



CANCER PREVENTION & RESEARCH INSTITUTE OF TEXAS

Award ID:
RP130123

Project Title:
Using Deep Sequencing Technology to Study Genes & Behavioral
Phenotypes Related to Smoking Cessation, Negative affect & Nicotine
Withdrawal

Award Mechanism:
Individual Investigator

Principal Investigator:
Cinciripini, Paul M

Entity:
The University of Texas M.D. Anderson Cancer Center

Lay Summary:

The overarching goal of this study is to investigate whether or not certain genes can influence a smoker's ability to quit smoking and the extent to which they experience symptoms of nicotine withdrawal when they attempt to quit. We have learned in past clinical studies that in addition to cravings, many people experience symptoms of depression, anxiety, agitation, restlessness, and difficulty concentrating when they stop smoking. These symptoms can last up to a few weeks or longer and may even return long after someone has abstained from smoking. Many people report that the experience of these negative moods is one of the primary reasons they relapse and go back to smoking. There are several genes that may be involved in determining why certain people may quit more easily than others and we believe they may be related to the control of certain processes in the brain which help determine our mood, the extent to which we find smoking pleasurable, and other aspects of the smokers experience while taking in nicotine. How nicotine affects the brain is fundamental in determining who smokes and these processes may be largely influenced by our genetic makeup. If we can determine which genes do this, and there are likely to be several since there are many aspects of brain function that are affected by nicotine, we may be in a better position to develop new pharmacological treatments to help people stop smoking that are directed specifically at the biological activity controlled by these genes. This research is one of the first studies to directly look at people's experience while quitting and relate that to genetic factors and if successful, could help us identify new biological targets for medication development.