

2020 Nutrition Symposium

UNIVERSITY OF ILLINOIS AT URBANA-CHAMPAIGN | DIVISION OF NUTRITIONAL SCIENCES

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Nutritional Sciences

COLLEGE OF AGRICULTURAL, CONSUMER
& ENVIRONMENTAL SCIENCES



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Nutritional Sciences Graduate Student Association

Special Note about Nutrition Symposium 2020

Due to the impact of COVID-19, the Nutritional Sciences Symposium Planning Committee made the difficult decision to cancel the in-person 2020 Nutrition Symposium. While we were disappointed not to have a physical opportunity to get together, it was still our goal to highlight the exciting and groundbreaking research taking place within our nutrition community at the University of Illinois. Here we present all of the scientific abstracts for the talks and posters that would have been part of the 2020 Nutrition Symposium. Thank you to all of our sponsors who continue to support this vital research event. We look forward to seeing you at the 2021 Nutrition Symposium.

Welcome

On behalf of the Nutritional Sciences Graduate Student Association (NSGSA), the Division of Nutritional Sciences (DNS), and all participating presenters, we would like to welcome you to the 2020 Nutrition Symposium at the University of Illinois!

The Nutrition Symposium is an important event for sharing ideas across disciplines and with the community. Started in 1994 by NSGSA, the symposium offers students within DNS and related disciplines on campus an opportunity to present their nutrition research prior to national meetings held annually in the spring. This symposium offers a first glance at exciting research in areas including metabolic regulation, cancer, gastrointestinal physiology, immunology, physical activity, public health, and bioactive plant compounds. Students will be traveling to present their work at a variety of national and international conferences.

This year, we are honored to have Dr. Catherine J. Field deliver the keynote address, “Improving immune development in the infant by altering the content of docosahexaenoic acid and form

of choline in the maternal diet.” Additionally, NSGSA is proud to highlight the work of world-class faculty members through a mini-symposium. This year’s presentations highlight the field of personalized nutrition and will feature Drs. Manabu Nakamura, Margarita Teran-Garcia, Yuan-Xiang Pan, and Zeynep Madak-Erdogan.

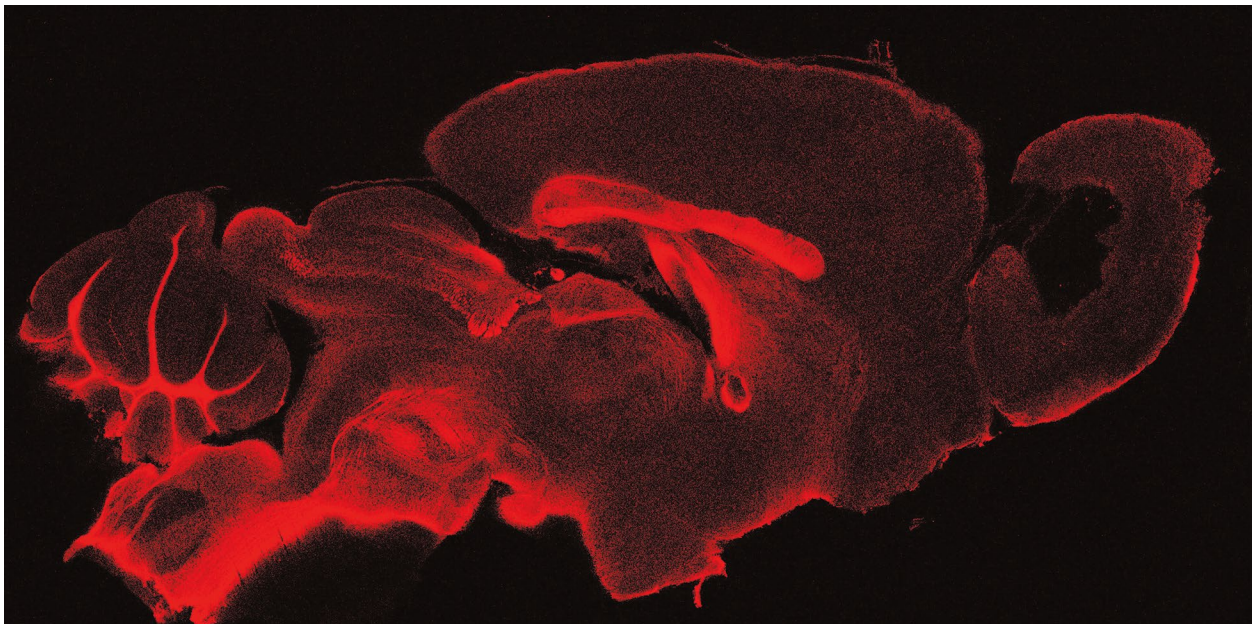
We are grateful to the many people involved with this meeting and program. We would first like to thank our keynote speaker, Catherine J. Field. Thank you also to our sponsors – their support is essential to the success and quality of the program. We would also like to recognize the NSGSA executive board and the symposium planning committee, whose members have worked long and hard to organize an excellent program. Most of all, we would like to thank our session chairs, judges, presenters, and attendees for participating in this year’s event and making them a success.

The Nutritional Sciences Graduate Student Association Steering Committee

<http://www.nutritionalsciences.illinois.edu>

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Research image produced by Allison Louie. "One of the challenges of looking into how the brain works is, quite literally, looking into it. The brain is a dense, lipid-rich structure, which can make it difficult to visualize its fine, intricate connections on a large but sensitive scale. In order to study how environmental factors such as diet and infection might affect myelination processes of the brain, I utilize a tissue-clearing technique called CLARITY (Clear Lipid-exchanged Acrylamide-hybridized Rigid Imaging/Immunostaining-compatible Tissue-hYdrogel), which essentially renders the tissue "see-through" while maintaining an intact protein scaffold. After staining with anti-proteolipid protein, I can measure attributes of many individual myelinated fibers across relatively large regions of the brain. This confocal tile scan of a sagittal brain section of a cuprizone-fed mouse shows characteristic demyelination in the caudal aspect of the corpus callosum. The mouse was sacrificed during the partial remyelination phase."

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Nutritional Sciences Graduate Student Association

The Nutritional Sciences Graduate Student Association (NSGSA) was founded in the spring of 1973 by students in the program. The mission of the organization is to provide a means of communication among graduate students, faculty, and alumni of the Division of Nutritional Sciences (DNS), which spans multiple colleges and departments.

