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Walking pace (Timmins, 2020)

Iain Timmins, et al.
Communications Biology

Behavior

STUDY SUMMARY

Identification of 70 regions of the genome associated with walking pace.

YOUR RESULT

STUDY DESCRIPTION

Walking is an excellent leisure activity that is associated with benefits to overall health and fitness. For example, previous studies found that an increased pace of walking is associated with a decreased risk of death from cardiovascular diseases and various forms of cancer. To identify the genetic factors that influence walking pace, this study enrolled over 450,000 individuals of European descent. After correlating genetic information with self-reported walking speeds, the study identified 70 genetic variants associated with walking pace, 11 of which are novel. The study also examined the connections between walking pace and various traits/conditions. Researchers found that genetic predisposition to increased walking pace is correlated with a lower risk of adiposity, higher education attainment, and longer lifespan.

DID YOU KNOW?

According to the American Council on Exercise, people who track their steps (such as with a pedometer or fitness app) may walk as many as 2,500 more steps a day than people who don't.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to faster walking pace we summed up the effects of genetic variants that were linked to faster walking pace 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 faster walking pace. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to faster walking pace. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to faster walking pace. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for faster walking pace to be 0.24**. 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 faster walking pace is in the **84th percentile**. This means that it is higher than the polygenic scores 84% of people. We consider this to be an **above average genetic predisposition to faster walking pace**. 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
rs13107325_C	C / C	0.02 (↑)	7%	6.31×10^{-24}
rs784257_T	C / C	0.01 (–)	19%	1.03×10^{-16}
rs2280406_G	G / G	0.01 (↑)	49%	6.10×10^{-16}
rs9972653_G	G / T	0.01 (↑)	40%	8.58×10^{-16}
rs11039324_G	G / A	0.01 (↑)	40%	3.94×10^{-15}
rs273512_C	C / C	0.01 (↑)	40%	6.91×10^{-14}
rs7924036_G	G / T	-0.01 (↓)	50%	1.15×10^{-13}
rs7187776_A	A / G	0.01 (↑)	40%	1.80×10^{-13}
rs9366651_G	G / T	-0.01 (↓)	49%	2.00×10^{-13}
rs1243184_T	T / C	0.01 (↑)	32%	8.81×10^{-13}
rs12127073_C	C / C	-0.01 (↓)	11%	1.40×10^{-12}
rs7795394_T	A / A	-0.01 (–)	38%	2.43×10^{-12}
rs12739999_G	G / G	0.01 (↑)	17%	3.44×10^{-12}
rs1652376_G	G / T	-0.01 (↓)	46%	2.54×10^{-11}
rs113825410_A	A / A	0.01 (↑)	22%	5.52×10^{-11}
rs6763292_A	G / G	-0.01 (–)	22%	5.81×10^{-11}
rs57800857_A	A / A	-0.01 (↓)	37%	6.38×10^{-11}
rs11636600_G NEW	G / A	0.01 (↑)	13%	9.73×10^{-11}
rs4839898_G	G / G	-0.01 (↓)	11%	1.95×10^{-10}
rs10750025_C	C / C	0.01 (↑)	32%	2.03×10^{-10}
rs10862220_T	G / G	-0.01 (–)	32%	2.50×10^{-10}
rs10452738_A	A / A	0.01 (↑)	32%	2.99×10^{-10}
rs6798941_C	C / C	0.01 (↑)	30%	3.32×10^{-10}
rs10883618_G	G / G	-0.01 (↓)	37%	4.10×10^{-10}
rs205262_A	A / A	0.01 (↑)	27%	4.11×10^{-10}
rs2054079_C	C / C	-0.01 (↓)	32%	4.30×10^{-10}
rs11548200_T	T / T	0.02 (↑)	7%	5.51×10^{-10}
rs376942435_A	A / A	-0.01 (↓)	30%	6.26×10^{-10}
rs6539771_C	C / T	0.01 (↑)	36%	7.51×10^{-10}
rs7492565_G	G / G	0.01 (↑)	39%	9.37×10^{-10}
rs4715208_A	G / G	0.01 (–)	25%	1.04×10^{-9}
rs362307_C	C / T	0.01 (↑)	8%	1.11×10^{-9}
rs8010773_T	C / C	0.01 (–)	38%	1.12×10^{-9}
rs12461902_G	G / A	0.01 (↑)	33%	1.13×10^{-9}
rs143384_A	G / A	-0.01 (↓)	40%	1.68×10^{-9}
rs61954974_T	T / C	0.01 (↑)	26%	1.76×10^{-9}
rs12883788_C	C / T	0.01 (↑)	46%	2.43×10^{-9}
rs4516268_C	C / A	-0.01 (↓)	19%	2.44×10^{-9}
rs55680124_C	C / C	0.01 (↑)	16%	2.57×10^{-9}
rs2304507_T	C / C	0.01 (–)	40%	2.72×10^{-9}

