

Researchers identify genetic clues associated with cigarette addiction

1 September 2015, by Cynthia McMullen



Researchers at the Virginia Commonwealth University School of Pharmacy have identified specific sets of genetic variants that are significantly associated with cigarette addiction. Pinpointing these genetic variants could eventually assist in identifying the biological mechanism behind nicotine addiction and in generating novel drug therapy targets to help people break their addiction to nicotine.

The study, "Deep Sequencing of Three Loci Implicated in Large-Scale Genome-Wide Association Study Smoking Meta-Analyses," was published in August as an advanced online publication in the Oxford University Press journal *Nicotine & Tobacco Research*.

"We dug deeper into genes known to be associated with smoking," said Shauna L. Clark, Ph.D., research assistant professor, Center for Biomarker Research and Precision Medicine, VCU School of Pharmacy. Previous large-scale, genomewide association studies have identified three genes that are related to cigarette addiction,

but the VCU-led study is the first to identify specific sets of genetic variants that might be responsible.

Researchers at the CBRPM sequenced the three genes and their adjacent regions to get a complete catalog of all the [genetic variation](#) that could be contributing to addiction. Sequencing the entire gene allowed Clark and her colleagues to examine variants that other studies had not addressed, such as rare variants not commonly found in the population and regulatory variants that can increase or decrease gene expression.

"We found that the tendency toward [nicotine addiction](#) is likely caused by many variants, each with a small effect," Clark said. "Thus, multiple variants within the same gene are related to smoking."

More information: "Deep Sequencing of Three Loci Implicated in Large-Scale Genome-Wide Association Study Smoking Meta-Analyses." *Nicotine Tob Res* first published online August 17, 2015 [DOI: 10.1093/ntr/ntv166](https://doi.org/10.1093/ntr/ntv166)

Provided by Virginia Commonwealth University

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