

August 16 2021, by David Bradley



DNA, which has a double-helix structure, can have many genetic mutations and variations. Credit: NIH

An analysis of the DNA of thousands of people who have been infected with the coronavirus, SARS-CoV-2, and shown a positive test for the disease it causes, COVID-19, shows that they have several DNA characteristics in common. The study, based on samples from the UK Biobank, is detailed in the *International Journal of Data Mining and*

Bioinformatics and could offer up a way to genetically profile individuals for susceptibility to the disease.

Taewan Goo, Kyulhee Han, Catherine Apio, and Taesung Park of Seoul National University in South Korea carried out a [genome-wide association study](#) as well as gene-level association and pathway analyses with common and rare variants of the virus to reveal how certain genetic characteristics associated with some of the body's metabolic pathways are present in those who contracted the disease more often than in those who had not. Moreover, they identified other genetic characteristics, most notably, ones associated with cellular signaling that had not been associated with viral infection previously.

Follow-up work to investigate those pathways may well reveal important pathophysiological factors associated with infection with SARS-CoV-2 and subsequent COVID-19. It might also be used to identify people who are more susceptible to the ravages of the disease than others and so allow them to be advised on protecting themselves better.

As other researchers have suggested, understanding how [human genetics](#) influence infectious disease susceptibility might give us the opportunity for better understanding this illness and other emerging infectious diseases. It might also guide us to potential drug targets, risk stratification, and a better understanding of patient response to therapy and vaccination.

More information: Taewan Goo et al, Analysis of COVID-19 genetic risk susceptibility using UK Biobank SNP genotype data, *International Journal of Data Mining and Bioinformatics* (2021). [DOI: 10.1504/IJDMB.2021.116879](#)

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