CANCER PREVENTION & RESEARCH INSTITUTE OF TEXAS

Award ID:
RP140556

Project Title:
DNA Methylation and Telomere Length in Peripheral Blood as Predictors of Aggressive Prostate Cancer

Award Mechanism:
Individual Investigator

Principal Investigator:
Gu, Jian

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

Lay Summary:

The overall 5-year survival rate of prostate cancer patients is nearly 100%. However, accompanying the excellent prognosis is overtreatment in many patients, as the majority of screening-detected PCa are localized, slow growing, and pose little or no threat to the health or longevity of the patients. Most patients die of diseases other than PCa, yet about 90% of men with localized PCa receive upfront treatment with prostatectomy or radiotherapy that often causes significant morbidity, including urinary dysfunction, rectal bleeding, and impotence. Clinical parameters are not sufficient to accurately distinguish men who can be spared initial therapy from those needing aggressive therapy, resulting in overtreatment of many truly indolent PCa patients and undertreatment in those who may benefit from early intervention. Biomarkers are urgently needed to augment clinical parameters in distinguishing aggressive and life-threatening PCa from indolent PCa. DNA methylation is the most common molecular mechanism regulating gene expression. Telomere is the protective cap at each chromosome end. DNA methylation can regulate telomere length. Both aberrant DNA methylation and short telomere length lead to genomic instability and may be promising biomarkers for aggressive PCa. The purpose of this project is to screen and validate DNA methylation in peripheral blood white cells as predictors of aggressive PCa, and evaluate telomere length as a biomarker of aggressive PCa. Furthermore, we will decipher the relationship of DNA methylation in specific chromosome regions with telomere length. This study leverages one of the largest PCa patient cohorts in the U.S. with well-annotated biospecimens linked to epidemiological and clinical data. A total of 3,800 patient samples will be used. This project will go a long way towards more accurate prediction of aggressive PCa at diagnosis, allowing better-informed clinical decision-making and avoiding overtreatment.