



National Institute on Drug Abuse  
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FOR IMMEDIATE RELEASE  
Monday, December 4, 2006

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**NIDA Researchers Complete Unprecedented Scan of Human Genome That May Help Unlock the Genetic Contribution to Tobacco Addiction**

Results of a new genetic study bring scientists one step closer to understanding why some smokers become addicted to nicotine, the primary reinforcing component of tobacco. The research, funded by the National Institute on Drug Abuse, part of the National Institutes of Health, represents the most powerful and extensive evidence to date of genetic risk factors for tobacco addiction. The study not only completed the first scan of the human genome to identify genes not previously associated with nicotine dependence (or addiction), it also focused on genetic variants in previously suspected gene families. The research results appeared in the December 1 online issue of the *Journal of Human Molecular Genetics*.

“This genome wide association scan is an important step in a large-scale genetic examination of nicotine addiction,” says Dr. Elias A. Zerhouni, Director of the NIH. “As more genomic variations are discovered that are associated with substance abuse, including smoking, we will be better able to understand how to prevent and treat human addictive disorders.”

Smoking behaviors, including the onset of smoking, smoking persistence (current smoking versus past smoking), and nicotine addiction, cluster in families. Studies of

twins indicate that this clustering partly reflects genetic factors. To identify those genes that could potentially contribute to nicotine dependence, scientists combined a comprehensive genome-wide scan with a more traditional approach that focuses on a limited number of candidate genes, using unrelated nicotine-dependent smokers as cases and unrelated non-dependent smokers as controls. A candidate gene has one or more variant forms, which, according to current scientific evidence, appear to be linked to a genetic disease.

“When two teenage friends experiment with smoking at the same age, one can become addicted and the other might not,” says NIDA Director Dr. Nora D. Volkow. “We want to know why. This systematic survey of the genome coupled with the ongoing identification of variants in candidate genes brings us closer to understanding what factors increase a person’s risk of transitioning from experimentation to nicotine addiction.”

Tobacco use, primarily in the form of cigarette smoking, is a leading contributor to death and disability worldwide. Each year, approximately 440,000 Americans die of smoking-related illnesses and about 5 million deaths are attributed to tobacco worldwide. Although the prevalence of cigarette smoking in the United States has decreased over the last 30 years, adolescents continue to initiate cigarette use, with more than 20 percent of high school seniors reporting cigarette smoking in the last month.

Efforts to understand nicotine addiction are important so that new approaches can be developed to reduce tobacco use. Tailoring of smoking cessation medications to an individual's genetic background may significantly increase the efficacy of treatment. “The hope is that continued identification of these genes that are associated with risk of addiction will not only help us predict who is more likely to become addicted but will also help identify who will respond best to specific cessation therapies,” says study leader Dr. Laura Jean Bierut, of Washington University School of Medicine in Saint Louis, Missouri.

NIDA will continue to commit resources to the study of genetic factors involved in smoking behaviors. “New technologies related to the study of the human genome have helped us collect new information related to nicotine addiction,” adds Dr. Volkow. “We must now determine how to translate these findings into approaches that will reduce smoking related disease and death.”

The term “genome” refers to the total genetic information of a particular organism. The normal human genome consists of about 3 billion base pairs of DNA in

each set of chromosomes from one parent. The term “genetic variation” is used to describe differences in the sequence of DNA among individuals. Genetic variation plays a role in whether a person has a higher or lower risk for getting particular diseases.

In addition to funding from NIDA, this research was also supported by a grant from the National Cancer Institute (NCI).

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The National Institute on Drug Abuse is a component of the National Institutes of Health, U.S. Department of Health and Human Services. NIDA supports most of the world’s research on the health aspects of drug abuse and addiction. The Institute carries out a large variety of programs to ensure the rapid dissemination of research information and its implementation in policy and practice. Fact sheets on the health effects of drugs of abuse and information on NIDA research and other activities can be found on the NIDA home page at [www.drugabuse.gov](http://www.drugabuse.gov).

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