

★ SARS coronavirus infection (Tu, 2015)

Xinyi Tu, et al.

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STUDY SUMMARY

Identification of 2 genetic variants associated with an increased risk of severe acute respiratory syndrome (SARS) *coronavirus* infection.

STUDY DESCRIPTION



Severe acute respiratory syndrome (SARS) *coronavirus* emerged in 2003 in China. During that year, more than 8000 infections across 26 countries were reported. SARS symptoms are flu-like and include fever and a dry cough. Severe cases are common and result in a ~ 10% mortality rate. This study examined the genetic data of nearly 1000 individuals of Chinese ancestry who were diagnosed with SARS. The study identified 2 variants that are associated with susceptibility to infection with the SARS *coronavirus*. One variant is in the CCL2 gene, which plays a role in attracting *macrophages* to an infection site. The other variant is in the MBL gene, which helps the immune system recognize molecular patterns that are commonly found on the surface of many viruses and bacteria. [Note: This study is not a genome-wide association study. Only a few variants were genotyped selectively.]

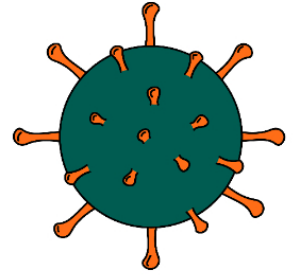
DID YOU KNOW?

The SARS coronavirus emerged as a result of an animal-to-human transmission. The original host is believed to have been a bat or a civet, a cat-like animal found in tropical Asia.

YOUR DETAILED RESULTS

The variants highlighted in green have **positive effect sizes** and increase your genetic predisposition to SARS infection susceptibility. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to SARS infection susceptibility. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to SARS infection susceptibility. 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 [⊙]
rs1024611_G 	A / G	G/G genotype associated with increased susceptibility.	0.39 (↑)	28%	1.60×10^{-4}
rs1800450_T 	C / C	T/T and C/T genotypes associated with increased susceptibility.	0.58 (-)	11%	4.90×10^{-8}



Coronaviruses are named after the crown-like spikes that protrude from their surface.