rs2301697_T	C / C	-0.01 (–)	42%	2.72 x 10^{-9}
rs830627_G	A / A	-0.01 (–)	42%	2.93 x 10^{-9}
rs17698630_A	A / A	-0.01 (↓)	18%	3.12 x 10^{-9}
rs11152989_C	C / T	0.01 (↑)	31%	3.13 x 10^{-9}
rs11881338_T	T / T	-0.01 (↓)	49%	3.68 x 10^{-9}
rs4134943_C	C / T	-0.01 (↓)	20%	4.99 x 10^{-9}
rs4109292_G	G / A	-0.01 (↓)	49%	7.82 x 10^{-9}
rs45583845_C	NA	0.02 (–)	3%	1.03 x 10^{-8}
rs2439823_A	A / G	0.01 (↑)	45%	1.12 x 10^{-8}
rs13005495_T	G / G	0.01 (–)	42%	1.16 x 10^{-8}
rs114547690_A	A / A	0.01 (↑)	12%	1.38 x 10^{-8}
rs10797999_C	C / T	-0.01 (↓)	41%	1.42 x 10^{-8}
rs115202226_A	NA	-0.05 (–)	1%	1.62 x 10^{-8}
rs5026760_A	A / G	-0.01 (↓)	17%	1.64 x 10^{-8}
rs798750_G	A / A	0.01 (–)	38%	1.82 x 10^{-8}
rs699785_G	G / G	-0.01 (↓)	24%	2.29 x 10^{-8}
rs35741895_A	A / A	0.01 (↑)	12%	2.30 x 10^{-8}
rs1531133_A	A / A	-0.01 (↓)	42%	2.46 x 10^{-8}
rs11264302_G	G / A	0.01 (↑)	47%	2.53 x 10^{-8}
rs1667369_A	A / C	0.01 (↑)	37%	2.72 x 10^{-8}
rs2920503_C	C / C	-0.01 (↓)	29%	2.91 x 10^{-8}
rs9844666_G	G / A	0.01 (↑)	24%	2.97 x 10^{-8}
rs8011870_G	G / G	0.01 (↑)	29%	3.16 x 10^{-8}
rs7804774_A	G / G	-0.01 (–)	19%	3.24 x 10^{-8}
rs34898535_C	T / T	-0.01 (–)	38%	3.30 x 10^{-8}
rs72636700_T	T / T	0.01 (↑)	17%	3.57 x 10^{-8}
rs2469878_C	C / T	0.01 (↑)	33%	3.59 x 10^{-8}
rs62246314_G	G / A	0.01 (↑)	10%	4.10 x 10^{-8}
rs67625472_T	T / T	0.01 (↑)	28%	4.22 x 10^{-8}
rs1061801_G	G / G	0.01 (↑)	19%	4.61 x 10^{-8}
rs8005131_G	G / C	-0.01 (↓)	34%	4.69 x 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.