6/2017

Insomnia (Hammerschlag, 2017)

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Nature Genetics

Sleep Mind

STUDY SUMMARY

Identification of multiple novel genetic variants that are associated with an increased risk of experiencing insomnia.

STUDY DESCRIPTION

Sleep plays a critical role in maintaining physical and mental health. Insomnia, characterized by difficulty falling asleep or staying asleep, is one of the most common sleeping disorders. Insomnia is also one of the most common mental disorders and a major risk factor for depression. This study gathered genetic data from 113,006 individuals of European ancestry and identified novel genetic variants that are linked to insomnia. In particular, variants in two genes were significantly associated with insomnia: MEIS1 and SCFD2. The MEIS1 gene has been linked by other studies to sleep disturbance. The study also analyzed each sex individually and discovered multiple variants in the WDR27 gene that are associated with insomnia in males. Finally, strong positive genetic correlations were identified between insomnia and multiple psychiatric disorders, including anxiety, depression and, *neuroticism*.

DID YOU KNOW?

Refraining from the use of electronic devices such as phones and computers an hour before bed may make it easier to fall asleep. Reading and meditating are excellent substitutes!

YOUR DETAILED RESULTS

The variants highlighted in green have **positive effect sizes** and increase your genetic predisposition to insomnia. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to insomnia. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to insomnia. 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
rs113851554_T NEW	G / T	0.17 (↑)	6%	2.14×10^{-18}
rs574763165_G NEW	NA	0.34 (-)	1%	4.98×10^{-9}

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.