💢 Menopause onset (Stolk, 2012)

Lisette Stolk, et al. Nature Genetics



STUDY SUMMARY

The timing of menopause may be influenced by genetic variants linked to DNA repair, immune function, and mitochondrial dysfunction.

YOUR RESULT

100th PERCENTILE Very high genetic redisposition to later

menopause onset

STUDY DESCRIPTION

Menopause is the end of the reproductive function of the ovaries in women. Menopause is defined to begin 1 year after a woman's periods have stopped. To find genetic variants that correlate with the age at which women's menstrual cycles stop, this study examined 38,968 women of European descent. The normal age range of menopause used in this study was 45-54, so menopause



before age 45 was considered early and after 54 was considered late. The genetic variants identified in this study explained less than 1.5% of the heritability of menopause. Many of the genetic variants associated with the timing of menopause were linked to DNA repair and immune function. In addition, mitochondrial dysfunction was found to be related to the age of menopause. The mitochondria is commonly referred to as the "powerhouse of the cell" - it is where most of the chemical energy in our cells is produced. If the mitochondrion do not function properly in the cell, it greatly influences the progress of a number of diseases and disorders, as well as the age of menopause.

DID YOU KNOW?

Some researchers claim that diet may influence the timing of menopause. Carbohydrates may result in earlier menopause, while fish, peas, green beans, and meat may delay menopause.

To calculate your genetic predisposition to later menopause onset we summed up the effects of genetic variants that were linked to later menopause onset 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 later menopause onset. The variants highlighted in blue have negative effects sizes and decrease your genetic predisposition to later menopause onset. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to later menopause onset. By adding up the effect sizes of the highlighted variants we calculated your polygenic score for later menopause onset to be 2.42. 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 later menopause onset 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 later menopause onset. 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 ^①	VARIANT FREQUENCY [®]	SIGNIFICANCE [®]
rs16991615_A	G/A	0.95 (1)	7%	1.42 x 10 ⁻⁷³
rs11668344_G	A / G	-0.42 (↓)	36%	1.45 x 10 ⁻⁵⁹
rs365132_T	G/T	0.29 (1)	49%	9.11 x 10 ⁻³²
rs4246511_T 🐡	T/C	0.24 (1)	27%	9.08 x 10 ⁻¹⁷
rs2277339_G 🌼	T/T	-0.38 (-)	10%	2.47×10^{-19}
rs1046089_A 🙌	G/G	-0.21 (-)	35%	1.63 × 10 ⁻¹⁶
rs10183486_T 💮	C/T	-0.20 (↓)	37%	2.21 x 10 ⁻¹⁴
rs4693089_G 🙀	G / G	0.23 (1)	49%	2.38 x 10 ⁻¹⁹
rs2517388_G 📫	T/T	0.26 (-)	17%	9.31 x 10 ⁻¹⁵
rs10852344_C 💮	C/C	0.17 (1)	42%	1.01 × 10 ⁻¹¹
rs2153157_A	A / A	0.17 (1)	49%	7.76 x 10 ⁻¹²
rs2303369_T 💮	C/T	-0.17 (↓)	39%	2.25 x 10 ⁻¹²
rs1635501_C 🌼	T/T	-0.16 (-)	48%	8.46 x 10 ⁻¹⁰
rs12461110_A 🙌	G/G	-0.16 (-)	36%	8.74 × 10 ⁻¹⁰
rs12294104_T 💮	т/т	0.23 (1)	17%	1.46 × 10 ⁻¹¹
rs2307449_G 🙌	T / G	-0.18 (↓)	41%	3.56 x 10 ⁻¹³
rs4886238_A 🌼	A / A	0.17 (1)	33%	9.53 x 10 ⁻¹¹