

CPH Seminar in Precision Medicine

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

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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

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