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Peripheral artery disease (Klarin, 2019)

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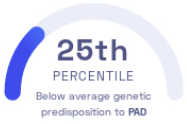
Nature Medicine

Vasculature

STUDY SUMMARY

The risk of peripheral *artery* disease is increased by genetic variants associated with LDL cholesterol levels.

YOUR RESULT



STUDY DESCRIPTION

Peripheral *artery* disease (PAD) is the narrowing of the arteries in the legs, stomach, arms, or head. It is generally caused by the buildup of *plaque* (from fats, cholesterol, or other substances) in the arteries and can lead to a heart attack or stroke. A predisposition to peripheral *artery* disease is known to be influenced by genetics, but few variants have been identified. This study looked for genetic variants that increase the risk of PAD in 243,060 military veterans of European, African, and Hispanic ancestry. Many of the variants identified were also associated with higher blood levels of low-density lipoprotein (LDL) cholesterol. LDL cholesterol is often referred to as "bad" cholesterol and can cause the formation of *plaque* in the arteries.

DID YOU KNOW?

You can reduce your LDL cholesterol levels (and therefore your risk of PAD) by eliminating trans fats (partially hydrogenated oil) from your diet. Losing weight, exercising regularly, and limiting your alcohol consumption can also lower your LDL cholesterol levels and PAD risk.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to PAD we summed up the effects of genetic variants that were linked to PAD 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 PAD. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to PAD. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to PAD. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for PAD to be 0.73**. 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 PAD is in the **25th percentile**. This means that it is higher than the polygenic scores 25% of people. We consider this to be a **below average genetic predisposition to PAD**. 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
rs118039278_A	G / G	0.23 (–)	7%	1.57×10^{-43}
rs1537372_T	G / G	0.11 (–)	42%	4.32×10^{-39}
rs10851907_A	G / A	0.06 (↑)	41%	1.49×10^{-13}
rs6025_T	NA	0.18 (–)	3%	1.63×10^{-12}
rs2107595_A	G / A	0.08 (↑)	19%	2.49×10^{-11}
rs7528419_A	A / A	0.07 (↑)	77%	2.54×10^{-11}
rs11066301_G	A / G	0.06 (↑)	41%	2.96×10^{-11}
rs4722172_G	A / A	0.08 (–)	20%	3.65×10^{-11}
rs7903146_T	C / T	0.06 (↑)	29%	3.76×10^{-11}
rs505922_C	C / C	0.06 (↑)	33%	7.10×10^{-11}
rs138294113_C	C / C	0.09 (↑)	88%	1.20×10^{-10}
rs62084752_C	G / G	0.07 (–)	22%	1.58×10^{-10}
rs3130968_T	C / C	0.07 (–)	14%	3.16×10^{-10}
rs1975514_C	T / T	0.05 (–)	36%	8.32×10^{-10}
rs7476_C	A / A	0.06 (–)	36%	8.33×10^{-10}
rs4842266_G	G / A	0.06 (↑)	39%	1.01×10^{-9}
rs322_A	C / C	0.06 (–)	71%	2.53×10^{-9}
rs566125_T	C / C	0.08 (–)	13%	4.37×10^{-9}
rs55784307_A	C / C	0.06 (–)	18%	2.93×10^{-8}

N/A indicates variants that could not be imputed using the 1000 genomes project datasets and variants that have a frequency of < 5%. Your genome was sequenced at 30x/100x coverage and is not imputed. However, to calculate percentiles, we need to compare your data with other users imputed data. To make the data comparable, we need to exclude some of the variants from your data.