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★ SARS coronavirus infection (Hamano, 2005)

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STUDY SUMMARY

Discovery of a genetic variant in the OAS-1 gene associated with increased risk of severe acute respiratory syndrome (SARS) *coronavirus* infection.

STUDY DESCRIPTION


In 2003, severe acute respiratory syndrome (SARS) *coronavirus* emerged in China and spread to countries in Asia, Europe, and North America, leading to a total of ~ 8,000 cases. SARS is an infectious disease that can cause flu-like symptoms, including fever, coughing, and shortness of breath. While multiple clinical risk factors for developing SARS, such as being over the age of 60 or having diabetes, have been identified, little is known about how genetics affects the susceptibility to SARS *coronavirus* infection. This study used genetic data from 147 Vietnamese individuals, 60 of which were SARS patients, and discovered a genetic variant (rs2660) in the OAS-1 gene that is associated with susceptibility to infection with the SARS *coronavirus*. Specifically, the G allele of the variant rs2660 was linked to increased susceptibility to infection with the SARS *coronavirus*. (Note: This study is not a genome-wide association study. Only a few variants were genotyped selectively.)

DID YOU KNOW?

The SARS-CoV virus which caused the 2003 SARS outbreak is very similar to SARS-CoV-2 which is responsible for coronavirus disease 2019 (COVID-19) pandemic.

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 [Ⓞ]	EFFECT SIZE [Ⓞ]	VARIANT FREQUENCY [Ⓞ]	SIGNIFICANCE [Ⓞ]
rs2660_G 	G / G	0.53 (↑)	24%	1.76×10^{-2}