Nutrition Science

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USDA Global Branded Food Products Database

Update on "A Partnership for Public Health: USDA Global Branded Food Products Database"

Brienna Larrick, Alison Kretser, Kyle McKillop. *Journal of Food Compos. & Analysis*. Volume 105, 1 November 2021, 104250. doi.org/10.1016/j.jfca.2021.104250. **Article link**

Signi icance: "A Partnership for Public Health: USDA Global Branded Food Products Database" is a public-private partnership between the US Department of Agriculture, the Institute for the Advancement of Food and Nutrition Sciences (IAFNS), GS1 US, 1WorldSync, NielsenIQ Label Insight, and the University of Maryland. This paper describes recent database enhancements and current Partnership initiatives.

IAFNS is a partner in this public-private partnership. The partnership is financially supported by USDA.

"A Partnership for Public Health: USDA Global Branded Food Products Database" is a public-private partnership between the US Department of Agriculture, the Institute for the Advancement of Food and Nutrition Sciences, GS1 US, 1WorldSync, Label Insight, and the University of Maryland. The goal of the Partnership is to improve public health and the sharing of open data by expanding and enhancing the USDA National Nutrient Database — now known as USDA FoodData Central — with nutrient composition and ingredient information on branded and private label foods to better reflect the food supply. Since its launch in 2016, the Partnership has made several enhancements to the USDA Global Branded Food Products Database, including improved database search functionality and new data attributes. The Partnership is currently working to expand the Database to international markets, fill identified data gaps, and enable federal interagency collaboration.

Protein

Evaluation of Protein Quality in Humans and Insights on Stable Isotope Approaches to Measure Digestibility – A Review

Sulagna Bandyopadhyay; Sindhu Kashyap; Juliane Calvez ; Sarita Devi; Dalila Azzout-Marniche. *Advances in Nutrition*, nmab134, doi.org/10.1093/advances/nmab134. 10 November 2021. **Article link**

Significance: This critical review evaluated the advantages and limitations of various isotope methods used for measuring protein quality in humans. To support future protein content label claims, further re-evaluation, and harmonization of findings from the different methods and protein sources will be necessary.

Recent Food and Agricultural Organization/World Health Organization/United Nations University expert consultations on protein requirements and quality have emphasized the need for the new Digestible Indispensable Amino Acid Score (DIAAS), as a measure of protein quality. This requires human measurements of the true ileal digestibility of individual indispensable amino acids (IAA) until the end of the small intestine. Digestibility is measured using standard oro-ileal balance methods, which can only be achieved by an invasive naso-ileal intubation in healthy participants or fistulation at the terminal ileum. Significant efforts have been made in last two decades to develop non-invasive or minimally invasive methods to measure IAA digestibility in humans. The application of intrinsically labeled (with stable isotopes like 13C, 15N and 2H) dietary proteins have helped in circumventing the invasive oro-ileal balance techniques and allowed for the differentiation between endo and exogenous protein digestibility. The non-invasive indicator amino acid oxidation (IAAO) technique, which is routinely employed to measure IAA requirements, has been modified to estimate metabolic availability (a sum of digestibility and utilization) of IAA in foods, but provide estimate for a single IAA at a time and burdensome for

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participants. The recently developed minimally invasive dual isotope tracer method measures small intestinal digestibility of multiple amino acids at once and is suitable for use in vulnerable groups and disease conditions. However, it remains to be validated against standard oro-ileal balance techniques. This review critically evaluates and compares the currently available stable isotope-based protein quality evaluation methods with a focus on the digestibility and metabolic availability measurements in humans. In the view of building reliable DIAAS database of various protein sources and subsequently supporting protein content claims in food labeling, a re-evaluation and harmonization of the available methods are necessary.

Carbohydrates

Effect of Dietary Carbohydrate and Lipid Modification on Clinical and Anthropometric Parameters in Nonalcoholic Fatty Liver Disease: A Systematic Review and Meta-Analysis

Lais S Garcêz, Camila R Avelar, Nedja S S Fonseca, Priscila R F Costa, André C Lyra, Carla M Cunha, Rosangela P Jesus, Lucivalda P M Oliveira. *Nutrition Reviews*, Vol. 79, Issue 12, November 2021, p1321–1337, doi.org/10.1093/nutrit/nuaa146. **Article link**

Significance: Many observed effects of nonalcoholic fatty liver disease are associated with low dietary caloric content.