NSGSA serves as a forum for student opinion and input and provides students the opportunity to expand their experiences as graduate students. Our activities reflect our desire to enrich our experiences as graduate students and promote the importance of the nutritional sciences discipline both within the university and among the surrounding communities of Champaign and Urbana.

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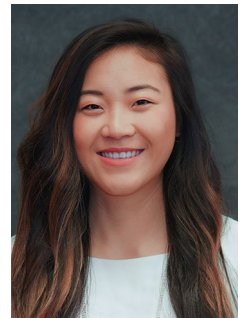
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This institution is an equal opportunity provider.

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SNAPSHOT FROM THE PAST

Winners of the 2019 University of Illinois Nutrition Symposium poster and oral competitions with keynote speaker, Dr. Corby Martin. Photo by L. Brian Stauffer.

Symposium Contributors

The University of Illinois Division of Nutritional Sciences and the Nutritional Sciences Graduate Student Association would like to acknowledge the generosity of the sponsors and friends of our 2020 Nutrition Symposium.

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Keynote Speaker

Dr. Catherine J. Field, PhD, RD

Department of Agricultural, Food and Nutritional Science, Faculty of Agriculture, Life and Environmental Science, University of Alberta

Catherine Field holds a Tier I Canada Research Chair in Human Nutrition and Metabolism and an Adjunct professorship in the Faculty of Medicine and Dentistry at the University of Alberta. Her research program centers on the effect of nutrition on the immune system. Current areas of research are: the role of polyunsaturated fats and breast milk bioactives on the development of the infant's immune system, the use of specific fatty acids in the prevention and treatment of breast cancer and identifying the association between nutritional status and maternal mental health and infant neuro-physical development. She is a co-PI of a large maternal infant cohort, APrON (Alberta Pregnancy Outcomes and Nutrition). She has published more than 250 peer-reviewed publications, been invited to speak more than 100 times nationally and internationally and has trained over 100 students, from high school to post-doctoral levels, in research. Dr. Field received the McCalla and Killam Professorships from the University of Alberta, the Earl Willard McHenry Award for Leadership in Nutrition from the Canadian Nutrition Society and the Mary Mitchell Award for service to the Dietetic Profession in Alberta. Dr. Field is currently the Past-President of, and only the second non-American, of the American Society for Nutrition. She currently serves as a member of the CIHR Institute for Nutrition, Metabolism and Diabetes Advisory Board, Associate Editor for *Advances in Nutrition* and as a scientific advisor for the International Life Science Institute North America and Dairy Farmers of Canada. She was one of the co-founding Directors of the Cancer Research Institute of Northern Alberta in 2012 that brought together cancer researchers from 10 different Faculties at the University of Alberta.



“Improving immune development in the infant by altering the content of docosahexaenoic acid and form of choline in the maternal diet”

The early postnatal period is critical for the development of the infant's immune system. One of the important immune functions that develops is that of 'oral tolerance', the ability to respond appropriately to dietary antigens. The failure to develop oral tolerance results in atopic diseases such as allergy. Our work and others has established that the intake of essential fatty acids, particularly docosahexaenoic acid (DHA), and choline alter immune development in infants. Breast milk is the optimal food for infants in the postnatal period, but the composition of these two nutrients is influenced by the maternal diet. Using a large maternal infant cohort, our group has established that the intake of DHA and choline by healthy women is not optimal at 3-month post-partum when all mothers reported to be 'exclusively' breastfeeding their infants. We have identified the major sources of DHA and both the sources and forms of choline in the maternal diet. Women consuming a daily supplement containing DHA had significantly more DHA in their breast milk. We have used these intakes to design maternal diets in pre-clinical studies in rodents. This alters the amount of DHA and the amount and form of choline in breast milk. Changing breast milk composition resulted in differences in immune development and 'programming' of the offspring's immune system, including the ability to successfully develop oral tolerance.

Faculty Mini-Symposium: Personalized Nutrition: Putting the ‘U’ in Nutrition”

Abstracts and Biographies

Multiscale approaches to identify novel biomarkers of metabolic and cardiovascular disease

Dr. Zeynep Madak-Erdogan

Department of Food Science and Human Nutrition, Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL

ABSTRACT: Currently, we lack clinical tests to assess a women’s breast cancer risk, or properly diagnose cardiac events due to microvascular disease of the heart. Gold standard tests used for diagnosis of gestational diabetes are not always successful in identifying the disease in individuals from certain racial backgrounds. Liquid biopsies, based on identifying changes in circulating biomarkers of various health conditions are gaining popularity in recent years due to real time disease risk and progression monitoring. In our lab, we are developing advanced computational methods to systematically evaluate electronic health records, and molecules in blood (metabolites, exosomes, proteins etc.) to identify potential circulating biomarkers for health outcomes. I will present data from clinical and preclinical studies related to identification and validation of circulating biomarkers for diagnosis of breast cancer risk, coronary microvascular disease and gestational diabetes. Thus, multiscale approaches that utilize combination of machine learning approaches, and preclinical and clinical studies provides opportunities for further validating identified biomarkers and promises improvement in women’s health by diagnosing conditions earlier before the disease onsets or progresses further.

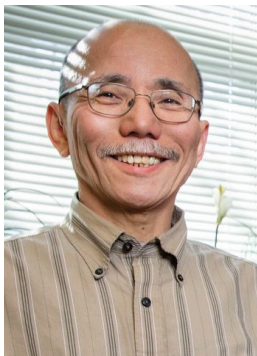


BIOGRAPHY: Dr. Zeynep Madak-Erdogan is an Assistant Professor of Nutrition and the Director of Women’s Health and Metabolism lab at University of Illinois, Urbana Champaign. She received her B.S. degree in Molecular Biology and Genetics from Bilkent University in 2002. After completing her PhD and Postdoctoral studies on Mechanisms of Estrogen Receptor Action, she joined Department of Food Science and Human Nutrition at UIUC, in 2014. Her lab uses “Systems Biology” approaches to understand how nutrients and hormones impact metabolic health and breast cancer outcomes. In addition to mentoring several undergraduate and graduate students she has taught courses in the areas of Diet, Nutrition and Cancer, Nutrition and Women’s health and Toxicology. She has received several awards including NIEHS, Pre- and Postdoctoral Research Training Program in Endocrine Developmental and Reproductive Toxicology Fellowship, Women in Endocrinology Young Investigator Award from Endocrine Society, National Center for Supercomputing Applications Fellowship, and Mary Swartz Rose Young investigator Award and Bio-serv Experimental Nutrition Award from American Society of Nutrition. She is the basic science editor-in-chief for Endocrine and Metabolic Science Journal and she serves as editorial board member for Journal of Endocrine, Steroids, Journal of Functional Foods and Scientific Reports.

