Principal Investigator: James G. Wilson

Institution Affiliation: University of Mississippi Medical Center

Ancillary Study Title: Genome Wide Association in the Jackson Heart Study

Project Overview

To perform whole-genome admixture scanning of all unrelated Jackson Heart Study participants and to seek quantitative trait loci for hypertension, HDL-cholesterol level, and left ventricular hypertrophy by admixture mapping. All consenting, unrelated JHS participants will be genotyped for 3,072 admixture mapping markers. The resulting data will be analyzed to seek chromosomal regions where the proportion of European or African ancestry is unexpectedly high in relation to a particular phenotype. Such regions are likely to contain the loci of risk alleles for the phenotype that were more common in the over-represented ancestral population. An Illumina bead station will be used to genotype a panel of genome wide single nucleotide polymorphisms (SNPs) selected and validated by Dr. Reich to be maximally informative for admixture mapping(1). SNP data will be analyzed for association with selected phenotypes by statistical methods that have been developed and published by Dr. Reich and colleagues (2). Admixture mapping has only recently become feasible, and available results are limited. However, calculations suggest that it may be as powerful as whole-genome haplotype-based mapping while requiring 200- to 500-fold fewer markers. Although the current proposal will focus on three phenotypes that are important in cardiovascular disease, once genome-wide admixture genotyping is complete, the data can be analyzed with respect to any phenotype of interest. Each new analysis will of course be subject to approval by the JHS Ancillary Studies or Publications Committee, as appropriate