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Spontaneous coronary artery dissection (Saw, 2020)

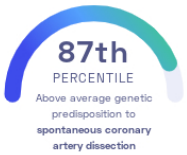
Jacqueline Saw, et al.
Nature Communications

Heart Vasculature

STUDY SUMMARY

Identification of 4 regions of the genome associated with spontaneous coronary artery dissection (SCAD).

YOUR RESULT



Above average genetic predisposition to **spontaneous coronary artery dissection**

STUDY DESCRIPTION

Arteries are blood vessels that carry blood from the heart to all parts of the body. Spontaneous coronary artery dissection (SCAD) is a condition in which a tear forms in an artery, causing blood to build up between the walls of the blood vessel. This build-up can lead to a blockage of blood flow, which can eventually lead to a heart attack. Though anyone can be affected by SCAD, the condition primarily affects women between the ages of 30 and 60. In fact, SCAD accounts for a quarter of all heart attacks in women under the age of 60. To better understand how genetics may affect SCAD, this study examined the genomes of over 5,500 individuals of European or East Asian ancestry. The study identified 4 unique regions of the genome that may impact an individual's risk of experiencing SCAD. One of the variants identified by this study (rs12740679) is near a gene known as ADAMTSL4, which plays a role in determining structure of our tissues, including our arteries.

DID YOU KNOW?

SCAD may be triggered by stressful situations, such as childbirth, the death of a family member, or even a strenuous workout. A 2014 study found that over half of all examined cases of SCAD followed a period of emotional and physical stress.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to spontaneous coronary artery dissection we summed up the effects of genetic variants that were linked to spontaneous coronary artery dissection 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 spontaneous coronary artery dissection. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to spontaneous coronary artery dissection. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to spontaneous coronary artery dissection. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for spontaneous coronary artery dissection to be 3.01**. 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 spontaneous coronary artery dissection is in the **87th percentile**. This means that it is higher than the polygenic scores 87% of people. We consider this to be an **above average genetic predisposition to spontaneous coronary artery dissection**. 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
rs12740679_G NEW	C / G	0.59 (↑)	26%	2.19×10^{-12}
rs9349379_A	A / G	0.40 (↑)	62%	4.36×10^{-8}
rs11172113_T NEW	T / T	0.41 (↑)	61%	2.63×10^{-8}
rs28451064_G NEW	G / G	0.60 (↑)	87%	1.19×10^{-7}