

Researchers Locate Genetic Link for Nicotine Dependence Among African Americans

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Scientists at the University of Virginia Health System have identified, for the first time ever, several genetic regions that are likely to carry the genes for nicotine dependence (ND) in an African American population. This is the first genome-wide study of such linkage and included the largest group of African Americans to participate in this type of linkage study. Until this study, participants in research to find genetic links to ND have been primarily of European origin.

This new study is important because there are known differences in smoking patterns and in ND risk across ethnic groups. Analysis of twin studies on smoking behavior showed that genetic factors are responsible for at least 50 percent of a person's tendency toward dependence on nicotine.

“Identifying the genes that predispose a person to nicotine dependence and understanding the molecular mechanisms are vital to prevention and treatment,” said lead author Ming Li, Ph.D., associate professor and head of the Neurobiology Section of the UVa Department of Psychiatric Medicine. “Given the potential ethnic differences in smoking patterns and nicotine metabolism, this study may suggest strategies for identifying genes for tobacco dependence, especially among African American smokers.” This could lead to potential targeted treatments in the future.

Such genome-wide studies are arduous, but they yield valuable information. “Without knowing these regions, we would have no place to start, given that everybody has 22 autosomal chromosomes and two sex chromosomes with about 40,000 genes located throughout the genome,” Dr. Li explained.

The researchers conducted a genome-wide scan of 1,261 individuals representing 402 nuclear families of African American origin, the largest sample collection of African-American smokers throughout the world. Their results revealed a region on chromosome 10 that showed a significant linkage to smoking quantity and other measures of smoking dependence. They also identified three other regions that met the criteria for linkage to at least one ND measure. Some of these regions have been linked to smoking behavior previously, which adds supporting data to the previous studies of nicotine dependence in other populations.

The article, which appears in the October issue of *American Journal of Human Genetics* (vol. 79, pages 745-751) noted that these linkage regions represent excellent candidate locations that might in the future become targets for treatments that could change a person’s tendency toward using nicotine. To identify susceptibility genes for ND from these regions, the UVA researchers have started a series of genetic analyses using a combination approach of fine mapping and genetics association studies.

To read the article, visit:

www.journals.uchicago.edu/AJHG.../43856/43856.web.pdf

Source: University of Virginia

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