Nonalcoholic fatty liver disease (NAFLD) is estimated to affect approximately 25% of the adult population, making it one of the most common chronic liver diseases worldwide and a major public health problem. Still, there is no consensus on the most appropriate nutritional intervention for disease treatment. Objective: To systematize and synthesize the results of randomized controlled trials that have evaluated the effect of dietary interventions with different, quantitative, macronutrient compositions on hepatic steatosis attenuation, serum levels of alanine aminotransferase, aspartate aminotransferase, lipid profile, glucose metabolism markers, and anthropometric parameters of adults and the elderly (age ≥ 60 years) with NAFLD. Data Sources: MEDLINE databases via PubMed, Embase, Science Direct, LILACS, Web of Science, ClinicalTrials.gov, and Cochrane Library were searched. Randomized controlled trials that compared interventions as diets with values ≤ 45% or 20% of the total daily energy intake from carbohydrates or lipids, respectively, compared with dietary reference intakes, were included. Data Extraction: Risk of bias was assessed through the Cochrane Collaboration tool. The meta-analysis was only performed to evaluate the effect of carbohydrate-modified diets on the outcome variables. The number of participants and mean values and respective standard deviations of the outcome variables were extracted and used to calculate weighted mean differences and their respective 95%CIs. Results: The search strategy resulted in 21146 studies, of which 10 were retained for qualitative analysis and 6 were included in the meta-analysis. From the analysis of 10 studies were identified 8 articles in which low-calorie diets were evaluated and 3 interventions that used an isocaloric diet. Only 3 studies were classified as having low risk of bias. Conclusion: The observed effects on hepatic steatosis, serum alanine aminotransferase and aspartate aminotransferase levels, parameters of lipid and glucose metabolism, and anthropometric variables were mostly related to a hypocaloric diet. The use of reduced macronutrient interventions had no efficacy.

Low and No-Calorie Sweeteners

Low- and No-Calorie Sweetener (LNCS) Presence and Consumption among the Portuguese Adult Population

María González-Rodríguez, Marina Redruello-Requejo, María de Lourdes Samaniego-Vaesken, Ana Montero-Bravo, Ana M. Puga, Teresa Partearroyo, et. al. *Nutrients*. 2021 Nov; 13(11): 4186. 2021 Nov 22. doi: 10.3390/nu13114186. **Article link**

Significance: A wide variety of foods and beverage in the Portuguese food supply contain LNCS. More information on the impacts of LNCS on health is needed, as well as the inclusion of these ingredients in food composition data bases with periodic updates to reflect changes in product formulations.

Background: The use of low and no-calorie sweeteners (LNCS) in food and beverages has become increasingly common in the development and reformulation of products to reduce energy derived from added sugars. Our aim was to identify the presence and consumption of LNCS through food and beverages according to consumption patterns in a representative sample (n = 256) of the Portuguese adult population. The study had a descriptive cross-sectional observational design and was based on the application of a Food Frequency Questionnaire. Overall, it was found that 4.1% of the foods and 16.7% of the beverages consumed by the Portuguese adult population contained LNCS. Food groups mostly contributing to LNCS consumption were non-alcoholic beverages such as soft drinks and juices (34.2%); milk and dairy products (16.5%); appetizers such as chips (8.6%); sugars and sweets such as chocolates, candies, or chewing gums (6.1%); meat and derivative products (2.2%); cereals and derivatives (1.2%) and canned fruits (1.2%). Main LNCS consumed were acesulfame-K, sucralose, and aspartame, single or combined, although their prevalence of use differs greatly among foods, beverages, or

tabletop sweeteners. In conclusion, LNCS were found across a wide variety of products available in the Portuguese market and their prevalence of inclusion in the diet of the population evidences the need to develop more studies on the evolution of LNCS intake and its impact on the full dietary model and health. Consequently, these food additives should be included in food composition databases and, periodically, updated to reflect the recurrent reformulation strategies adopted by the food industry in its efforts to reduce the energy contribution of added sugars.

Cognitive Health

Nutrition, Physical Activity, and Other Lifestyle Factors in the Prevention of Cognitive Decline and Dementia.

