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Summary of “Understanding COVID-19 through genome-wide association studies”

There are several commonly used phenotype definitions in COVID-19 genetics studies that represent either susceptibility to infection by the SARS-CoV-2 virus or just the risk of severe COVID-19 disease. Since COVID-19 was urgent and chaotic, early genome-wide association studies (GWAS) were focused on hospitalized cases with unscreened genotyped controls. The studies are designed for the biology of complications in COVID-19. With the focus on mild to no symptom patients with identification of household virus exposure as a high-risk measure, scientists were able to investigate susceptibility to SARS-CoV-2 by comparing patients who tested positive and comparing them to patients to tested negative. These tests confirmed that the ABO locus as a bona fide susceptibility or SARS-CoV-2 infection with also the suggestions of the hitherto unexplored pool of protective variants presence.

There was also the identification that there is an association with a non-coding X chromosome variant upstream from ACE2 and also the protection against the SARS-CoV-2 infections. Scientists discovered that using RNA sequencing data from liver tissue, a protective allele leads to a 40% reduction in ACE2. ACE2 is a membrane-bound that serves as the binding site for SARS-CoV-2 virus entry. The scientists then used rich phenotype data to dissect chromosome 3p21.31 into susceptibility signal and severity signal, which localized to SLC6A20 and LZTFL1. SLC6A20 directly interacts with ACE2 and shows that the risk allele is directly associated with increased expression of SLC6A20. It was also found that six established severity variants were associated with a 1.65-fold and 1.75-fold which result in a higher risk of severe disease in people with or without the presence of risk factors.

The main scientists that were involved in the tastings were Horowitz and Roberts, who both played an important role in better understanding the pathophysiology of SARS-CoV-2 infection. It is proven that vaccinations are the ultimate protection against SARS-CoV-2, but there is hope that the insights provided by COVID-19 GWAS will help facilitate the identification and development of treatment options for hospitalized and critically ill COVID-19 patients and also treatments that can prevent hospitalization.

In a peer-reviewed article about “the role of host genetics in the immune response to SARS-CoV-2 and COVID-19 susceptibility and severity, it is discussed that mutations among genomes of single-stranded RNA viruses lead to faster mutagen rates for the human genome. It leads to the accrual of numerous quasi-species within a single infected individual resulting in observed differences in symptoms and disease severity. Mutagens may also result in altered ACE2 binding interactions that promote more or less aggressive and widespread infections. This supporting article makes it believable to trust the popular press information is accurate for this specific case.

Works Cited

Karlsen, T. Understanding COVID-19 through genome-wide association studies. *Nature Genetics; https://www.nature.com/articles/s41588-021-00985-x (2022).*

Ovsyannikova, I; Haralambieva, I; Crooke, S; Poland, G; Kennedy, R. The role of host genetics in the immune response to SARS-CoV-2 and COVID-19 susceptibility and severity. *EBSCO Host*;https://web-s-ebscohost-com.proxy.lib.odu.edu/ehost/pdfviewer/pdfviewer?vid=0&sid=73d42d72-d62c-4465-a207-20c3349bfd09%40redis (2020).