Assisting sustainable dietary weight loss one at a time**Dr. Manabu Nakamura**

Department of Food Science and Human Nutrition, Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL

ABSTRACT: Obese individuals often develop chronic diseases such as diabetes, cardiovascular and musculoskeletal diseases. Although dietary weight loss is an effective treatment of obesity, a dietary weight loss program that can produce sustainable weight loss is yet to be developed. In the past years our lab has been developing a dietary weight loss program, Individualized Diet Improvement Program (iDip). Our long-term goal is to establish iDip as a reliable, affordable and widely accessible weight management program to improve health and quality of life of many. The approach of iDip is to help participants experiment and discover dietary changes they can sustain for a lifetime, instead of providing dieting products or strict dietary instructions. A core innovation to support this approach is the protein-fiber plot (PF plot), a two-dimensional display of protein and fiber per energy values for easy comparison of food properties to make an informed decision in food selection. We also replaced calorie counting with daily weighing for monitoring of daily energy balance. The iDip consists of 19 lecture sessions and 3 individual advising sessions over one year. iDip 1 (n=14) demonstrated feasibility of our approach. An ongoing trial, iDip 2 (n=30) succeeded in increasing the magnitude of weight loss. However, we observed large differences in weight loss outcome among participants. We have been analyzing our data to identify factors that affect participants' outcome so that we can develop a treatment algorithm. Also, we are shifting the iDip platform from on-site to online to increase accessibility and affordability. In conclusion, we have developed innovative dietary weight loss program. With an online platform and further individualized treatment plan, the program would become a reliable dietary weight loss program in the near future.



BIOGRAPHY: After receiving a degree in Veterinary Medicine from the University of Tokyo, Japan, Dr. Nakamura worked as a veterinarian for several years specializing in dairy cows. This experience helped him recognize the importance of nutrition in disease prevention, and led him to starting his graduate study in nutrition at the University of California, Davis. There, he was attracted to biochemical nutrition, which could explain nutrient metabolism in chemical terms, and has been studying it since then. His main research areas have been regulation of macronutrient metabolism and function of polyunsaturated fatty acids. Although research in biochemical and molecular nutrition was exciting, devastating effects of obesity epidemic and lack of an effective dietary weight loss program were a lingering concern to him. Thus, he switched his research focus to developing a weight loss program, and started a novel program, *Individualized Diet Improvement Program* (iDip) in 2018. The project has been making a rapid progress thanks to a dedicated team of graduate students and collaborators. In addition to his research, he enjoys teaching three graduate courses every year.

Genetic variation in pathways of lipid and lipoprotein metabolism are associated with lipid profiles of young Mexicans

Dr. Margarita Teran-Garcia

Division of Nutritional Sciences, Department of Human Development and Family Studies, University of Illinois at Urbana-Champaign, Urbana, IL; Carle Illinois College of Medicine, University of Illinois Urbana-Champaign, Urbana, Illinois

ABSTRACT: Obesity and other nutrition-related diseases, including non-communicable chronic diseases, are significant causes of morbidity and mortality worldwide. The adverse impacts of obesity and associated comorbidities on health remain a major concern due to the lack of effective interventions for prevention and management. Specifically, there is a need for well-tolerated and effective therapies.

In Mexico, 65% of the adult population has low high-density lipoprotein cholesterol (HDL-C), and 43.6% have hypercholesterolemia, clinical markers of metabolic syndrome and risk factors for cardiovascular disease. Similar patterns are present among young Mexicans, aged 20 to 29 years old, with 62% having low HDL-C and 22% high levels of triglycerides (TG). The rapid increase in the prevalence of overweight and obesity, coupled with dyslipidemia, highlights the need to understand risk factors amenable to intervention in this population. In European groups, research on the genetic predisposition to the development of dyslipidemia has identified over 95 loci to be associated with either low-HDL-C, high LDL-C, high TG, or high TC. Most of the genetic association research has been conducted in populations of European descent. Recent genome-wide association studies in Mexicans have identified several genetic loci associated with blood lipid levels in adults. Despite reports of genetic association with lipid profiles in other ethnicities, there is no data on the fatty acid desaturase (FADS) gene cluster in this population. The FADS gene cluster includes 3 genes FADS1, FADS2, and FADS3. The role of the FADS gene cluster is the elongation and formation of long-chain fatty acids from both dietary and endogenous precursors. Thus, its role in plasma fatty acid concentration is essential. Our data indicate that a genetic variant in the fatty acid cluster gene (FADS1-rs174546) is associated with TG and very-low-density lipoprotein cholesterol (VLDL) concentrations in healthy young Mexicans. New findings of genetic associations in pathways of lipid and lipoprotein metabolism with blood lipid concentrations and dietary interactions will be presented.

BIOGRAPHY: Dr. Terán is an Extension Specialist for Hispanic Health Programs, faculty of the Department of Human Development and Family Studies, the Carle Illinois College of Medicine, member of the Division of Nutritional Sciences and Affiliate to the Family Resiliency Center, the Department of Psychology and the Center for Latin American Affairs at the University of Illinois Urbana-Champaign.



She obtained her Medical Degree by the Universidad Nacional Autónoma de México (U.N.A.M.) and did her Pediatric fellowship at the National Institute of Pediatrics in Mexico. Her Ph.D. focused on nutrient-gene interactions and lipogenesis at the University of Texas at Austin. During her postdoctoral training, she acquired expertise in genetic epidemiology methods and tools while she investigated the role of individual genotype in cardiovascular and metabolic responses to exercise.

Dr. Terán participates and leads multi-disciplinary projects that are collecting primary longitudinal data relevant to children (STRONG KIDS), college-age individuals (UP AMIGOS), and families of Hispanic-Heritage (ABRIENDO CAMINOS USDA-NIFA, multi-state Grant # 2015-68001-23248) on weight status and weight-related health outcomes. Dr. Teran's primary research focuses on the joint influence of genetics (nature) and the environment (nurture, culture, family) on the development of unhealthy behaviors in dietary intake, physical (in)activity, or family dynamics. She has published more than 70 peer-review articles. Her scholarly work applies a competent multicultural and transdisciplinary perspective towards family health and wellness in the community.

