The Relationship Of Trends In ARIC Community Coronary Heart Disease Surveillance To Changes In Risk Factors Distributions Based On The ARIC Cohort

b. Abbreviated Title (Length 26 characters): CHD Risk Factors and Surveillance

2. Writing Group (list individual with lead responsibility first): Nina Paynter, Josef Coresh, A. Richey Sharrett, Thomas Louis, Wayne Rosamond, Aaron Folsom (others welcome)

Lead: Nina Paynter
Address: 2024 E. Monument St.
        Suite 2-600
        Baltimore, MD 21205
        Phone: 410-502-6705   Fax: 410-955-0476
        E-mail: npaynter@jhsph.edu

Corresponding/senior author (if different from first author correspondence will be sent to both the first author & the corresponding author): Josef Coresh
Address: 2024 E. Monument St.
        Suite 2-600
        Baltimore, MD 21205
        Phone: 410-955-0495   Fax: 410-955-0476
        E-mail: coresh@jhu.edu

3. Timeline: begin analysis upon approval, circulate draft in August 2005, complete by March 2006

4. Rationale:

Coronary heart disease (CHD) disease remains the leading cause of death in the United States. While the relationships between CHD mortality and morbidity and the individual risk factors of blood pressure, total and HDL cholesterol, smoking and diabetes have been well established in cohort studies, estimating the extent to which individual risk factors explain community CHD rates has been difficult. Explaining differences in CHD rates across communities and changes in CHD rates over time within communities is an important public health goal and underlies many public health initiatives, including Healthy People 2010. A greater understanding of the effects of risk factor levels in the community can help assess the extent to which monitoring and controlling risk factor
levels in the community might affect future CHD incidence in the United States. Finally, the development of methods for relating cohort data to surveillance outcomes could be useful for risk factor monitoring for other outcomes.

5. Main Hypothesis/Study Questions:
1) Are CHD event rate differences across the four ARIC geographical areas explained by differences in established CHD risk factors (smoking, blood pressure, diabetes, and lipids)?
2) Are trends in CHD event rates within each of the ARIC geographical areas explained by trends in CHD risk factors over time?
3) If event rate differences across geographical areas and calendar time are not fully explained by this set of CHD risk factors, what are some alternative scenarios which would account for the observed pattern of differences?

6. Data (variables, time window, source, inclusions/exclusions):

Both the surveillance and the cohort data will be used for this analysis, along with census data. The community surveillance study population includes, at any given time, all of the individuals aged 35 to 74 living in the four defined geographic areas. The data framework of this project relies on the concept of the community cohort, the portion of the community surveillance study population which is restricted to the age range of the ARIC cohorts which were examined and followed. The ARIC examined cohorts comprise a subset of and have the same age range as the community cohort at any given time. This allows us to generalize the risk factor profile of the examined cohorts to the community cohort only, rather than the entire community surveillance study population.

The overall structure of the main analysis is as follows. The cohort data will be used to generate the relationship between the outcome of incident CHD events and the risk factors and to summarize that relationship over each demographic group, generating a probability of an outcome given their age, gender and race, which takes into account the distribution of risk factors within each demographic group. The census will provide the demographic distribution in the community cohort. Combining these census demographics with the cohort risk factor-CHD relationships will give us the predicted events in the community cohort. The resulting predicted CHD incidence rates can then be compared to the events observed from the surveillance data, and this process can be repeated for different time periods to look at trends. In order to address the third question of exploring what scenarios would generate our observed results, we will simulate a variety of options including: an unmeasured community factor, the healthy participant effect, and selective migration. This will allow us to quantify the magnitude of each of these effects needed to generate the observed results. We can also identify relative differences between predicted and observed event rates across demographic and geographic groups and time to explore where the greatest discrepancies lie. We will also look at time lagged effects. Preliminary statistical analysis will be done using R.

Cohort:
Exposures: smoking, blood pressure, hypertensive and lipid medication use, diabetes and lipids (total and HDL cholesterol)
Outcome: Incident CHD events (hospitalized MI and CHD death)
Covariates: age, race, gender, center
Analysis: Generation of model for each time period to predict CHD event rates in the community cohort using a CHD risk equation which includes age, gender, race, blood pressure, diabetes, cigarette smoking, and lipid levels.

Surveillance:
Outcomes: Incident CHD events
Covariates: age, race, gender
Analysis: comparison with projected CHD event rates for community cohort.

7.a. Will the data be used for non-CVD analysis in this manuscript? **Yes**

b. If Yes, is the author aware that the file ICTDER02 must be used to exclude persons with a value RES_OTH = “CVD Research” for non-DNA analysis, and for DNA analysis RES_DNA = “CVD Research” would be used? **Yes**

(This file ICTDER02 has been distributed to ARIC PIs, and contains the responses to consent updates related to stored sample use for research.)

8.a. Will the DNA data be used in this manuscript? **Yes**

8.b. If yes, is the author aware that either DNA data distributed by the Coordinating Center must be used, or the file ICTDER02 must be used to exclude those with value RES_DNA = “No use/storage DNA”? **Yes**

9. The lead author of this manuscript proposal has reviewed the list of existing ARIC Study manuscript proposals and has found no overlap between this proposal and previously approved manuscript proposals either published or still in active status. ARIC Investigators have access to the publications lists under the Study Members Area of the web site at: http://bios.unc.edu/units/csc/ARIC/stdy/studymem.html

**Yes**

10. What are the most related manuscript proposals in ARIC (authors are encouraged to contact lead authors of these proposals for comments on the new proposal or collaboration)?
None Found

11.a. Is this manuscript proposal associated with any ARIC ancillary studies or use any ancillary study data? **Yes**

11.b. If yes, is the proposal
A. primarily the result of an ancillary study (list number* __________)

B. primarily based on ARIC data with ancillary data playing a minor role (usually control variables; list number(s)* __________ __________ __________)

*ancillary studies are listed by number at [http://www.cscc.unc.edu/aric/forms/](http://www.cscc.unc.edu/aric/forms/)

12. Manuscript preparation is expected to be completed in one to three years. If a manuscript is not submitted for ARIC review at the end of the 3-years from the date of the approval, the manuscript proposal will expire.