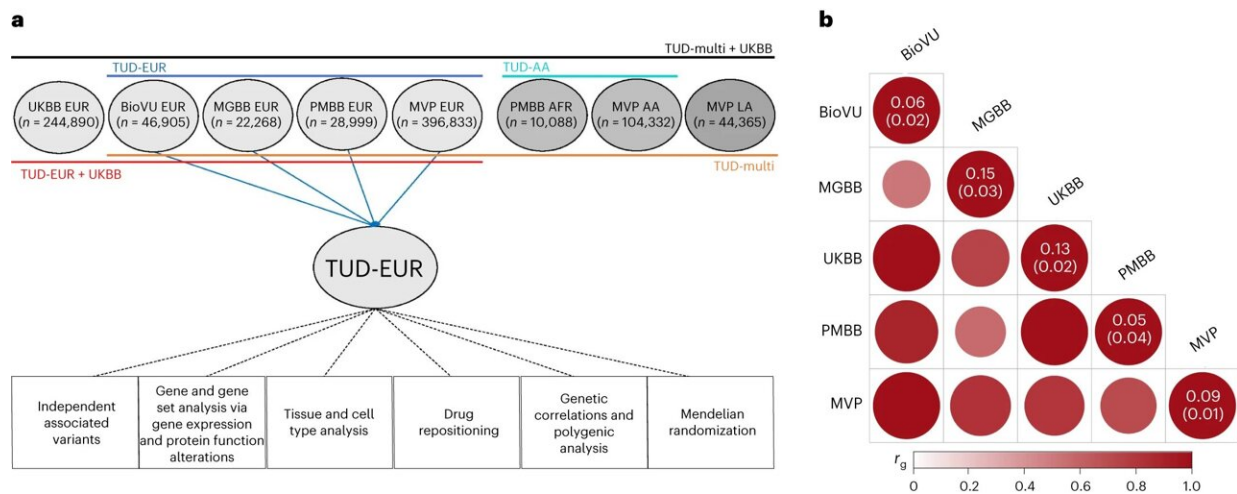


Electronic health records unlock genetics of tobacco use disorder

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Overview of the cohorts, analysis pipeline and genetic correlations among the sites. Credit: *Nature Human Behaviour* (2024). DOI: 10.1038/s41562-024-01851-6

By analyzing electronic health records, researchers at the University of California San Diego School of Medicine have identified hundreds of new genes associated with tobacco use disorder. They also identified hundreds of potential drug candidates that could help treat the disease. The study was [published](#) in *Nature Human Behavior*.

"Tobacco use disorder has an enormous impact on public health," said Sandra Sanchez-Roige, Ph.D., an associate professor in the Department of Psychiatry at UC San Diego School of Medicine. "However, it's challenging to develop new therapeutics for tobacco use disorder because so much of its underlying genetics is poorly understood."

According to the World Health Organization, there are about 1.3 billion tobacco users worldwide, and 80% of these people live in low and middle-income countries. The [public health](#) effects of tobacco use extend far beyond those who use it themselves; tobacco kills more than 8 million people each year, and an estimated 1.3 million of these deaths are nonsmokers who were exposed to [secondhand smoke](#).

The official criteria for tobacco use encompass a wide variety of behaviors associated with tobacco use, such as using more tobacco than intended or continuing to use it despite negative consequences. There are known genes associated with nicotine consumption on its own, but these don't tell researchers how nicotine use progresses to tobacco use disorder.

"A fraction of people are able to smoke occasionally without developing an addiction," said Sanchez-Roige. "We want to understand, from a genetic perspective, why occasional tobacco use becomes chronic misuse in some people."

The researchers leveraged large volumes of electronic health data from several [health systems](#) in the United States, which was enabled by the PsycheMERGE Network, an international consortium of researchers that aims to synthesize medical records and genomics data to understand better and treat neuropsychiatric illnesses. Sanchez-Roige leads the substance use disorder workgroup within PsycheMERGE.

For the current study, her team used an approach called genome-wide association, which allows researchers to scan the [entire genome](#) and look for variations in our genes associated with certain traits, behaviors, or diseases. This is one approach scientists have used to find genes associated with smoking, but this is the first time this approach has been able to reveal genes associated with tobacco use disorder.

In their study of 898,680 individuals, they found 461 candidate risk genes for tobacco use disorder, mostly expressed in the brain. These genes are associated with a myriad of other psychiatric and [medical conditions](#), such as HIV infection, heart disease, and chronic pain. Further, the researchers were able to validate known findings about genes associated with smoking behaviors, which helped validate their approach.

In addition to giving us a more comprehensive view of [tobacco use](#) disorder, the researchers were able to use their results to identify hundreds of potential drug candidates that could help doctors treat the disease. However, it will take more research to evaluate these drugs in the lab and the clinic.

In the meantime, the study also supports a growing idea in the field of genetics research: Electronic health records are an underutilized treasure trove of information.

"There's a world of information hidden in medical records, and we accumulate more of them every day as part of routine clinical care," said Sanchez-Roige. "They're also a relatively untapped resource due to how difficult it is to organize and analyze electronic health record data. This study is part of a growing movement to use this constantly expanding source of information to solve complex medical problems."

More information: Sylvanus Toikumo et al, Multi-ancestry meta-

analysis of tobacco use disorder identifies 461 potential risk genes and reveals associations with multiple health outcomes, *Nature Human Behaviour* (2024). [DOI: 10.1038/s41562-024-01851-6](https://doi.org/10.1038/s41562-024-01851-6)

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