

ARIC Manuscript Proposal #1812

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1.a. Full Title: Biomarkers of atrial fibrosis and risk of incident atrial fibrillation: the Atherosclerosis Risk in Communities Study (ARIC)

b. Abbreviated Title (Length 26 characters): Fibrosis and atrial fibrillation

2. Writing Group:

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I, the first author, confirm that all the coauthors have given their approval for this manuscript proposal. RH [**please confirm with your initials electronically or in writing**]

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3. Timeline:

Data analysis – 3 months

First draft of the manuscript – 3 months

4. Rationale:

Atrial fibrillation (AF) is a tachyarrhythmia characterized by uncoordinated atrial activation with consequent deterioration of atrial mechanical function. It is one of the most frequently sustained cardiac arrhythmias seen in clinical practice, affecting an estimated 2.2 million Americans [1]. Individuals with AF have between two to seven times the risk of stroke compared with unaffected individuals; moreover, AF doubles the rate of cardiovascular disease mortality and all-cause mortality [2,3]. AF is usually initiated by ectopic electrical activity, frequently originating in the pulmonary veins. In addition to this, AF requires the presence of an appropriate substrate, both structural and electrical, to persist. Structural abnormalities and factors such as atrial stretch and autonomic dysfunction are potentially involved in the development of ectopic cardiac activity that can trigger the onset of AF. If the substrate is adequate, the initial electrophysiological alterations will lead to the development and perpetuation of AF [4,5].

Although clinical studies have indicated a potential link between fibrosis and AF, they are limited by their cross-sectional design [4,5]. There are currently no prospective data on the relationship between atrial fibrosis and risk of subsequent AF. Fibrosis markers, such as the matrix metalloproteinases (MMP), are of particular interest since atrial fibrosis has been identified as a fundamental substrate for the development of AF. In addition, heart failure, a major cause of AF, leads to atrial fibrosis, which, in turn, increases the risk of AF.

The ARIC study provides an excellent setting for a prospective study of the association between markers of atrial fibrosis and incident AF in both whites and African-Americans. Further, information on a large number of socio-demographic, physiological, and biochemical risk factors will enable adjustment for known and unknown confounders allowing a more accurate estimate of the association to be determined.

5. Main Hypothesis/Study Questions:

We hypothesize that markers of atrial fibrosis, namely MMP-1, MMP-2, MMP-9, tissue inhibitor of metalloproteinase (TIMP)-1, TIMP-2 and C-terminal propeptide of collagen type 1 (CICP), will be independently associated with risk of incident AF.

6. Design and analysis (study design, inclusion/exclusion, outcome and other variables of interest with specific reference to the time of their collection, summary of data analysis, and any anticipated methodologic limitations or challenges if present).

We will assess the association between markers of fibrosis and AF risk using a case-cohort design. The aforementioned biomarkers have been measured in 630 incident AF cases and a random sample of 630 cohort participants in serum samples from visit 2. Cases will be defined as individuals who developed incident AF during the follow-up through the end of 2005. The subcohort was randomly selected from eligible individuals at visit 2, and frequency matched by age (<55, >=55), sex, and race.

Exclusions

The following individuals will be excluded from all analyses:

- Those with missing or unreadable ECGs at visit 1 or 2
- Those with prevalent AF at visit 2 (defined as AF by ECG in visit 1 or 2, or AF hospitalization between visits 1 and 2)
- Those with missing variables for any of the covariates

Sensitivity analyses

- Given that HF is a major cause of fibrosis, and that in turn, fibrosis is postulated to increase the risk of AF [5], we will repeat the analyses in those with and without prevalent HF.

Statistical analysis

We will follow appropriate methodology for the analysis of case-cohort studies [6]. In brief, we will define risk sets (study participants at risk of the outcome) at each time point, such that the cases outside the sub-cohort are excluded from the risk set before failure; cases outside the sub-cohort are included in the risk set at failure; cases inside the sub-cohort are included in the risk set at failure; cases in the sub-cohort before failure as well as non-cases in the sub-cohort are included in the risk set with a weight equal to the inverse of the sampling frequency. The sampling frequency is the proportion of people in the sub-cohort relative to the full cohort. All sub-cohort individuals are assumed to enter the study at visit 2 (baseline for this analysis). Cases not in the sub-cohort begin contributing event time just prior to their failure time. All individuals (in the sub-cohort or non-sub-cohort cases) complete their follow up time at the event time or when censored.

For each biomarker, we will estimate Cox models adjusting for age, sex, race and study center to study the nature of the association between the biomarker and AF risk. Then, we will add other covariates potentially associated with the risk of AF and with markers of fibrosis (education, physical activity, smoking, BMI, systolic/diastolic BP, BP medications, diabetes, prevalence of coronary heart disease, prevalence of heart failure, left ventricular hypertrophy) and other biomarkers (C-reactive protein and NT-proBNP), also measured in these participants in visit 2 samples.

We will initially explore the dose-response relationship between each exposure-outcome pair using restricted cubic splines. The spline terms will allow us to examine the functional shape of the dose response curve and, potentially determine appropriate categorizations of the biomarkers. Depending on the shape of the biomarker outcome association, we will include the biomarker in the regression models as a continuous variable (after a log transformation if appropriate) if a linear association is found, or we will create quintiles according to the distribution of the biomarker. Finally, we will

