

Genes associated with COVID-19 risk identified

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Having genetic risk variants in the ABO gene might significantly increase the chances of developing COVID-19, and other genes may also increase COVID-19 risk, according to research presented at the ATS 2021 International Conference.

Much about COVID-19 remains a medical mystery, including whether certain genes place individuals at greater risk of contracting the SARS-CoV-2 virus, which causes COVID-19. Ana Hernandez Cordero, Ph.D., postdoctoral fellow with the Centre for Heart Lung Innovation, University of British Columbia, and colleagues used integrative genomics combined with proteomics to identify these genes.

Genomic research identifies [specific genes](#) that may play a role in biological processes such as the development of disease, while proteomics does the same for proteins. Researchers can get a fuller picture of disease processes by integrating tools to investigate both.

"DNA is a big, complex molecule and so, genetic associations alone cannot pinpoint the exact gene responsible for COVID-19," said Dr. Hernandez. "However, by combining COVID-19 genetic information with gene expression and proteomic datasets, we can figure out which genes are driving the relationship with COVID-19."

The researchers combined [genetic information](#) with an examination of lung gene expression to identify genetic variants that were controlling gene expression in the lung that were responsible for COVID-19. The researchers identified specific genes' markers that share their effects on gene expression and protein levels with COVID-19 susceptibility. For the analysis, they used bioinformatics to integrate: (1) a genomic dataset

obtained from patients who were infected with SARS-CoV-2 as well as non-infected individuals (controls); (2) lung and blood tissue gene expression datasets from clinical populations (non-COVID-19); and (3) a proteome dataset obtained from blood donors (non-COVID-19).

By doing this, they found that several genes responsible for the immune system's response to COVID-19 are also involved in COVID-19 susceptibility. What they discovered was supported by the findings of previous research.

Looking for candidate genes in blood proteins, they were able to go one step further in connecting the effects of genes to susceptibility to COVID-19. Blood proteomics can also help identify markers in the blood that can be easily measured to indicate disease status, and potentially, to monitor the disease.

"By harnessing the power of genomic information, we identified genes that are related to COVID-19," said Dr. Hernandez. "In particular, we found that the ABO gene is a significant risk factor for COVID-19. Of particular note was the relationship between the blood group ABO and COVID-19 risk. We showed that the relationship is not just an association but causal."

In addition to the ABO gene, Dr. Hernandez and colleagues found that people carrying certain genetic variants for SLC6A20, ERMP1, FCER1G and CA11 have a significantly higher risk of contracting COVID-19. "These individuals should use extreme caution during the pandemic. These genes may also prove to be good markers for disease as well as potential drug targets."

Several of the genes identified in the researchers' analysis have already been linked with respiratory diseases. For example, ERMP1 has been linked to asthma. CA11 may also elevate COVID-19 risk for people with

diabetes.

Genetic associations for COVID-19 and gene and protein expression were combined using integrative genomics (IG). IG aims to identify mechanisms (for example: [gene expression](#) levels) that connect the effects of the genetic code to a complex disease. These methods, although complex, are also fast and their outcomes can help researchers to prioritize candidate genes for in vitro (in the lab) and in vivo (in living organisms) testing.

Dr. Hernandez added, "Our research has progressed since the time that we first conducted this analysis. We have now identified even more interesting candidates for COVID-19 such as IL10RB, IFNAR2 and OAS1. These [genes](#) have been linked to severe COVID-19. Their role in the immune response to viral infections and mounting evidence suggest that these candidates and their role in COVID-19 should be further investigated."

More information: A. I. Hernandez Cordero et al. Integrative Genomic Analysis Highlights Potential Genetic Risk Factors for Covid-19. [conference.thoracic.org/progra ... search.php?sid=P9325](https://conference.thoracic.org/progra...search.php?sid=P9325)

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