Ligia J Dominguez, Nicola Veronese, Laura Vernuccio, Giuseppina Catanese, Flora Inzerillo, Giuseppe Salemi, Mario Barbagallo. *Nutrients* 2021, 13(11), 4080; doi. org/10.3390/nu13114080. 15 November 2021. DOI: 10.3390/nu13114080. **Article link**

Significance: This review of current evidence for the effects of several factors (dietary, sleep and lifestyle) on the prevention or delayed onset of age-related cognitive decline found no single food or nutrient alone can prevent or delay the onset of dementia. However modifiable somatic and lifestyle factors are strong predictors of all-cause dementia including dietary patterns with plant-based, less-processed foods, better sleep, education, exercise, no history of hypertension, diabetes, obesity, smoking and social engagement.

Multiple factors combined are currently recognized as contributors to cognitive decline. The main independent risk factor for cognitive impairment and dementia is advanced age followed by other determinants such as genetic, socioeconomic, and environmental factors, including nutrition and physical activity. In the next decades, a rise in dementia cases is expected due largely to the aging of the world population. There are no hitherto effective pharmaceutical therapies to treat age-associated cognitive impairment and dementia, which underscores the crucial role of prevention. A relationship among diet, physical activity, and other lifestyle factors with cognitive function has been intensively studied with mounting evidence supporting the role of these determinants in the development of cognitive decline and dementia, which is a chief cause of disability globally. Several dietary patterns, foods, and nutrients have been investigated in this regard, with some encouraging and other disappointing results. This review presents the current evidence for the effects of dietary patterns, dietary components, some supplements, physical activity, sleep patterns, and social engagement on the prevention or delay of the onset of age-related cognitive decline and dementia.

Lipids

Host Immunomodulatory Lipids Created by Symbionts from Dietary Amino Acids.

Sungwhan F. Oh, T. Praveena, Heebum Song, Ji-Sun Yoo, Da-Jung Jung, Deniz Erturk-Hasdemir, Yoon Soo Hwang, et. al. *Nature* (2021) 2021 Nov 10. doi: 10.1038/s41586-021-04083-0. **Article link**

Significance: Little is known about the mechanism involved in control of immune development in the host–microbiota environment. In this study the authors present a structural and molecular-level model for immunomodulatory control by interactions of endobiotic metabolites with diet, microbiota and the immune system.

Background: Small molecules derived from symbiotic microbiota critically contribute to intestinal immune maturation and regulation1. However, little is known about the molecular mechanisms that control immune development in the host–microbiota environment. Here, using a targeted lipidomic analysis and synthetic approach, we carried out a multifaceted investigation of immunomodulatory α-galactosylceramides from the human symbiont Bacteroides fragilis (BfaGCs). The characteristic terminal branching of BfaGCs is the result of incorporation of branched-chain amino acids taken up in the host gut by B. fragilis. A B. fragilis knockout strain that cannot metabolize branched-chain amino acids showed reduced branching in BfaGCs, and mice monocolonized with this mutant strain had impaired colonic natural killer T (NKT) cell regulation, implying structure-specific immunomodulatory activity. The sphinganine chain branching of BfaGCs is a critical determinant of NKT cell activation, which induces specific immunomodulatory gene expression signatures and effector functions. Co-crystal structure and affinity analyses of CD1d–BfaGC–NKT cell receptor complexes confirmed the interaction of BfaGCs as CD1d-restricted ligands. We present a structural and molecular-level paradigm of immunomodulatory control by interactions of endobiotic metabolites with diet, microbiota and the immune system.

Sodium

24-Hour Urinary Sodium and Potassium Excretion and Cardiovascular Risk.

Yuan Ma, Feng J He, Qi Sun, Changzheng Yuan, Lyanne M Kieneker, Gary C Curhan, Graham A MacGregor et. al. *N Engl J Med*. 2021 Nov 13. doi: 10.1056/NEJMoa2109794 **Article link**

Significance: Higher sodium and lower potassium intakes, as measured from multiple 24-hour urinary collections, were correlated, in a dose-response manner, with higher cardiovascular risk. These findings support a reduction in sodium intake and an increase in potassium intake.

