CANCER PREVENTION & RESEARCH INSTITUTE OF TEXAS

Award ID:
RP130502

Project Title:
Role of MicroRNA in Lung Cancer Risk & Clinical Outcome Prediction

Award Mechanism:
Individual Investigator

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

Lay Summary:

Smoking accounts for 90% of lung cancer cases, but only about 10-15% of heavy smokers develop lung cancer, suggesting individual genetic susceptibility. Identifying genetic predisposition loci to lung cancer will help predict a person's risk of developing lung cancer. In this project, we will first identify inherited genetic susceptibility factor of lung cancer using two of the largest lung cancer studies with 6,000 cases and 6,000 healthy controls. We designed a three-stage study to screen and validate inherited genetic variations in microRNA pathway as susceptibility loci of lung cancer. MicroRNAs are a class of small non-coding RNAs that regulate gene expression and play important roles in cancer development. The ability to identify high-risk individuals for lung cancer will provide immense public health benefit for those high-risk people who may be subjected to intense surveillance, screening and chemoprevention. Lung cancer accounts for nearly 30% or all cancer deaths. Non-small cell lung cancer (NSCLC) comprises over 80% of lung cancer cases. Surgical resection remains the best treatment for operable early stage NSCLC patients. However, 50% to 60% of surgically resected early stage NSCLC patients have a recurrence and eventually die from this disease. Adjuvant chemotherapy is recommended for routine use in stage II NSCLC patients with modest survival benefit, often accompanied by significant side effect. Clinical variables alone cannot satisfactorily predict patients' prognosis. Our second goal is to identify inherited genetic predictors of recurrence in surgically resected early stage NSCLC patients. Blood-based biomarkers have the potential to complement clinical variables and improve prediction of recurrence. If a patient's genetic makeup permits a better prediction of recurrence before therapy starts, physicians could potentially customize therapy to maximize efficacy and avoid unnecessary toxicity of therapy.