Principal Investigator: Herman Taylor/ James Wilson

Institution Affiliation: University of MS Medical Center

Ancillary Study Title: Whole exome sequencing in the Jackson Heart Study

Project Overview: Genome wide association studies (GWAS) have now identified hundreds of common variants that contribute to cardiovascular disease-related phenotypes. However, despite this rapid pace of discovery, in almost every case the variants that have been identified, in aggregate, fail to account for more than about 10% of the heritability of the phenotypes being analyzed. In trying to account for the "other 90%", scientists have proposed that a substantial proportion of the variance of most phenotypes may be determined by the sum of the effects of a large number of rare variants (i.e., variants with minor allele frequencies <1%) in the population. In the current project we will identify a large number of medically significant rare variants by sequencing every protein coding exam in the genome (i.e. "the exome") in potentially every consenting JHS participant, and analyzing the identified variants with respect to a broad array of CVE-related phenotypes. Sequencing will use highly parallel platforms such as Illumina/Solexa, Roche® 454 or ABI SOLiD. While the exome includes only about 1% of the genome (the functions of the remaining 99% are not well understood), it is estimated that perhaps as much as 50% of medically significant variation may be discovered within the exome. Thus the current project should yield rich findings that will continue to develop over a number of years, as the sequencing data produced are analyzed more and more deeply.