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## ★ SARS coronavirus infection (Ching, 2010)

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Infection Lungs

### STUDY SUMMARY

Identification of a genetic variant associated with a decreased risk of SARS *coronavirus* infection.

### STUDY DESCRIPTION


The severe acute respiratory syndrome (SARS) *coronavirus* emerged in 2003 in China, infecting over 8000 people and causing over 900 deaths across the world. Typical symptoms include high fever, headache, and a dry cough. Previous studies have shown that *interferons* can inhibit the replication of the SARS *coronavirus* by inducing production of antiviral proteins like MxA. This study demonstrated that a genetic variant (rs17000900) near the MxA gene influences its activity when cells are exposed to *interferons*. The study also examined the genetic information of over 1200 individuals of Chinese descent and established a relationship between this genetic variant and risk of SARS *coronavirus* infection. The results suggest that the A allele of the rs17000900 variant is linked to a decreased susceptibility to SARS *coronavirus* infection. (Note: This study is not a genome-wide association study. Only a few variants were genotyped selectively.)

### DID YOU KNOW?

Coronaviruses are also responsible for the MERS (Middle East Respiratory Syndrome) pandemic in the early 2010s.

### 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 <sup>Ⓞ</sup>	YOUR GENOTYPE <sup>Ⓞ</sup>	EFFECT SIZE <sup>Ⓞ</sup>	VARIANT FREQUENCY <sup>Ⓞ</sup>	SIGNIFICANCE <sup>Ⓞ</sup>
rs17000900_A 	C / A	-0.39 (↓)	13%	7.00 x 10 <sup>-3</sup>