Role of epigenetics in development of personalized cancer management

Yuan-Xiang Pan, PhD

Department of Food Science and Human Nutrition, Division of Nutritional Sciences, Illinois Informatics Institute (I3), University of Illinois at Urbana-Champaign, Urbana, IL

ABSTRACT: Cancer is a heterogeneous group of diseases whose causes, pathogenesis, metastatic potential, and responses to treatment can be very different among individuals. These differences make cancer an ideal target for the application of personalized cancer management (PCM). Constituting some of this PCM are screening, diagnosis, prognosis, prediction of treatment efficacy, patient follow-up after surgery for early detection of recurrence, and the stratification of patients into specific smaller subgroups, thus allowing for individualization of treatment. Epigenetic patterns, such as DNA methylation, histone modifications, and non-coding RNAs, can be both driver factors and characteristic features of cancer. Multiple patterns of these epigenetic factors occur specifically in certain cancers, which allows their potential use as biomarkers for PCM. Each group of epigenetic factors that are currently available or in development can be used in early cancer detection, prediction, prognosis, and response to treatment. Alteration of DNA methylation, histone modifications, and miRNAs often helps to differentiate tumor subtypes better and bring new prognostic information related to patient survival in relation to age, sex, etc. On the other hand, there are also a few epigenetic biomarkers that predict response to chemotherapeutic agents. The availability of blood-based biomarkers also allows sampling invasiveness to be reduced and the sampling procedure to be simplified. The reversal of epigenetic changes represents a potential target for novel preventive and therapeutic strategies, as well as medication design as PCM. Epigenetic drugs represent authentic 'genomic medicines' and will almost certainly exhibit the most significant efficacy when used in combination and when used jointly with other therapies such as standard chemotherapy or immunotherapy.



BIOGRAPHY: Dr. Pan is an Associate Professor in the Department of Food Science and Human Nutrition (FSHN), a member of the Division of Nutritional Sciences (DNS) and Illinois Informatics Institute (I3) at University of Illinois at Urbana-Champaign (UIUC). Dr. Pan's research is to understand the adaptation of epigenetic modifications in mammalian gene regulation to the environment, with a focus on the impact of these adaptive processes in health and disease. His lab uses experimental, statistical, and computational analyses to explore the epigenome, to integrate comparative and high-throughput epigenomics data. Dr. Pan is an investigator in NIEHS/EPA Children's Environmental Health Research Center at Illinois and receives grant support from the National Institutes of Health (NIH), the United States Department of Agriculture, and industry. Dr. Pan received the 2012 Norman Kretchmer Memorial Award in Nutrition and Development with potential relevance to improving children's health from the American Society of Nutrition.

Graduate Student Oral Session Abstracts

Oral Session 1

Impact of dietary tomato on prostate carcinogenesis and progression in lean and overweight/obese TRAMP mice

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INTRODUCTION: Despite decreasing trends of diagnosis, prostate cancer (PCa) is the most commonly diagnosed male cancer in the United States. The 2018 revision to the 2014 Prostate Cancer Continuous Update Project (WCRF/AICR) maintained that there was strong evidence to support that being overweight or obese increases the risk for advanced, high-grade, and fatal PCa. Abundant epidemiological and pre-clinical evidence exists to show that physiologically relevant levels of dietary tomato intake reduce the risk for PCa, with some evidence suggesting that tomato intake is beneficial for reducing the risk for advanced PCa. The primary objective was to determine the effect of dietary tomato on PCa development and progression in overweight/obese, transgenic mice prone to PCa (TRAMP mice). Secondary objectives included assessing histological, inflammatory, angiogenic, and metabolic changes in prostate tumors at different time points of cancer progression.

METHODS: Four-week-old TRAMP mice were randomly assigned to consume one of four diets (n=45/diet): control (CON) or obesogenic (OB), both with and without 10% freeze-dried tomato powder (TP). Prostate tumor incidence and growth were monitored via ultrasound imaging. Mice were terminated one or four weeks following tumor development to assess early and later molecular changes in the tumors.

RESULTS: OB diets led to greater body weight over time (45.2 ± 1.0 g at 24 weeks of age) when compared with CON diets (33.2 ± 0.8 g; $p < 0.0001$ by 2-way ANOVA), with TP inclusion having no impact on body weight within diets. OB diets resulted in greater tumor incidence (64.8% vs. 42.5%), earlier age at tumor onset (16.9 ± 1.0 weeks vs. 18.6 ± 0.7 weeks), higher body weight at tumor detection (38.6 ± 1.0 g vs. 30.8 ± 1.2 g), and greater post-mortem periprostatic adipose weight (2.0 ± 0.1 g vs. 0.9 ± 0.1 g). TP intake was protective only in lean animals, with CON-TP-fed animals having exhibited lower tumor volume at detection (28.7 ± 5.2 mm³ vs. 47.3 ± 15.5 mm³) and lower tumor weight at both one (0.1 ± 0.02 g vs. 0.2 ± 0.06 g) and four (1.5 ± 0.3 g vs. 2.1 ± 0.5 g) weeks following tumor detection compared with CON-fed animals. Conversely, TP was not protective in animals with obesity, with OB-TP-fed animals having exhibited no differences in tumor weight one week following tumor detection (0.3 ± 0.06 g vs. 0.3 ± 0.07 g) and greater tumor weight four weeks following tumor detection (2.5 ± 0.7 g vs. 2.0 ± 0.3 g) when compared with OB-fed animals.

CONCLUSIONS: TRAMP mice fed obesogenic diets have higher body weight and earlier onset of PCa. While tomato intake led to smaller tumors in lean animals, the opposite effect was observed in animals with higher body weight.

Diisononyl phthalate exposure affects colonic health in adult female miceKaren Chiu^{1,2} and J.A. Flaws^{1,2,3}¹ Department of Comparative Biosciences, University of Illinois at Urbana-Champaign, Urbana, IL² Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL³ Carl R. Woese Institute of Biology, University of Illinois at Urbana-Champaign, Urbana, IL

INTRODUCTION: Diisononyl phthalate (DiNP) is a common phthalate that is used to make polyvinyl chloride flexible. DiNP is used in many end products such as toys, faux leather, and building materials. Exposure to DiNP has been shown to aggravate immune responses in humans. However, little is known about DiNP and its effects on the gastrointestinal tract. Thus, this study tested the hypothesis that subchronic exposure to DiNP alters colon histology, hormone levels, and gene expression related to inflammation and cell cycle regulation.

