

# Marijuana use linked to epigenetic changes

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Recent and long-term marijuana use is linked to changes in the human epigenome, a new Northwestern Medicine study published in *Molecular Psychiatry* has found.

Marijuana is the most used drug in the United States, according to the

Centers for Disease Control and Prevention, with roughly 48.2 million people (about 18% of all Americans) having used it at least once in 2019, the most recent year for which data is available.

Although multiple states have legalized marijuana, the health consequences of marijuana use are not well understood, said Lifang Hou, MD, Ph.D., chief of Cancer Epidemiology and Prevention in the Department of Preventive Medicine and senior author of the study.

"Despite its growing popularity, as well as recent legalization by several states, the effect of marijuana on [epigenetic factors](#) has not been well studied," said Hou, who is also Director of the Center for Global Oncology in the Robert J. Havey, MD, Institute for Global Health. "We previously identified associations between marijuana use and the [aging process](#) as captured through DNA methylation. We wanted to further explore whether specific epigenetic factors were associated with marijuana and whether these factors are related to health outcomes."

In the study, investigators analyzed whole [blood samples](#) taken five years apart from people who previously participated in the Coronary Artery Risk Development in Young Adults (CARDIA) study. The current study included data from more than 900 adults.

The scientists surveyed each participant for recent marijuana use and estimated cumulative use and then performed DNA methylation profiling on their blood samples to reveal epigenetic changes associated with marijuana use.

By studying changes in DNA methylation, the [biological process](#) by which [methyl groups](#) are added to DNA molecules, thereby altering [gene expression](#), scientists were able to link marijuana use to changes in the human epigenome.

Overall, investigators observed 22 and 31 DNA methylation markers associated with recent and cumulative marijuana use, respectively, from the first samples and 132 and 16 methylation markers in the second batch of samples, according to the study.

Many of the epigenetic changes were found in pathways previously linked to cellular proliferation, hormone signaling, infections and mental health disorders such as schizophrenia, [bipolar disorder](#) and substance use disorders, Hou said.

"In our study, we observed associations between cumulative marijuana use and multiple epigenetic markers across time," Hou said.

"Interestingly, we consistently identified one marker that has previously been associated with tobacco use, suggesting a potential shared epigenetic regulation between tobacco and marijuana use. The observed marijuana markers were also associated with [cell proliferation](#), infection and psychiatric disorders, however, additional studies are needed to replicate and verify these findings."

While the study does not establish a causal relationship between marijuana use and epigenetic changes, nor between those epigenetic changes and observed health outcomes, the findings may be useful in future research into the epigenetic effects of marijuana use, said Drew Nannini, DO, Ph.D., a postdoctoral fellow in the Hou lab and first author of the study.

"This research has provided novel insights into the association between marijuana use and epigenetic factors," Nannini said. "Additional studies are needed to determine whether these associations are consistently observed in different populations. Moreover, studies examining the effect of marijuana on age-related [health outcomes](#) may provide further insight into the long-term effect of marijuana on health."

**More information:** Drew R. Nannini et al, Genome-wide DNA methylation association study of recent and cumulative marijuana use in middle aged adults, *Molecular Psychiatry* (2023). [DOI: 10.1038/s41380-023-02106-y](https://doi.org/10.1038/s41380-023-02106-y)

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