Background: The relation between sodium intake and cardiovascular disease remains controversial, owing in part to inaccurate assessment of sodium intake. Assessing 24-hour urinary excretion over a period of multiple days is considered to be an accurate method. **Methods:** We included individual-participant data from six prospective cohorts of generally healthy adults; sodium and potassium excretion was assessed with the use of at least two 24-hour urine samples per participant. The primary outcome was a cardiovascular event (coronary revascularization or fatal or nonfatal myocardial infarction or stroke). We analyzed each cohort using consistent methods and combined the results using a random-effects meta-analysis. **Results**: Among 10,709 participants, who had a mean (±SD) age of 51.5±12.6 years and of whom 54.2% were women, 571 cardiovascular events were ascertained during a median study follow-up of 8.8 years (incidence rate, 5.9 per 1000 person-years). The median 24-hour urinary sodium excretion was 3270 mg (10th to 90th percentile, 2099 to 4899). Higher sodium excretion, lower potassium excretion, and a higher sodium-to-potassium ratio were all associated with a higher cardiovascular risk in analyses that were controlled for confounding factors (P≤0.005 for all comparisons). In analyses that compared quartile 4 of the urinary biomarker (highest) with quartile 1 (lowest), the hazard ratios were 1.60 (95% confidence interval [CI], 1.19 to 2.14) for sodium excretion, 0.69 (95% CI, 0.51 to 0.91) for potassium excretion, and 1.62 (95% CI, 1.25 to 2.10) for the sodium-to-potassium ratio. Each daily increment of 1000 mg in sodium excretion was associated with an 18% increase in cardiovascular risk (hazard ratio, 1.18; 95% CI, 1.08 to 1.29), and each daily increment of 1000 mg in potassium excretion was associated with an 18% decrease in risk (hazard ratio, 0.82; 95% CI, 0.72 to 0.94). **Conclusions**: Higher sodium and lower potassium intakes, as measured in multiple 24-hour urine samples, were associated in a dose-response manner with a higher cardiovascular risk. These findings may support reducing sodium intake and increasing potassium intake from current levels.

Gut Microbiome

Gut Microbiome Diversity and Composition Are Associated with Habitual Dairy Intakes: A Cross-Sectional Study in Men

Hajara Aslam, Fiona Collier, Jessica A Davis, Thomas P Quinn, Martin O'Hely, Julie A Pasco, Felice N Jacka, Amy Loughman. *The Journal of Nutrition,* Vol. 151, Issue 11, November 2021, p3400–3412, doi.org/10.1093/jn/nxab252. **Article link**

Significance: A study in Australian men reported total dairy intake was not associated with gut microbiome, but individual food type (milk, yogurt, cheese) has differential influence in shaping the gut microbiome.

Background: At a population level, the relation between dairy consumption and gut microbiome composition is poorly understood. Objectives: We sought to study the cross-sectional associations between individual dairy foods (i.e., milk, yogurt, and cheese), as well as total dairy intake, and the gut microbiome composition in a large, representative sample of men living in south-eastern Australia. **Methods:** Data on 474 men (mean ± SD: 64.5 ± 13.5 y old) from the Geelong Osteoporosis Study were used to assess the cross-sectional association between dairy consumption and gut microbiome. Information on dairy intake was self-reported. Men were categorized as consumers and nonconsumers of milk, yogurt, cheese, and high- and low-fat milk. Milk, yogurt, and cheese intakes were summed to calculate the total dairy consumed per day and categorized into either low (<2.5 servings/d) or high (≥2.5 servings/d) total dairy groups. Fecal samples were analyzed using bacterial 16S ribosomal RNA (rRNA) gene sequencing. After assessment of α and β diversity, differential abundance analysis was performed to identify bacterial taxa associated with each of milk, yogurt, and cheese consumption compared with nonconsumption, low compared with high total dairy, and low- compared with high-fat milk consumption. All analyses were adjusted for potential confounders. **Results:** α Diversity was not associated with consumption of any of the dairy groups. Differences in β diversity were observed between milk and yogurt consumption compared with nonconsumption. Taxa belonging to the genera Ruminococcaceae UCG-010 and Bifidobacterium showed negative and weak positive associations with milk consumption, respectively. A taxon from the genus Streptococcus was positively associated with yogurt consumption, whereas a taxon from the genus Eisenbergiella was negatively associated

with cheese consumption. No specific taxa were associated with low- compared with high-fat milk nor low compared with high total dairy consumption. **Conclusions:** In men, community-level microbiome differences were observed between consumers and nonconsumers of milk and yogurt. Bacterial taxon-level associations were detected with milk, yogurt, and cheese consumption. Total dairy consumption was not associated with any microbiome measures, suggesting that individual dairy foods may have differential roles in shaping the gut microbiome in men.