METHODS: To test this hypothesis, 39-40 day old female CD-1 mice were orally dosed with corn oil vehicle, 20 µg/kg/day, 200 µg/kg/day, 2 mg/kg/day, 20 mg/kg/day, or 200 mg/kg/day (n=6 mice/treatment group) DiNP for 10-14 days and then euthanized during diestrous immediately after dosing. Distal colons were collected for histological examination, hormone analyses, and gene expression analyses of *Ifng*, *Tnf*, *Il22*, *Il10*, *Bcl2*, *Ccnd2*, *Cdkn1a*, *Ccnb1*, *Bcl2l10*, *Ccne1*, *Cdk4*, *Ki67*, and *Pcna*.

RESULTS: Histological analysis showed that DiNP exposure at 20 and 200 µg/kg/day increased colonic damage compared to control (p=0.02 and p≤0.05, respectively). Colonic damage was mainly attributed to cellular infiltration and edema. However, enterocyte sloughing and aberrant colon walls were also observed in the DiNP treatment groups. DiNP exposure did not significantly affect cytokine gene expression (*Ifng*, *Tnf*, *Il22*, *Il10*) in the colon compared to control. However, DiNP exposure increased *Ifng* and *Tnf* expression in a dose-dependent manner compared to control. Lipid extractions from the distal colon revealed that the 200 µg/kg, 2 mg/kg, 20 mg/kg, and 200 mg/kg treatment groups exposed to DiNP had significantly decreased estradiol concentrations compared to control. Testosterone concentrations were unaffected by treatment. Further, 200 µg/kg/day DiNP significantly downregulated *Ccnd2* compared to control. High levels of DiNP did not alter the expression of *Bcl2*, *Cdkn1a*, *Ccnb1*, *Bcl2l10*, *Ccne1*, *Cdk4*, and *Pcna* compared to control.

CONCLUSIONS: These data suggest that DiNP exposure causes colonic damage and may interfere with cell growth in the colon. Supported by NIH T32 ES 007326, NIH R01 ES028661, and Vision 20/20.

Resistance exercise-induced apelin is not modulated by higher dietary protein density in overweight adultsColleen F. McKenna¹, A.F. Salvador², A.R. Keeble², R.A. Alamilla², S.E. Scaroni¹, N.A. Khan^{1,2,3}, N.A. Burd^{1,2}¹ Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL² Department of Kinesiology and Community Health, University of Illinois at Urbana-Champaign, Urbana, IL³ Neuroscience Program, University of Illinois at Urbana-Champaign, Urbana, IL

INTRODUCTION: Apelin is a bioactive peptide related to chronic diseases and metabolic status. Furthermore, it has recently been demonstrated as an exercise-sensitive myokine associated with physical independence during aging. Physical performance is highly dependent on muscle strength, with a clear role of dietary protein (i.e., > Recommended Dietary Allowance) for the maintenance of age-related muscle strength. However, the influence of dietary protein density on exercise-induced apelin remains unknown. Therefore, our objective was to evaluate plasma apelin concentrations and its relationship with muscle strength in middle-aged adults consuming differential protein intake during progressive resistance training.

METHODS: 41 overweight middle-aged adults (50 ± 2 y, BMI 28 ± 1 kg·m⁻², M = 19, F = 22) were stratified and randomized to consume either high protein (1.68 ± 0.06 g·kg⁻¹·d⁻¹) or moderate protein (1.16 ± 0.04 g·kg⁻¹·d⁻¹) during a 10-week weight-maintenance nutrition counseling-controlled resis-

tance training program. Body composition was assessed by dual-energy x-ray absorptiometry. Muscle strength was assessed by one-repetition maximum (1RM) and isometric maximal voluntary contraction (MVC) at 60° knee angle. Oral glucose tolerance tests were performed at baseline and post-intervention.

RESULTS: Main effects of time were observed for increases in lean body mass ($P = 0.003$), upper and lower body 1RM (all $P \leq 0.001$), isometric MVC flexion ($P = 0.013$), and plasma apelin concentrations ($P = 0.007$). There were no changes in body adiposity or glucose-insulin regulation (e.g., HOMA-IR, Matsuda) with the intervention (all $P \geq 0.152$). Apelin was positively and significantly associated with isometric MVC (extension: $r = 0.233$, $P = 0.047$; flexion: $r = 0.308$, $P = 0.008$), but not 1RM.

CONCLUSIONS: Our results show that resistance training increases circulating apelin concentrations, which is related to isometric strength gain. While resistance exercise has the capacity to increase lean mass, muscle strength, and apelin, our results suggest that higher dietary protein does not potentiate these adaptations.

Benefits of home-delivered, low sodium meals in patients on hemodialysis

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BACKGROUND: Patients undergoing maintenance hemodialysis (HD) therapy are routinely counseled to reduce dietary sodium intake to reduce sodium retention, volume overload (VO), and hypertension. Unfortunately, low-sodium trials in HD are sparse and mostly indicate that dietary education and behavioral counseling alone are ineffective in reducing sodium intake. The purpose of this study is to determine if 4-weeks of low-sodium home delivered meals will reduce VO and hypertension in patients undergoing HD. We also examined the secondary effects of meal provision on nutrient intakes as well as serum potassium and phosphorus levels.

METHODS: Thirteen subjects have been recruited to date (53±14 years, BMI 39.1±13.2 kg/m², 64% male, 55% AA, DM% AA, 55% CVD) from a HD clinic in central IL. PurFoods, LLC prepared and shipped 3 low-sodium kidney meals (<700 mg Na, K, and Phosphorus each) per day to patients for 4 weeks. We collected interdialytic weight gain (monthly average), bioelectrical impedance, standardized blood pressure, and 3 days (HD, non-HD, and weekend day) of dietary recalls (USDA automated multiple-pass method), and blood pre-(OM) and post-(1M) intervention.

RESULTS: Home-meal delivery significantly reduced both dietary sodium intake (OM 3776±1244 vs 1M 1831±256 $p < 0.001$) and interdialytic weight gain (OM 3.46±0.99 vs 1M 2.53±0.85 $p < 0.001$). This was accompanied by a trend for reduction in total body water (OM 58.60±14.85 vs 1M 55.58±12.50 $p = 0.07$), but a non-significant reduction in calculated VO (OM 1.46±4.33 vs 1M 0.96±4.09 $p = 0.28$). There were also significant reductions in systolic blood pressure (OM 166±32 vs 1M 147±23 $p < 0.05$), with no change in diastolic blood pressure (OM 92±13 vs 1M 90±13 $p < 0.37$). Meal provision did not change calorie or protein intake ($p > 0.05$). Patients had no changes in pre- or post-dialysis serum potassium ($p > 0.05$) but did have significant reductions in pre-dialysis serum phosphorus (OM 7.04±1.44 vs 1M 4.98±1.39 $p < 0.001$).

