

Researchers find genetic variants linked to smoking behaviors

April 26 2010

(PhysOrg.com) -- In a paper published in the journal *Nature Genetics*, a UNC team reported that three genetic regions were associated with the number of cigarettes smoked per day, one region was associated with smoking initiation and one variant was associated with smoking cessation.

A team of scientists has used data from genome-wide association studies to identify genetic variants associated with key smoking behaviors that have a significant impact on health.

UNC-Chapel Hill genetics faculty members and UNC Lineberger members Helena Furberg, PhD and Patrick Sullivan, MD led the largest genetic study of smoking, called the Tobacco and Genetics Consortium (TAG), collaborating with scientists from 16 large genetic studies worldwide. They compared the [DNA marker](#) profiles between [smokers](#) and non-smokers to examine whether genetic variants affect whether people start to smoke. They also compared the DNA among smokers to see if genetic variants affected the number of cigarettes smoked per day, the age when people began to smoke and whether smokers were able to quit.

“In a paper published today in the journal *Nature Genetics*, the team reported that three genetic regions were associated with the number of cigarettes smoked per day, one region was associated with smoking initiation and one variant was associated with [smoking cessation](#). The variants on chromosome 15 that were associated with heavy smoking lie within a region that contains nicotinic receptor genes, which other

scientists have previously associated with [nicotine](#) dependence and [lung cancer](#).

“We hope that this work will allow researchers from multiple disciplines to develop a better understanding of the genetics of addiction and evaluate how drug-gene interactions could be used to create and tailor therapies to improve the rates of smoking cessation,” said Furberg.

“More work needs to be done before these findings can be used to treat smokers who wish to quit. At this time, testing for these variants will not tell you anything meaningful about your risk of smoking or [nicotine dependence](#). Of course, all smokers should be encouraged to quit regardless of their genetic make-up,” she added.

Genome-wide association studies (GWAS) search for genetic variants involved in a disease which may ultimately help prevent, diagnose, and treat the disease. Because smoking behavior is associated with many diseases, such as heart disease and cancer, the researchers were able to assemble more data to test the links between genetic variants and smoking than any one study could provide alone. The Tobacco and Genetics Consortium also collaborated with two other groups from Europe to confirm their findings; all three papers appear in *Nature Genetics*.

Provided by University of North Carolina at Chapel Hill School of Medicine

Citation: Researchers find genetic variants linked to smoking behaviors (2010, April 26) retrieved 2 May 2024 from <https://medicalxpress.com/news/2010-04-genetic-variants-linked-behaviors.html>

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