DESIGN OF A FAMILY STUDY AMONG HIGH-RISK CARIBBEAN HISPANICS: 
THE NORTHERN MANHATTAN FAMILY STUDY

Stroke continues to kill disproportionately more Blacks and Hispanics than Whites in the United States. Racial/ethnic variations in the incidence of stroke and prevalence of stroke risk factors are probably explained by both genetic and environmental influences. Family studies can help identify genetic predisposition to stroke and potential stroke precursors. Few studies have evaluated the heritability of these stroke risk factors among non-White populations, and none have focused on Caribbean Hispanic populations. The aim of the Northern Manhattan Family Study (NOMAFS) is to investigate the gene-environment interaction of stroke risk factors among Caribbean Hispanics. The unique recruitment and methodologic approaches used in this study are relevant to the design and conduct of genetic aggregation studies to investigate complex genetic disorders in non-White populations. The aim of this paper is to describe the NOMAFS and report enrollment and characteristics of the participants. The NOMAFS will provide a data resource for the exploration of the genetic determinants of highly heritable stroke precursor phenotypes that are less complex than the stroke phenotype. Understanding the gene environment interaction is the critical next step toward the development of new and unique approaches to disease prevention and interventions. (Ehn Dis. 2007;17:351–357)

Key Words: Stroke, Hispanic, Genetics

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BACKGROUND

Stroke continues to kill disproportionately more Blacks and Hispanics than Whites in the United States.1–4 Racial/ethnic variations in the incidence of stroke and prevalence of stroke risk factors are probably explained by both genetic and environmental influences. Some variation in well-known and highly heritable risk factors for stroke, including hypertension, diabetes, and lipids, can be explained by lifestyle factors, such as diet or lack of physical activity. Family studies can help identify genetic predisposition to stroke and stroke precursors.

Given the extreme complexity of genetic and non-genetic contributions to stroke, the evaluation of risk factors (ie, intermediate phenotypes for stroke) may reduce complexity and facilitate gene discovery. Subclinical markers, such as carotid intima media thickness (IMT), carotid distensibility (CD), and left ventricular mass (LVM), are risk factors for stroke and vascular disease. These markers may be less complex than the stroke phenotype. Few studies have evaluated the heritability of stroke risk factors among non-White populations, and none have focused on Caribbean Hispanic populations, the second largest ethnic group in the northeastern United States.5–9 Caribbean Hispanics, including Cubans, Dominicans, and Puerto Ricans, account for 15% of the 35 million US Hispanics and are the fastest growing ethnic group in the northeastern United States.10–11

The main goals of Northern Manhattan Family Study (NOMAFS) are to evaluate high-risk Caribbean Hispanic families to: 1) systematically measure stroke precursor phenotypes; 2) determine heritability of these phenotypes; 3) collect DNA in families for preliminary genome-wide linkage analysis; and 4) identify new quantitative trait loci linked to these phenotypes. The unique recruitment and methodologic approaches are relevant to the design and conduct of genetic aggregation studies to investigate complex genetic disorders in non-White populations. The aim of this manuscript is to describe NOMAFS and to report enrollment and characteristics of the participants.

METHODS

Enrollment of the Caribbean Family Cohort

The Northern Manhattan Family Study (NOMAFS) cohort was derived from the 1727 Caribbean Hispanic probands already enrolled in the multiethnic, community-based Northern Manhattan Study (NOMAS).12 The Northern Manhattan Study (NOMAS) was assembled between 1993 and 2001 from a population-based random sample by using random digit dialing methods. At baseline, the cohort was characterized as: 1) White, Black, or