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**Institution Affiliation:** University of Virginia

**Ancillary Study Title:** Jackson Heart Study sample inclusion for Genetic Prediction of Essential Hypertension

**Project Overview**

We characterized a proprietary set of gene polymorphisms, the hypertension single-nucleotide polymorphism (SNP) “panel” that we believe are largely responsible for the pathogenesis of essential hypertension (1). This hypertension SNP panel, by themselves or via an interaction with genes controlling the renin-angiotensin system, has a strong positive association with essential hypertension across racial and ethnic subpopulations including Japanese, Caucasians, and Ghanaians (where 60% of African Americans can trace their roots).

To test our hypertension SNP panel in an African American cohort to determine if they associate with the expression of the hypertensive phenotype. We intend to replicate our existing set of SNPs within the JHS. We would like to have the right to add several SNPs to our study if new SNPs with promise as being predictive of hypertension appear in peer reviewed published literature. However, we will approach the JHS again if more than three SNPs need to be added to our testing panel.

Our study is designed with the inclusion criteria of African American hypertensive subjects between the age of 55 and 70 consisting of approximately 50% male and 50% female with body mass indices between 18 and 25, and a matched normotensive control cohort. (See Part III, section 4 for cohort details.)

We will use our automated genotyping platform to examine a panel of SNPs associated with essential hypertension with or without salt sensitivity.

Through the use of predictive genetic diagnostics, there is a growing trend of changing medicine from an episode-based practice to a service that provides consumers with tools that emphasize wellness. Genetic testing has been demonstrated to increase personal awareness of the potential for disease and to result in motivation to initiate healthy lifestyle changes. The results could also be used as a basis for pharmacogenetic studies in the future.