Developing Diagnostic Tools for Vascular Disease Using RNA Markers, Year Two

Rathinasabapathi, Brindha (School: Eastside High School)

Cardiovascular disease (CVD) is the leading cause of death worldwide, killing 17.9 million people annually and costing billions of dollars. The main cause of CVD is atherosclerosis, the buildup of plaque in the arteries. Current diagnostic tools are suited to detect the later stages of this disease. Unfortunately, diagnostic methods to comprehensively define the earliest stages of atherosclerosis are lacking. Thus, the objective of this study was to develop a simple blood test for detection of early atherosclerosis. I hypothesized that the expression levels of genes related to the earliest stage of the disease (F11R, NFKB1, TNFAIP6, and ITGA6) could be used to create a comprehensive model to predict atherosclerosis severity. Quantitative RT-PCR was used to measure the relative expression levels of the four target genes in 50 clinical human leukocyte RNA samples. Subjects' carotid intima-media thickness (CIMT) scores, an indicator of atherosclerosis severity, and other medical parameters were used to define patients' overall disease severity. Sample data was also stratified using relevant factors (e.g. sex). Then, multiple linear regression in RStudio was used to examine the relationship between gene expression and disease severity in sample subsets. Two significant models for the prediction of atherosclerosis were produced, one using F11R and NFKB1 ($p = 0.003$, R-squared = 0.50) and the other using F11R and TNFAIP6 ($p = 0.003$, R-squared = 0.53). The novel approach of this study, integrating transcriptomic biomarkers, clinical data, and computational analyses, resulted in unique models that hold the key to the preventative, personalized treatment of CVD.