ILSI North America

Nutrition Briefs

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Energy Balance

A Novel Approach to Predict 24-Hour Energy Expenditure Based on Hematologic Volumes: Development and Validation of Models Comparable to Mifflin-St Jeor and Body Composition Models

Chang DC, Piaggi P, Krakoff J. *J Acad Nutr Diet*. 2017 May 29. pii: S2212-2672(17)30349-0. Article Link

Significance: Prediction equations based on hematologic volumes were developed, validated, and found to be comparable to Mifflin-St Jeor and body composition models in this population of healthy adults.

Accurate prediction of 24-hour energy expenditure (24EE) relies on knowing body composition, in particular fat-free mass (FFM), the largest determinant of 24EE. FFM is closely correlated with hematologic volumes: blood volume (BV), red cell mass (RCM), and plasma volume (PV). However, it is unknown whether predicted hematologic volumes, based on easily collected variables, can improve 24EE prediction. The aim was to develop and validate equations to predict 24EE based on predicted BV, RCM, and PV and to compare the accuracy and agreement with models developed from FFM and with the Mifflin-St Jeor equation, which is recommended for clinical use by the Academy of Nutrition and Dietetics. BV, RCM, and PV were calculated from five published equations. Native American and white men and women were studied (n=351). Participants were healthy adults aged 18 to 49 years from the Phoenix, AZ, metropolitan area. Regression models to predict 24EE from hematologic and body composition variables were developed in half the dataset and validated in the other half. Hematologic volumes were all strongly correlated with FFM in both men and women (r≥0.94). Whereas the accuracy of FFM alone was 69%, four hematologic volumes were individually more accurate (75% to 78%) in predicting 24EE. Equations based on hematologic volumes plus demographics had mean prediction errors comparable to those based on body composition plus demographics; although the Mifflin-St Jeor had modestly better mean prediction error, body composition, hematologic, and Mifflin-St Jeor models all had similar accuracy (approximately 80%).

The Role of Energy Intake and Energy Misreporting in the Associations Between Eating Patterns and Adiposity

Leech RM, Worsley A, Timperio A, McNaughton SA. *Eur J Clin Nutr*. 2017 May 31. doi: 10.1038/ejcn.2017.90. Article Link

Significance: Longitudinal research that considers the impact of EI and energy misreporting is needed to better understand the relationship between eating patterns and obesity.

Research examining associations between eating occasion (EO) frequency and adiposity is inconclusive; studies examining the impact of energy misreporting are rare. This study examined associations between eating patterns and adiposity, with adjustment for energy misreporting, in a nationally representative sample of Australian adults. Dietary intake was assessed via two 24-h recalls collected during the 2011-12 National Nutrition and Physical Activity Survey (n=4050 adults, aged ≥19 years). Frequencies of all EOs, meals and snacks were calculated. Energy misreporting was assessed as the ratio of energy intake to predicted energy expenditure (EI:EE). Energy misreporters were identified by EI:EE ratios, <0.68 or >1.32. Multivariate regression models assessed associations between eating patterns and body mass index (BMI), WC, overweight/obesity (BMI ≥25 kg m-2) and central overweight/obesity (WC ≥94 cm in men and ≥80 cm in women). Meals (women only) and snacks were positively associated with WC and BMI (all P<0.01). Snack, but not meal frequency, was also associated with overweight/obesity (men: OR=1.22, 95% CI 1.07-1.39; women: OR=1.26, 95% CI 1.10-1.43) and central overweight/obesity (men: OR=1.17, 95% CI 1.04-1.32; women: OR=1.21, 95% CI 1.06-1.37). Multivariate analysis that excluded energy misreporters and adjusted for EI yielded either null or inverse associations (P<0.05). These findings suggest that the associations between eating patterns and adiposity are complicated by the role of EI and energy misreporting.

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Fortification/Supplementation

Definition of a Tolerable Upper Intake Level of Niacin: A Systematic Review and Meta-Analysis of the Dose-Dependent Effects of Nicotinamide and Nicotinic Acid Supplementation

Minto C, Vecchio MG, Lamprecht M, Gregori D. *Nutr Rev*. 2017 May 25. doi: 10.1093/nutrit/nux011. Article Link

Significance: The study authors suggest reconsideration of the UL of nicotinic acid for nutritional supplements, possibly differentiating between ULs in healthy and unhealthy individuals.

Nicotinic acid and nicotinamide are soluble compounds of the vitamin B group, widely used to regulate the lipid profile in hyperlipidemic individuals. Higher doses of nicotinic acid are associated with adverse effects, especially flushing. A unique tolerable upper intake level (UL) of nicotinic acid has not been defined. This meta-analysis aims to evaluate adverse effects and their incidence after supplementation with different doses of nicotinic acid and nicotinamide, comparing results with current ULs in Europe and the United States. A total of 2670 citations were selected for screening. Two primary outcomes were considered: occurrence of adverse effects following nicotinic acid or nicotinamide supplementation, and dose at which adverse effects occurred. After screening, 47 articles involving 11,741 individuals were included. Meta-analysis was based on estimation of benchmark doses for the probability of adverse effects after supplementation. In individuals with dyslipidemia or cardiovascular disease, nicotinic acid monotherapy seems to be protective against any adverse effects considered, as adverse events occurred at doses above those used with other treatments. In healthy individuals treated with nicotinic acid alone, major adverse effects occurred at doses below 1000 mg/d. Results may indicate a high degree of conservativeness in the UL of nicotinic acid, fixed at 35 mg/d in United States and 10 mg/d in Europe. Reconsideration of the UL of nicotinic acid for nutritional supplements, possibly differentiating between ULs in healthy and unhealthy individuals, may be warranted.

