



CPH Seminar in Precision Medicine

Genetic Variants in microRNA Genes and Targets associated with Cardiovascular Disease risk factors in the African American population

Chang Li Ph.D

University of Texas Health Science Center at Houston
School of Public Health
Epidemiology

The purpose of our study was to identify microRNA (miRNA) related polymorphism, namely, single-nucleotide variants (SNVs) in mature miRNA-encoding sequences or in miRNA target sites, and their association with CVD risk factors. To achieve our objective, we examined 1,900 African-Americans from the Atherosclerosis Risk in Communities (ARIC) study using SNVs identified from whole-genome sequencing (WGS) data. A total of 971 SNVs found in 726 different mature miRNA-encoding sequences and 16,057 SNVs found in the 3'UTR of 3,647 protein coding genes were identified and used in our discovery analysis. We reported 5 SNVs in miRNA-encoding sequences to be significantly associated with serum Lp(a) (NR_030387.1:n.27A>G), HDL (NR_039943.1:n.66T>C; NR_039880.1:n.18A>C) or triglycerides

Friday, September 8, 2017. 12p – 1p. UCT1414

Arlisa.K.Ross@uth.tmc.edu
713 500-3912

 #SBMIseminar

