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MedGenome, SGRF predict COVID-19 susceptibility

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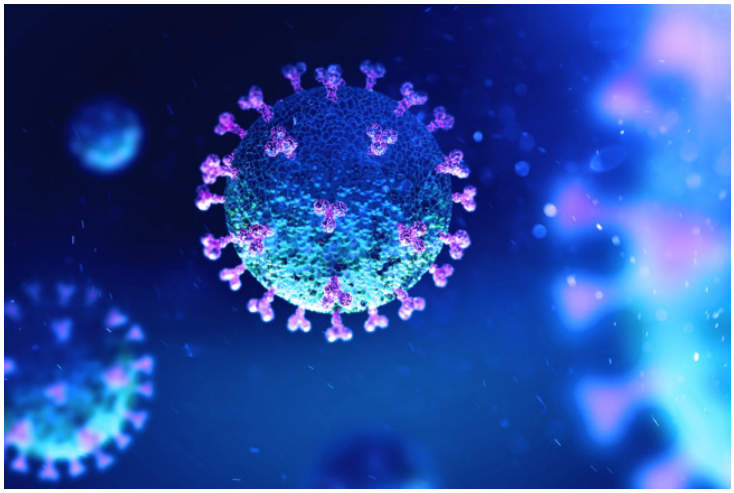

A group of Indian and US researchers from MedGenome and SciGenom Research Foundation (SGRF) collaborated to analyze DNA sequence and variation data from over 300,000 individuals to predict susceptibility to the COVID-19 disease caused by the SARS-CoV-2 virus. The group identified variations in the ACE-2 protein gene that are predicted to make individuals more susceptible to the virus – their findings are published online at https://biorxiv.org/cgi/content/short/2020.04.07.024752v1. They also report variants in the ACE2 gene that will protect individuals carrying some of those variants.

SARS-CoV-2 is a highly contagious virus and is the cause of the current COVID-19 pandemic. Symptoms caused by the virus include fever, chills, cough, diarrhea and pneumonia. While some infected individuals are asymptomatic, about 10% need hospitalization and ~1-5% of the cases are fatal. Understanding why some individual are more severely affected than others by the virus is important for managing at risk individuals. In this study posted in bioRxiv, the research team has attempted to understand how genetic factors affect susceptibility to the virus.

SARS-CoV-2 enters human cells by binding to ACE2, a cell surface protein that functions like a door to the cells for the virus. ACE2, an enzyme created by the ACE2 protein, usually plays a role in the maintenance of blood pressure but is tricked by the virus into becoming an entrance. One of the reasons the SARS-CoV-2 virus is highly infectious is because it can bind to the ACE2 cell receptor with higher affinity compared to the previous SARS-CoV virus which caused the disease called SARG which was less contagious, even though it caused an epidemic in 2003. Natural human ACE2 protein variation encoded in an individual's DNA can allow the virus to bind to ACE2 either strongly or weakly and hence alter their susceptibility to the disease which has caused the current pandemic.

"We analyzed ACE2 protein altering variants from over 300,000 individuals variant data from across the world and have found variants that are predicted to bind to the virus less tightly and hence make individuals less susceptible – giving these individuals natural protection against the invading virus" said Dr. Sekar Seshagiri, President, SciGenom Research

Foundation, India and lead study author. “The converse is also true; in this data set, we found ACE2 variants that will render individuals more susceptible to the virus” said Dr. Eric Stawiski, Vice President Bioinformatics, MedGenome.

The team used its world class bioinformatics capabilities to accelerate the analysis and complete this study in very short order. The variants in ACE2 identified are not common, but this work sets the stage for larger studies that can focus on understanding the role and impact of these variants in patients. by studying variations in clinical outcomes and data in patients with the different genetic variants identified. The team is continuing to conduct more research to build on these findings to help fight COVID-19 and is also supporting Pharma and Biotech companies help find solutions for COVID-19 through its research support services teams.

“Our finding on ACE2 variants can help enable the development of a rationally engineered soluble ACE2 that can quickly be developed as a therapeutic against this deadly virus” added Dr. Sekar Seshagiri. “We are in discussions with Pharma partners to advance their drug development work with genomics insights and capabilities, in particular in the context of this COVID-19 crisis. I think we have a potential drug solution that should work and can be developed quickly with the right Pharma/Biotech partner.” said Sam Santhosh, Chairman, MedGenome.