02/2016

Pancreatic cancer (Childs, 2016)

Erica J. Childs, et al.
Nature Genetics

Pancreas Cancer

STUDY SUMMARY

Pancreatic cancer may be influenced by variants in the LINC00673, SUGCT, and TP63 genes.

YOUR RESULT

STUDY DESCRIPTION

The pancreas is an organ behind the stomach that helps with digestion and control of blood-sugar levels. To better understand the genetics that help determine pancreatic cancer risk, this study examined 21,494 individuals of European and Asian descent. It identified three new genetic variants associated with an increased risk of pancreatic cancer. One of these variants was in the LINC00673 gene, which has previously been found to play a role in cancer. Another significant variant was located in the SUGCT gene. The SUGCT protein is involved in the metabolism of the *amino acid* glutarate. Finally, a variant in the TP63 gene was found to be linked to pancreatic cancer. TP63 is also known as p63 and it plays a role in regulating the cell-cycle and the progression of tumors. Collectively, the identified variants accounted for roughly 2% of the heritability of pancreatic cancer.

DID YOU KNOW?

Not smoking, staying at a healthy weight, limiting your alcohol consumption, and avoiding exposure to certain chemicals in the workplace are all ways in which you can reduce your risk of pancreatic cancer.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to pancreatic cancer we summed up the effects of genetic variants that were linked to pancreatic cancer 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 pancreatic cancer. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to pancreatic cancer. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to pancreatic cancer. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for pancreatic cancer to be 0.61**. 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 pancreatic cancer is in the **100th percentile**. This means that it is higher than the polygenic scores 100% of people. We consider this to be a **very high genetic predisposition to pancreatic cancer**. 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
rs11655237_T NEW	T / T	0.23 (↑)	15%	1.42×10^{-14}
rs1486134_G	G / G	0.13 (↑)	30%	3.36×10^{-9}
rs17688601_A NEW	C / C	-0.13 (–)	24%	1.41×10^{-8}
rs9854771_A NEW	G / A	-0.12 (↓)	33%	2.35×10^{-8}