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Critical COVID-19 illness (Pairo-Castineira, 2020)

Erola Pairo-Castineira, et al.
Nature

Infection | Inflammation

STUDY SUMMARY

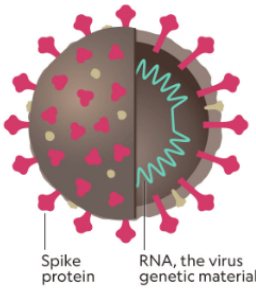
Identification of 8 genetic variants associated with critical illness following COVID-19 infection.

YOUR RESULT

7th
PERCENTILE
Low genetic predisposition to **critical COVID-19 illness**

STUDY DESCRIPTION

COVID-19 is a transmissible disease caused by the SARS-CoV-2 virus. Though symptoms vary from person to person, many develop a fever, cough, difficulty breathing, and a loss of taste/smell. For most people, these symptoms are only mild and resolve within a few weeks. However, around 5% of infected individuals develop a more severe disease, which can include respiratory failure, septic shock, and multi-organ failure. While comorbidities such as obesity and asthma make individuals more susceptible to critical illness, genetics is also believed to contribute to disease severity. This genome-wide association study examined 2,244 individuals of European, South Asian, East Asian, or African ancestry, all of whom were critically ill following SARS-CoV-2 infection. The study found 8 regions of the genome that appear to be associated with severity of the disease. Many of the identified genes are crucial for the function of the immune system. These include OAS1/3 and IFNAR2 genes, that play a role in the body's antiviral defense.



COVID-19 is caused by a novel coronavirus that first emerged in 2019. The virus has an RNA genome and characteristic spike proteins on the surface.

DID YOU KNOW?

Another study found that individuals with type O blood group may have a decreased risk of infection with the SARS-CoV-2 virus compared to individuals with blood types A, B, and AB. The same study also found that type O blood group is also associated with a decreased risk of severe illness in those who did contract COVID-19.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to critical COVID-19 illness we summed up the effects of genetic variants that were linked to critical COVID-19 illness in the study that this report is based on. These variants can be found in the table below. The variants highlighted in green have **positive effect sizes** and increase your genetic predisposition to critical COVID-19 illness. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to critical COVID-19 illness. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to critical COVID-19 illness. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for critical COVID-19 illness to be 1.31**. To determine whether your score is high or low, we compared it to the scores of 5,000 other Nebula Genomics users. We found that your polygenic score for critical COVID-19 illness is in the **7th percentile**. This means that it is higher than the polygenic scores 7% of people. We consider this to be a **low genetic predisposition to critical COVID-19 illness**. However, please note that genetic predispositions do not account for important non-genetic factors like lifestyle. Furthermore, the genetics of most traits has not been fully understood yet and many associations between traits and genetic variants remain unknown. For additional explanations, click on the column titles in the table below and visit our Nebula Library tutorial.

VARIANT	YOUR GENOTYPE	COMMENTS	EFFECT SIZE	VARIANT FREQUENCY	SIGNIFICANCE
rs73064425_T	C / C	Near LZTFL1	0.74 (–)	15%	4.80×10^{-30}
rs143334143_A	G / A	Near CCHCR1	0.64 (↑)	12%	8.80×10^{-18}
rs2109069_A NEW	G / G	Near DPP9	0.34 (–)	38%	4.00×10^{-12}
rs10735079_A NEW	G / G	Near OAS1/3	0.26 (–)	68%	1.60×10^{-8}
rs74956615_A	T / T	Near TYK2	0.47 (–)	8%	2.30×10^{-8}
rs3131294_G	A / G	Near NOTCH4	0.41 (↑)	90%	2.80×10^{-8}
rs9380142_A	A / G	Near HLA-G	0.26 (↑)	74%	3.20×10^{-8}
rs2236757_A NEW	G / G	Near IFNAR2	0.26 (–)	34%	5.00×10^{-8}