Dietary Patterns

Dietary Patterns and Cardiovascular Disease Risk among Chinese Adults: A Prospective Cohort Study

Significance: This prospective look at cardiovascular disease in Chinese adults finds that a traditional dietary pattern and rice consumption is associated with reduced CVD risk, whereas a modern diet with wheat consumption is associated with increased CVD risk.

Background and Objective: We aimed to examine the prospective association between dietary patterns and cardiovascular disease (CVD) risk in Chinese adults. Methods: Adults aged ≥20 years in the China Health and Nutrition Survey (open cohort) were followed between 1991 and 2011. Participants may enter the cohort at any wave. Dietary intakes were obtained from a 3-day, 24-h recall combined with household weighing for oil and condiments. CVD was defined as having either myocardial infarction or stroke. Two sets of dietary patterns were derived using reduced rank regression and factor analysis. Iron-related dietary pattern (IDP) was generated using iron intake as a response variable. Multivariable Cox regression was used to analyse the relation between dietary patterns and CVD risk. Results: In total, 13,055 adults were followed for a median of 9 years. During 115,368 person years of follow-up, 502 participants developed CVD. Two dietary patterns were derived and labeled as traditional dietary pattern (high intake of rice, pork, fish, poultry, and fresh vegetable but low intake of wheat) and modern dietary pattern (high intake of fruit, soymilk, and fast food). Across the quartiles of intake, the hazard ratio (95% CI) for CVD were 1.0, 0.84 (0.64-1.0), 0.57 (0.42-0.77), and 0.58 (0.42-0.79) for traditional pattern (p for trend <0.001) and 1.0, 1.56 (1.16-2.09), 1.56 (1.13-2.14), and 1.68 (1.16-2.44) (p for trend = 0.118) for modern pattern. IDP was characterised by high intake of fresh vegetable, wheat, legume, beverage, offal, rice, and whole grain. IDP intake was not associated CVD. Comparing extreme quartiles, high rice intake was associated with halved while wheat intake was associated with a doubled risk of CVD. Conclusions: Traditional dietary pattern and rice intake are inversely but modern dietary pattern and wheat is directly associated with CVD risk. IDP is not related to CVD in Chinese adults.

Protein

Adjusting for Protein Quality by Food Source May Affect Nutrient Density Metrics

Significance: Quantitative approaches that use protein content to reflect nutrient density may require a protein-quality adjustment.

Methods to assess nutrient density of foods, commonly known as nutrient profiling (NP), typically include protein as a component. In this study, the goal was to apply a correction for protein quality by food source to selected NP algorithms. Analyses of 378 component foods of the Fred Hutch food frequency questionnaire showed that animal-source foods (ie, meat, eggs, and dairy) along with some soy products and nuts were the only foods that provided > 20% of the daily value (DV) of protein per 100 g or per 100 kcal. Most beans, pulses, legumes, grains, and vegetables provided <10% DV of protein per 100 g or per 100 kcal. Adjusting for protein quality using a simplified Protein Digestibility Corrected Amino Acid Score (PDCAAS) had consequences for point-based NP models (namely, Nutri-Score) and for continuous nutrient density scores (namely, Nutrient Rich Foods). Quantitative methods that use protein content to capture nutrient density may require a protein-quality adjustment, especially when adapted for use in low- and middle-income countries where protein quality is an issue of public health concern.
Lipids

A Lipid-Related Metabolomic Pattern of Diet Quality


Significance: Researchers uncovered metabolites associated with both healthy and unhealthy diets, allowing for an objective measure complementary to diet questionnaires.

Background: Adherence to a healthy diet has been associated with reduced risk of chronic diseases. Identifying nutritional biomarkers of diet quality may be complementary to traditional questionnaire-based methods and may provide insights concerning disease mechanisms and prevention. Objective: To identify metabolites associated with diet quality assessed via the Alternate Healthy Eating Index (AHEI) and its components. Methods: This cross-sectional study used FFQ data and plasma metabolomic profiles, mostly lipid related, from the Nurses’ Health Study (NHS, n = 1460) and Health Professionals Follow-up Study (HPFS, n = 1051). Linear regression models assessed associations of the AHEI and its components with individual metabolites. Canonical correspondence analyses (CCAs) investigated overlapping patterns between AHEI components and metabolites. Principal component analysis (PCA) and explanatory factor analysis were used to consolidate correlated metabolites into uncorrelated factors. We used stepwise multivariable regression to create a metabolomic score that is an indicator of diet quality. Results: The AHEI was associated with 83 metabolites in the NHS and 96 metabolites in the HPFS after false discovery rate adjustment. Sixty-three of these significant metabolites overlapped between the 2 cohorts. CCA identified “healthy” AHEI components (e.g., nuts, whole grains) and metabolites (n = 27 in the NHS and 33 in the HPFS) and “unhealthy” AHEI components (e.g., red meat, trans fat) and metabolites (n = 56 in the NHS and 63 in the HPFS). PCA-derived factors composed of highly saturated triglycerides, plasmalogens, and acylcarnitines were associated with unhealthy AHEI components while factors composed of highly unsaturated triglycerides were linked to healthy AHEI components. The stepwise regression analysis contributed to a metabolomics score as a predictor of diet quality. Conclusion: We identified metabolites associated with healthy and unhealthy eating behaviors. The observed associations were largely similar between men and women, suggesting that metabolomics can be a complementary approach to self-reported diet in studies of diet and chronic disease.

