

10/2020

★ Cannabis use disorder (Johnson, 2020)

Emma Johnson, et al.
The Lancet Psychiatry

Addiction

STUDY SUMMARY

Identification of 2 genomic regions associated with cannabis use disorder.

STUDY DESCRIPTION


In the United States, over 20 million people consume cannabis every month. About 1 in 10 users of cannabis will become dependent, leading to a condition known as cannabis use disorder. Individuals afflicted by cannabis use disorder may develop irritability, memory problems, and depression. It is estimated that over 50% of an individual's risk of developing cannabis use disorder can be explained by genetic factors. This genome-wide association study found 2 regions of the genome associated with cannabis use disorder after examining genetic data of over 380,000 individuals of European and African ancestries. One of the discovered genetic variants is located in a gene known as FOXP2, which has previously been shown to play a role in speech and language development. The study also found a positive association between the risk of developing cannabis use disorder and the risk of developing ADHD, schizophrenia, and depression.

DID YOU KNOW?

Cannabis use can greatly affect coordination. Driving or use of other machinery under the influence of cannabis can be extremely dangerous. A 1990 study found that employees who tested positive for cannabis on a pre-employment drug test were prone to 55% more industrial accidents and 85% more injuries than their co-workers who tested negative.

YOUR DETAILED RESULTS

The variants highlighted in green have **positive effect sizes** and increase your genetic predisposition to cannabis use disorder. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to cannabis use disorder. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to cannabis use disorder. 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 [ⓘ]	COMMENTS	EFFECT SIZE [ⓘ]	VARIANT FREQUENCY [ⓘ]	SIGNIFICANCE [ⓘ]
rs7783012_A 	G / A	In the FOXP2 gene	5.97 (↑)	64%	2.43×10^{-9}
rs4732724_C	G / G	Near CHRNA2 gene	-5.95 (-)	37%	2.64×10^{-9}