ARIC Manuscript Proposal # 3145

PC Reviewed: 4/10/18	**Status: _____**	**Priority: 2**
SC Reviewed: _____	**Status: _____**	**Priority: ____**

1.a. Full Title: Serum Metabolomic Markers of Diet Quality

b. Abbreviated Title (Length 26 characters): Metabolomics of diet quality

2. Writing Group:
Writing group members:

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

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3. Timeline: Analyses will begin after the manuscript proposal is approved. We anticipate that a first draft of the manuscript will be available within approximately one year of manuscript proposal approval.

4. Rationale:
Diet is an important modifiable risk factor for cardiovascular disease and other chronic diseases.[1,2] The American Heart Association and the U.S. Dietary Guidelines for Americans have endorsed the DASH diet and a prudent diet for the prevention of cardiovascular disease and

related health outcomes.[3-5] Further research is necessary to examine the metabolic disturbances associated with these purported healthy dietary patterns.

Metabolomics allows for the comprehensive characterization of small metabolic compounds in biological specimens (serum).[6] The metabolome is responsive to dietary intake and therefore is a useful method for detecting biomarkers of dietary patterns and metabolic pathways that are potentially modifiable by diet.[7] The untargeted and unbiased metabolomic approach maximizes the potential for discovery of novel markers of dietary intake and could provide insights about metabolic pathways underlying the diet-disease relationship.

5. Main Hypothesis/Study Questions:
We hypothesize that we will be able to identify known and novel metabolites associated with overall measures of diet quality and components of diet quality scores. We hypothesize that there will be metabolites that are similarly associated with diet quality across the three diet quality indices (HEI-2015, AHEI, DASH).

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).

Study Design: cross-sectional analysis of metabolomics and measures of diet quality, which both were assessed at study visit 1 (1987-1989)

Eligibility Criteria: Approximately 4,000 African-American and Caucasian ARIC study participants with metabolomic profiling data from visit 1 serum specimens (ancillary study #2014.20 and 2008.16; two "batches")

Exposures: The exposures are three measures of diet quality: 1) Healthy Eating Index-2015, 2) Alternative Healthy Eating Index, and 3) DASH Diet. The Healthy Eating Index-2015 assesses adherence to the 2015-2020 U.S. Dietary Guidelines for Americans. The HEI-2015 score ranges from 0 to 100 based on twelve factors: total fruit, whole fruit, total vegetables, greens and beans, whole grains, dairy, total protein foods, seafood and plant proteins, refined grains, added sugars, fatty acids, sodium, and saturated fat.[1] The Alternative Healthy Eating Index scores 11 foods and nutrients that have been shown to be related to chronic disease risk and has a total score of 110: vegetables, fruit, whole grains, sugar-sweetened beverages and fruit juice, nuts and legumes, red/processed meat, trans fat, long-chain fats, polyunsaturated fatty acids, sodium, and alcohol.[8] The Dietary Approaches to Stop Hypertension (DASH) was tested in two feeding trials and was shown to reduce blood pressure.[9,10] The DASH diet score captures 8 components: fruits, vegetables, nuts and legumes, low-fat dairy, whole grains, sodium, sweetened beverages, and red and processed meats.[11] Dietary intake was assessed at study visit using an interview-administered, in-person, 66-item, semi-quantitative, food frequency questionnaire 1, which was modified from an instrument developed by Willett et al.[12]

[1] https://epi.grants.cancer.gov/hei/hei-2015-table1.html

Outcomes: Metabolites were measured from stored fasting serum samples by Metabolon, Inc. (Durham, North Carolina) using an untargeted, ultra-performance liquid chromatography tandem mass spectrometry approach. This untargeted approach identified approximately 600-800 named and unnamed metabolites. In the present study, we will primarily focus on the ~200 named metabolites with limited missing values, reasonable reliability, and present in both batches.

Other Variables of Interest: In multivariable linear regression models, we will consider adjusting for the following variables: age, sex, race, center, body mass index, total energy intake, estimated glomerular filtration rate (eGFR), and batch (batch represents when the metabolomic profiling was conducted).

Statistical Analysis: We will use multivariable linear regression models to estimate the cross-sectional association between diet quality (exposure) and metabolites (outcome). Diet quality will be quantified using *a priori* defined scores for the HEI-2015, the AHEI, and the DASH diet. In addition to the overall diet quality scores, we will assess the association between metabolites and individual components of the diet quality scores. Effect estimates will be calculated per one unit increase in the diet quality score. Metabolites will be log-transformed for analysis. We will adjust for the following covariates in the multivariable regression model: age, sex, race, center, body mass index, total energy intake, eGFR, and batch. We will examine potential effect modification using statistical tests for interaction and by stratifying by sex, race, age group, BMI group, and kidney function. Analyses will be conducted by batch (1st batch: discovery, 2nd batch: replication). All analyses will be run in Houston, Texas using scripts provided by the first author.

Anticipated Methodologic Limitations or Challenges: Given the large number of metabolites, there is a high likelihood of detecting a false positive association. We will adjust the significance threshold by the Bonferroni method (dividing by the number of metabolites) to account for multiple comparisons (0.05/number of metabolites).[13]

7.a. Will the data be used for non-CVD analysis in this manuscript? ____ Yes __X__ No

b. If Yes, is the author aware that the file ICTDER03 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 ____ No
(This file ICTDER 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 __X__ No

8.b. If yes, is the author aware that either DNA data distributed by the Coordinating Center must be used, or the file ICTDER03 must be used to exclude those with value RES_DNA = "No use/storage DNA"? ____ Yes ____ No

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://www.cscc.unc.edu/ARIC/search.php

___X___ Yes _____ No

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)?

#2034: The human metabolome is associated with dietary intake among African Americans in the Atherosclerosis Risk in Communities Study (lead author: Yan Zheng)

The manuscript based on this proposal has already been published [Zheng Z, Yu B, Alexander D, Steffen LM, Boerwinkle E. Human metabolome associates with dietary intake habits among African Americans. Am J Epidemiol 2014;179(12):1424-1433.] It was focused on food groups and food items, whereas the present manuscript proposal is focused on dietary patterns. In addition, it included data on African Americans only, whereas the present manuscript proposal will include data on both African Americans and Caucasians.

11.a. Is this manuscript proposal associated with any ARIC ancillary studies or use any ancillary study data? __ X __ Yes __ __ No

11.b. If yes, is the proposal

_X__ A. primarily the result of an ancillary study

2014.20: Genomics, Metabolomics, and Cardiovascular Disease (PI: Eric Boerwinkle)

2008.16: Metabolomics & Heart Failure: A Novel Approach to Biomarker Discovery (PI: Jennifer Nettleton)

___ 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/

12a. 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.

12b. The NIH instituted a Public Access Policy in April, 2008 which ensures that the public has access to the published results of NIH funded research. It is **your responsibility to upload manuscripts to PubMed Central** whenever the journal does not and be in compliance with this policy. Four files about the public access policy from http://publicaccess.nih.gov/ are posted in http://www.cscc.unc.edu/aric/index.php, under Publications, Policies & Forms.

http://publicaccess.nih.gov/submit_process_journals.htm shows you which journals automatically upload articles to PubMed central.

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