Carbohydrates

Exploring Changes in the Human Gut Microbiota and Microbial-Derived Metabolites in Response to Diets Enriched in Simple, Refined, or Unrefined Carbohydrate-Containing Foods: A Post Hoc Analysis of a Randomized Clinical Trial


Significance: Simple carbohydrate– and refined carbohydrate–rich diets have different effects on the gut microbiome, suggesting separate mechanisms mediate their effects on cardiometabolic health.

Background: Dietary carbohydrate type may influence cardiometabolic risk through alterations in the gut microbiome and microbial-derived metabolites, but evidence is limited. Objectives: We explored the relative effects of an isocaloric exchange of dietary simple, refined, and unrefined carbohydrate on gut microbiota composition/function, and selected microbial metabolite concentrations. Methods: Participants [n = 11; age: 65 ± 8 y; BMI (in kg/m²): 29.8 ± 3.2] were provided with each of 3 diets for 4.5 wk with 2-wk washout, according to a randomized, crossover design. Diets [60% of energy (%E) carbohydrate, 15%E protein, and 25%E fat] differed in type of carbohydrate. Fecal microbial composition, metatranscriptomics, and microbial-derived SCFA and secondary bile acid (SBA) concentrations were assessed at the end of each phase and associated with cardiometabolic risk factors (CMRFs). Results: Roseburia abundance was higher (11% compared with 5%) and fecal SBA concentrations were lower (lithocolic acid –50% and deoxycholic acid –64%) after consumption of the unrefined carbohydrate diet relative to the simple carbohydrate diet (false discovery rate (FDR): all P < 0.05), whereas Anaerostipes abundance was higher (0.35% compared with 0.12%; FDR: P = 0.04) after the simple carbohydrate diet relative to the refined carbohydrate diet. Metatranscriptomics indicated upregulation of 2 cellular stress genes (FDR: P < 0.1) after the unrefined carbohydrate diet compared with the simple carbohydrate or refined carbohydrate diets. The microbial expression of 3 cellular/oxidative stress and immune response genes was higher (FDR: P < 0.1) after the simple carbohydrate diet relative to the refined carbohydrate diet. No significant diet effect was observed in fecal SCFA concentrations. Independent of diet, we observed 16 associations (all FDR: P < 0.1) of taxon abundance (15 phylum and 1 genera) with serum inflammatory markers and also with fecal SCFA and SBA concentrations. Conclusions: Consuming an unrefined carbohydrate–rich diet had a modest effect on the gut microbiome and SBAs, resulting in favorable associations with selected CMRFs. Simple carbohydrate– and refined carbohydrate–rich diets have distinctive effects on the gut microbiome, suggesting differential mechanisms mediate their effects on cardiometabolic health.
**Low-Calorie Sweeteners**

**Perspective: Measuring Sweetness in Foods, Beverages, and Diets: Toward Understanding the Role of Sweetness in Health**


**Significance:** This article proposes a future direction for improving methods for measuring sweetness in the diet to support evidence-based dietary recommendations.

This work was supported by ILSI North America Low-Calorie Sweeteners Committee.

Various global public health agencies recommend minimizing exposure to sweet-tasting foods or beverages. The underlying rationale is that reducing exposure to the perception of sweet tastes, without regard to the source of sweetness, may reduce preferences for sweetness, added sugar intake, caloric intake, and body weight. However, the veracity of this sequence of outcomes has yet to be documented, as revealed by findings from recent systematic reviews on the topic. Efforts to examine and document the effects of sweetness exposure are needed to support evidence-based recommendations. They require a generally agreed-upon methodology for measuring sweetness in foods, beverages, and the overall diet. Although well-established sensory evaluation techniques exist for individual foods in laboratory settings, they are expensive and time-consuming, and agreement on the optimal approach for measuring the sweetness of the total diet is lacking. If such a measure could be developed, it would permit researchers to combine data from different studies and populations and facilitate the design and conduct of new studies to address unresolved research questions about dietary sweetness. This narrative review includes an overview of available sensory techniques, their strengths and limitations, recent efforts to measure the sweetness of foods and diets across countries and cultures, and a proposed future direction for improving methods for measuring sweetness toward developing the data required to support evidence-based recommendations around dietary sweetness.