CONCLUSIONS: Low-sodium home-meal delivery appears to be an effective method to reduce dietary sodium intake, interdialytic weight gain, and blood pressure in HD patients. It will be important to determine if these changes can be sustained long-term with additional counseling, and the cost-effectiveness of this approach needs to be evaluated.

Graduate Student Oral Session Abstracts

Oral Session 2

Effect of natural vs. synthetic α -tocopherol on neurogenesis-related genes in cerebella of juvenile α -tocopherol transfer protein-null mice

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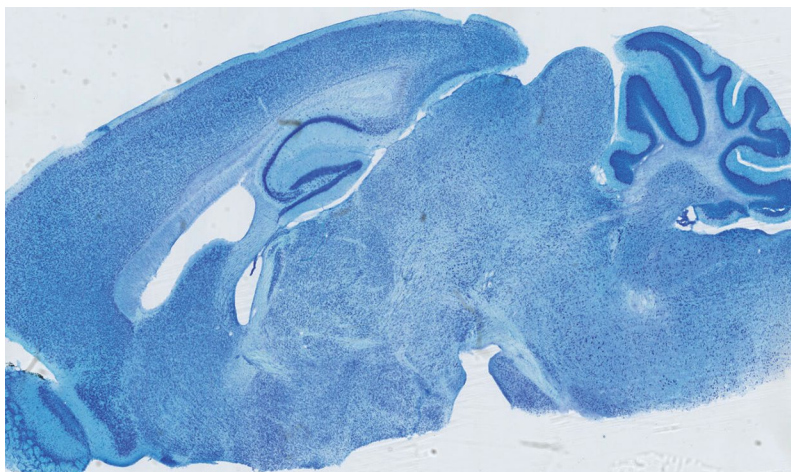
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INTRODUCTION: Vitamin E (α -tocopherol, α -T) restriction during brain development alters the expression of neurogenesis-related genes in cerebella of juvenile α -tocopherol transfer protein-null ($Ttpa^{-/-}$) mice. Synthetic α -T (SYN), compared to natural α -T (NAT), downregulates cerebellar myelin genes in adolescent $Ttpa^{-/-}$ mice. We studied how early-life exposure to SYN or NAT affects the expression of neurogenesis-related genes in juvenile $Ttpa^{-/-}$ mice.

METHODS: Male and female $Ttpa^{+/+}$ and $Ttpa^{-/-}$ mice were nursed by $Ttpa^{+/-}$ dams fed AIN-93G-based diets containing either SYN (~816 mg α -T/kg diet) or NAT (~600 mg α -T/kg diet). Homogenized brain tissues from 21 day old weanlings (n = 9/group) were used to measure total α -T concentrations via HPLC-PDA. The expression of genes critical for brain development (*Rora*, *Shh*), myelination (*Plp1*, *Cntnap1*, *Mbp*, *Mobp*, *Nr1h3*), and synaptic function (*Cplx1*, *Necab1*, *Prkcg*) were measured in the cerebellum via real-time qPCR.

RESULTS: α -T concentrations were significantly lower in brains of $Ttpa^{-/-}$ mice (17.7 nmol/g) compared to $Ttpa^{+/+}$ mice (37.5 nmol/g) ($P < 0.001$). Exposure to SYN vs. NAT resulted in similar total α -T brain levels within each genotype ($Ttpa^{-/-}$: 19.8 vs. 15.6 nmol/g; $Ttpa^{+/+}$: 42.5 vs. 32.6 nmol/g). Consistent with previous studies, *Necab1* was significantly downregulated in $Ttpa^{-/-}$ mice ($P < 0.05$). The other selected neurogenesis-related genes were similarly expressed between all groups, regardless of genotype or dietary α -T source.

CONCLUSIONS: Brain α -T concentrations at weaning depended on the presence of *Ttpa*. α -T source did not modulate the selected neurogenesis genes, possibly because the natural and synthetic α -T diets each provided sufficient total α -T during development.



Adult mouse brain stained with Methylene Blue/Azure II (sagittal section). This cell body stain will be one endpoint for our study comparing the effects of dietary natural versus synthetic vitamin E in the adult central nervous system. Research image by Katherine M. Ranard.

Resistance exercise does not up-regulate YAP expression in aged human skeletal muscle

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OBJECTIVES: Yes-Associated Protein (YAP) is implicated as a regulator of the post-exercise skeletal muscle response through mechanical transduction. We recently observed that resistance exercise (RE) increased both total (t) and phosphorylated (p) muscle YAP content, which correlated with extracellular signal-regulated kinase 1/2 (Erk1/2). Other anabolic signaling pathways (i.e. mTORC1) are known to be potentiated by the combined stimuli of RE and protein ingestion during post-exercise recovery. However, the impact of protein ingestion on t- and p-muscle YAP content during recovery from RE is unknown. Therefore, we aimed to determine the nutrient sensitivity of YAP in both an acute and chronic exercise setting in aging skeletal muscle.

METHODS: Acute study: 13 untrained older women (59.8 ± 0.5 y) were randomized to perform an acute bout of unilateral RE (3 sets \times 12 repetitions at 65% of one repetition maximum) followed by the ingestion of whey protein (0.3 g/kg lean body mass) or water. Muscle biopsies of both the rested and exercised legs were collected before and during the postprandial period. Chronic study: 20 untrained middle-aged men and women (47.5 ± 0.3 y) performed 3 weeks of whole body RE (3 d/wk) with moderate or high protein intake set at 1.2 g/kg/d or 1.6 g/kg/d, respectively. Muscle biopsies were taken weekly in the rested state. Total and phosphorylated YAP^{Ser127} and Erk1/2^{Thr202/Tyr204} were examined by western blotting.

RESULTS: Acute study: Protein ingestion decreased t- and p-YAP compared to the water condition in the non-exercised leg (main effect: $P < 0.04$). There was no change in t- or p-YAP, regardless of condition, in the exercised-leg throughout recovery ($P = 0.88$). There was no change in p/t ratio of Erk1/2 in the exercised or non-exercised leg. Chronic study: There was no change in either p- or t-YAP in moderate and high protein conditions throughout training (both, $P > 0.05$). There was a decrease in t-Erk1/2 irrespective of condition ($P = 0.04$). There was no change in p/t ratio of Erk1/2 throughout training. There was a significant correlation between t-Erk1/2 and t-YAP ($r = 0.741$ and $P < 0.001$).