Microbiome

Dietary Metabolites Derived From Gut Microbiota: Critical Modulators of Epigenetic Changes in Mammals

Bhat MI, Kapila R. *Nutr Rev*. 2017 May 1;75(5):374–389. doi: 10.1093/nutrit/nux001. Article Link

Significance: The review provides insights into the current understanding of the microbiota and its association with mammalian epigenomics as well as the interaction of pathogens and probiotics with host epigenetic machinery.

The mammalian gastrointestinal tract harbors trillions of commensal microorganisms, collectively known as the microbiota. The microbiota is a critical source of environmental stimuli and, thus, has a tremendous impact on the health of the host. The microbes within the microbiota regulate homeostasis within the gut, and any alteration in their composition can lead to disorders that include inflammatory bowel disease, allergy, autoimmune disease, diabetes, mental disorders, and cancer. Hence, restoration of the gut flora following changes or imbalance is imperative for the host. The low-molecular-weight compounds and nutrients such as short-chain fatty acids, polyamines, polyphenols, and vitamins produced by microbial metabolism of nondigestible food components in the gut actively participate in various epigenomic mechanisms that reprogram the genome by altering the transcriptional machinery of a cell in response to environmental stimuli. These epigenetic modifications are caused by a set of highly dynamic enzymes, notably histone acetylases, deacetylases, DNA methylases, and demethylases, that are influenced by microbial metabolites and other environmental cues. Recent studies have shown that host expression of histone acetylases and histone deacetylases is important for regulating communication between the intestinal microbiota and the host cells. Histone acetylases and deacetylases influence the molecular expression of genes that affect not only physiological functions but also behavioral shifts that occur via neuroepigenetic modifications of genes. The underlying molecular mechanisms, however, have yet to be fully elucidated and thus provide a new area of research.

Bioactives

Flavones: Food Sources, Bioavailability, Metabolism, and Bioactivity

Hostetler GL, Ralston RA, Schwartz S. *Adv Nutr*. 2017 May 15;8(3):423–435. doi: 10.3945/an.116.012948. Article Link

Significance: A better understanding of flavone sources and bioavailability is needed to understand mechanisms of action and nutritional intervention.

Flavones are a class of flavonoids that are a subject of increasing interest because of their biological activities in vitro and in vivo. This article reviews the major sources of flavones and their concentrations in food and beverages, which vary widely between

studies. It also covers the roles of flavones in plants, the influence of growing conditions on their concentrations, and their stability during food processing. The absorption and metabolism of flavones are also reviewed, in particular the intestinal absorption of both O- and C-glycosides. Pharmacokinetic studies in both animals and humans are described, comparing differences between species and the effects of glycosylation on bioavailability. Biological activity in animal models and human dietary intervention studies is also reviewed.

Personalized Nutrition

Can Genetic-Based Advice Help You Lose Weight? Findings From the Food4Me European Randomized Controlled Trial

Celis-Morales C, Marsaux CF, Livingstone KM, et al. *Am J Clin Nutr.* 2017 May;105(5):1204–1213. doi: 10.3945/ajcn.116.145680. Article Link

Significance: Results indicated that there are greater body weight and waist circumference reductions in risk carriers than in non-risk carriers of the fat-mass and obesity associated gene.

There has been limited evidence about whether genotype-tailored advice provides extra benefits in reducing obesity-related traits compared with the benefits of conventional one-size-fits-all advice. Researchers determined whether the disclosure of information on fat-mass and obesity-associated (FTO) genotype risk had a greater effect on a reduction of obesity-related traits in risk carriers than in nonrisk carriers across different levels of personalized nutrition. A total of 683 participants (women: 51%; age range: 18-73 y) from the Food4Me randomized controlled trial were included in this analysis. Participants were randomly assigned to 4 intervention arms as follows: level 0, control group; level 1, dietary group; level 2, phenotype group; and level 3, genetic group. FTO (single nucleotide polymorphism rs9939609) was genotyped at baseline in all participants, but only subjects who were randomly assigned to level 3 were informed about their genotypes. Level 3 participants were stratified into risk carriers (AA/AT) and nonrisk carriers (TT) of the FTO gene for analyses. Height, weight, and waist circumference (WC) were self-measured and reported at baseline and months 3 and 6. Changes in adiposity markers were greater in participants who were informed that they carried the FTO risk allele (level 3 AT/AA carriers) than in the nonpersonalized group (level 0) but not in the other personalized groups (level 1 and 2). Mean reductions in weight and WC at month 6 were greater for FTO risk carriers than for noncarriers in the level 3 group [-2.28 kg (95% CI: -3.06, -1.48 kg) compared with -1.99 kg (-2.19, -0.19 kg), respectively ($P = 0.037$); and -4.34 cm (-5.63, -3.08 cm) compared with -1.99 cm (-4.04, -0.05 cm), respectively, ($P = 0.048$)].

Scientific Integrity

Peer Review: A System Under Stress

Gropp RE, Glisson S, Gallo S, Thompson L. *BioScience.* 2017;67(5):407–410. Article Link

The American Institute of Biological Sciences (AIBS) convened a meeting in Washington, DC, on 6 December 2016 to explore The Role of Peer Review in Informed Decision-making. The participants included representatives from AIBS member organizations, government agencies, research funders, scholarly publishers, and scholars of peer review.