**Bioactives**

**Neuroprotective Effects of Coffee Bioactive Compounds: A Review**


**Significance:** This review highlights potential molecular mechanism(s) by which coffee bioactive components may provide neuroprotection.

Coffee is one of the most widely consumed beverages worldwide. It is usually identified as a stimulant because of a high content of caffeine. However, caffeine is not the only coffee bioactive component. The coffee beverage is in fact a mixture of a number of bioactive compounds such as polyphenols, especially chlorogenic acids (in green beans) and caffeic acid (in roasted coffee beans), alkaloids (caffeine and trigonelline), and the diterpenes (cafestol and kahweol). Extensive research shows that coffee consumption appears to have beneficial effects on human health. Regular coffee intake may protect from many chronic disorders, including cardiovascular disease, type 2 diabetes, obesity, and some types of cancer. Importantly, coffee consumption seems to be also correlated with a decreased risk of developing some neurodegenerative conditions such as Alzheimer’s disease, Parkinson’s disease, and dementia. Regular coffee intake may also reduce the risk of stroke. The mechanism underlying these effects is, however, still poorly understood. This review summarizes the current knowledge on the neuroprotective potential of the main bioactive coffee components, i.e., caffeine, chlorogenic acid, caffeic acid, trigonelline, kahweol, and cafestol. Data from both in vitro and in vivo preclinical experiments, including their potential therapeutic applications, are reviewed and discussed. Epidemiological studies and clinical reports on this matter are also described. Moreover, potential molecular mechanism(s) by which coffee bioactive components may provide neuroprotection are reviewed.

**Sodium**

**Associations of Sodium and Potassium Consumption with the Gut Microbiota and Host Metabolites in a Population-Based Study in Chinese Adults**


**Significance:** Sodium and potassium consumption is associated with gut microbiome taxa and metabolites implicated in cardiometabolic health, providing insights into the potential roles of gut microbiota and host metabolites in related diseases.
**Gut Microbiome**

**Gut Microbiome Responses to Dietary Intake of Grain-Based Fibers with the Potential to Modulate Markers of Metabolic Disease: A Systematic Literature Review**


**Significance:** A review of cereal fiber studies indicate cereal fibers may modulate the gut microbiome. However, evidence of the link between this and metabolic outcomes is limited.

**Context:** Cereal fiber modulates the gut microbiome and benefits metabolic health. The potential link between these effects is of interest. **Objective:** The aim for this systematic review was to assess evidence surrounding the influence of cereal fiber intake on microbiome composition, microbiome diversity, short-chain fatty acid production, and risk factors for metabolic syndrome. **Data Sources and Extraction:** The MEDLINE, PubMed, CINAHL, and Cochrane Library databases were searched systematically, and quality of studies was assessed using the Cochrane Risk of Bias 2.0 tool. Evidence relating to study design, dietary data collection, and outcomes was qualitatively synthesized on the basis of fiber type. **Data Analysis:** Forty-six primary publications and 2 secondary analyses were included. Cereal fiber modulated the microbiome in most studies; however, taxonomic changes indicated high heterogeneity. Short-chain fatty acid production, microbiome diversity, and metabolic-related outcomes varied and did not always occur in parallel with microbiome changes. Poor dietary data were a further limitation. **Conclusions:** Cereal fiber may modulate the gut microbiome; however, evidence of the link between this and metabolic outcomes is limited. Additional research is required with a focus on robust and consistent methodology.

**Should There Be a Recommended Daily Intake of Microbes?**


**Significance:** To test the hypothesis that the inclusion of safe, live microbes in the human diet supports and improves health, the researchers propose assessment of the types and evidentiary quality of the data available on microbe intake.

The collective findings from human microbiome research, randomized controlled trials on specific microbes (i.e., probiotics), and associative studies of fermented dairy consumption provide evidence for the beneficial effects of the regular consumption of safe live microbes. To test the hypothesis that the inclusion of safe, live microbes in the diet supports and improves health, we propose assessment of the types and evidentiary quality of the data available on microbe intake, including the assembly and evaluation of evidence available from dietary databases. Such an analysis would help to identify gaps in the evidence needed to test this hypothesis, which can then be used to formulate and direct initiatives focused on prospective and randomized controlled trials on live microbe consumption. Outcomes will establish whether or not the evidence exists, or can be generated, to support the establishment of dietary recommendations for live microbes.