CONCLUSION: Protein ingestion mediated an acute down-regulation of YAP in the postprandial-state. However, resistance training did not modulate YAP content in aged skeletal muscle tissue.

Can tomato powder reduce radiation-induced effects in a murine model of prostate cancer?

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INTRODUCTION: Tomatoes contain carotenoids and other potent antioxidants that may protect the surrounding tissue from the detrimental effects of external beam radiation therapy, while reducing rates of prostate carcinogenesis. The objective of this study was to determine whether dietary lyophilized tomato paste (TP) alters early inflammatory and oxidative events following a single dose of radiation and leads to a more successful therapeutic outcome.

METHODS: Male Transgenic Adenocarcinoma of the Mouse Prostate (TRAMP) mice ($n = 76$) were provided a powdered AIN-93G diet (Control) or a modified AIN-93G diet containing 10% TP (w/w) at 4 weeks of age. Mice were monitored by ultrasound for *in vivo* tumor detection and 3-D volumetric

measurement biweekly. Once tumors reached a volume of 1000 mm³, the caudal half of the mouse was irradiated with 7.5 Gy (Rad, n = 18-19 per diet) or 0 Gy (sham, n = 16-20 per diet) with a Cobalt-60 source. Mice were euthanized 24 hours after radiation or sham treatment. Antioxidants (carotenoids and α -tocopherol) were measured by high performance liquid chromatography (HPLC) in the serum, tumor, prostate, and liver. Sections of tumor, liver, kidneys, bladder, lymph, bladder and intestines were stained by hematoxylin and eosin (H&E) and cleaved-caspase 3 were assessed for radiation-induced changes and apoptosis. Inflammatory markers (C-reactive protein, IL-6, IL-17A, TNF α , IFN γ , and IL-10) were measured in serum, liver, prostate, tumor, and epididymal adipose tissues by ELISA.

RESULTS: This study is the first to explore the effects of TP on the tumor microenvironment following irradiation. Initial results suggest that TP consumption does not alter circulating or tissue (liver and prostate) concentrations of inflammatory markers (C-reactive protein, TNF α , IFN γ , IL-6, IL-17, or IL-10). We hypothesize that TP-Rad will maintain similar levels of circulating concentrations of antioxidants (carotenoids and α -tocopherol) compared to sham-treated mice. Additionally, we hypothesize that TP will reduce markers of cell damage in surrounding tissues.

CONCLUSIONS: This study will provide important preclinical data to inform future clinical trials evaluating approaches to lessen extra-prostatic damage from radiation therapy and thus improve therapeutic outcomes.

The impact of fresh Hass avocado on the fecal metabolome among adults with overweight and obesity: a randomized, controlled trial

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OBJECTIVE: Avocados are nutrient-rich fruits that have been recently linked to beneficial alterations to the gastrointestinal microbiota. However, previous research on shifts in the fecal metabolome with avocado intake has largely been conducted in *in vitro* or preclinical models and little is known about their metabolomic impact in human subjects.

METHODS: Adult participants (n = 109) 25-45 years of age with BMI \geq 25.0 kg/m² were enrolled in an investigator-blinded, parallel arm, randomized, controlled trial. Participants consumed isocaloric meals with or without fresh Hass avocado once daily for 12-weeks and reported \geq 80% meal consumption over the intervention period. Untargeted fecal metabolites were quantified in a subsample of participants (n=48) using gas chromatography mass spectroscopy and were normalized by sample weight. Kruskal-Wallis tests and false discovery rate type I error correction were conducted and orthogonal partial least squares discriminant analysis (OPLS-DA) was used to predict treatment group by fecal metabolite concentrations (RStudio, version 3.6.2).

RESULTS: A total of 292 metabolites were identified at intervention follow-up. Of these, three metabolites differed significantly between treatment groups. Fecal concentrations of lanosterol (p = 0.0004, q = 0.04) and the fatty alcohols hexadecanol (p = 0.001, q = 0.04) and octadecanol (p = 0.001, q = 0.04), were greater in the group consuming avocado as compared to control. Seventeen additional metabolites, including nine fecal lipids, two fat soluble vitamin derivatives, and three monosaccharides/disaccharides differed at p < 0.05 but did not meet the q < 0.05 threshold. Treatment group assignment was predicted correctly in 70% of cases (R² = 72%, Q² = 33%) using the trained OPLS-DA model.

CONCLUSIONS: Fresh Hass avocado intake increased fecal lipid and sterol concentrations among healthy adults with overweight and obesity, demonstrating diet-related modifications to the fecal metabolome.

Graduate Student Poster Session Abstracts

Fecal microbiota enterotypes of preterm infants at the neonatal intensive care unit (NICU) in association with dietary and clinical factors

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INTRODUCTION: The gut microbiota of preterm infants (PTI) differs from that of term infants, with higher abundances of pathogenic bacteria and late acquisition of beneficial bacteria. This dysbiosis is affected by different types of milk and milk fortifiers fed to PTI, exposure to antibiotics after birth, and long hospitalization periods. Different enterotypes have been proposed to classify the gut bacteria ecosystems in adults, but little data exists regarding the PTI gut microbiota. Thus, the objective herein was to investigate gut microbial enterotypes of PTI infants.

METHODS: PTI were followed from birth until NICU discharge. Data including daily feeding information and medications were obtained from the medical records. Freshly voided stool samples were collected, bacterial DNA was extracted and the V3-V4 regions of the 16S rRNA were sequenced. Enterotypes were determined using the partitioning around medoids clustering algorithm and the Jensen-Shannon divergence method using RStudio.

RESULTS: A total of 551 stool samples were collected from 97 PTI. At genus level, two enterotypes were obtained; enterotype A (EA) was characterized by a high abundance (62%) of *E. shigella* and *Staphylococcus*, whereas *Enterobacteriaceae*, *Clostridium sensu stricto 1* and *Klebsiella* accounted 55% of relative abundance for Enterotype B (EB). Alpha diversity (Shannon index) was higher ($p < 0.0001$) in EB. In the earliest sample collected after birth (2.2 ± 1.1 weeks of life), the majority of PTI (64%) belonged to EB, but 37% of PTI switched enterotypes during their hospital stay, most of these changed from EA to EB. The change on enterotypes occurred at 4.6 ± 2.7 weeks of life. Bovine milk-based fortifier (BMF) and abundance of *E. shigella* were positively associated in EA, whereas, this correlation was negative for EB. Similarly, *Enterobacteriaceae* abundance was positively correlated with the use of antibiotics in EA, but was negatively correlated in EB.

CONCLUSIONS: The gut microbiota of PTI was more likely to belong to a more diverse enterotype. There were opposite effects between both enterotypes to exposure to BMF and antibiotics. This suggests that responses to dietary and clinical factors could be dependent upon the characteristics of the gut microbiota of PTI.



SNAPSHOT FROM THE PAST

1999 Nutrition Symposium
at the University of Illinois

The role of liver in atherosclerosis regressionAsma'a Gh. Albakri¹ and J. Amengual^{1,2}¹ *Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL*² *Department of Food Science and Human Nutrition, University of Illinois at Urbana-Champaign, Urbana, IL*

INTRODUCTION: Atherosclerosis is characterized by the accumulation of proatherogenic lipoproteins such as low-density lipoproteins (LDL) in the arterial wall, which promotes macrophage infiltration and plaque development. This disease is the main cause of myocardial infarction, the leading cause of death worldwide. While the molecular mechanisms leading to atherosclerosis progression has been studied extensively, those implicated in atherosclerosis regression are poorly characterized. Most studies on atherosclerosis regression are focused on the resolution of the local inflammatory status of the plaque, but little is known about the role the liver plays in this process. Considering that the liver is responsible of the clearance of up to 70% of circulating LDL, we aimed to study whether the liver is involved in atherosclerosis regression. We hypothesize that hepatic function is required to promote atherosclerosis regression. The objectives of the current study are to determine the role of liver in atherosclerosis regression and the mechanistic pathways by which the liver enhance atherosclerosis regression.

METHODS: We will induce atherosclerosis in wild-type mice by injecting antisense oligonucleotide (ASO) targeting the LDL receptor (LDLR). After nine weeks, a subset of mice will be sacrificed (baseline), while the rest will undergo regression by injecting a single dose of the ASO LDLR antidote. Mice subjected to regression will be harvested at different time points to study the metabolic changes in regression compared to baseline. Flow cytometry, immunofluorescence, western blot, and qPCR will be applied to meet the objectives of the current study.

RESULTS: We expect to observe metabolic changes during atherosclerosis regression towards the resolution of systemic inflammation and LDL hepatic catabolism, overall contributing to the positive effects of atherosclerosis regression in the plaque.

Identifying the factors that hinder sustainable dietary modification and successful weight loss in obese adultNouf W. Alfouzan¹, A. Shaffer¹, M.H. Lee¹, S. Habib¹, M.T. Nakamura¹¹ *Department of Food Science and Human Nutrition, University of Illinois at Urbana-Champaign, Urbana, IL*

INTRODUCTION: The Individualized Diet Improvement Program (iDip) is a year-long, group session-based weight loss program to help participants experiment and discover a sustainable dietary modification. We observed a large difference among participants in weight loss success. The objective is to identify factors that explain the difference in weight loss magnitude among participants.

METHODS: 30 participants (enrolled in an ongoing iDip study). A self-reflection survey was designed and administrated at eight months to determine the factors that could account for the differential weight loss outcome. The survey consisted of 19 dietary implementation statements and 19 behavior change statements. A degree of dietary implementation was scored from 0 (Have not tried) to 3 (Well implemented). Difficulty in a behavior change was scored from 0 (Strongly agree) to 4 (Strongly disagree). The survey scores were compared between top and bottom tertile groups in weight loss success. Two-tailed t-test was used for statistical analysis.

RESULTS: 21 out of 24 remaining participants (25-70y) returned the survey. Mean weight loss of the top, middle, and bottom tertiles (n=7 each) was -14.8±2.9, -5.2±0.6 and -1.3±0.6 kg (mean±SEM) at eight months, respectively. The sum of dietary implementation statement scores in the bottom tertile group (14.5±1.2) was significantly lower (p<0.05) than that of the top tertile group (17.7±1.1). The score of the bottom tertile group was also significantly lower than that of the top tertile group in the following statements: exchanging protein sources for leaner options (2.00vs.2.86), selecting higher protein and fiber density foods (1.71 vs. 2.43), making meals high in protein and fiber (1.57 vs. 2.29), and finding staple food high in protein and fiber (1.86vs.2.57). No difference was

observed in the sum of behavioral statement scores between the two groups. Only one statement, “it is demotivating when seeing others losing weight”, was found significant among individual behavioral statements (bottom and top tertile groups, 3.1 and 3.7, respectively).

CONCLUSIONS: The survey indicates that the main obstacles to successful weight loss are difficulty in establishing meal routine and selecting foods high in protein and fiber per energy. In addition, lack of success in weight loss is likely to decrease motivation.

Determination of honey varieties' impact on *Bifidobacterium animalis ssp lactis* survivability in commercial yogurt through simulated *in vitro* digestion

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INTRODUCTION: Consumption of yogurt containing the probiotic strain *Bifidobacterium animalis lactis* DN-173 010/CNCM I-2494 (*Bifidus*) has been shown to improve digestive health and improve quality of life in adults. To optimize the benefits of this probiotic, we aimed to test our hypothesis that adding honey to commercial yogurt would increase the survivability of *Bifidus* under simulated gastrointestinal tract digestion conditions.

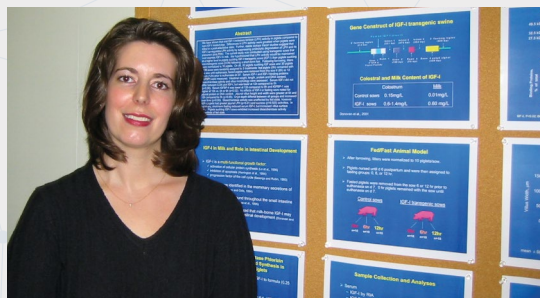
METHODS: Four honey varieties (alfalfa, buckwheat, clover, and orange) were added to a final concentration of 20% w/w in yogurt containing *Bifidus*. Undiluted yogurt and yogurt with added sucrose or water (20% w/w) were included as control treatments (all controls contained *Bifidus*). Yogurt samples were subjected to *in vitro* simulated oral, gastric, and intestinal phase digestion using simulated salivary, gastric, and intestinal fluids, respectively. At four time points—pre-digestion (baseline), and then after each phase of digestion (i.e., oral, gastric, and intestinal)—probiotic cells were enumerated first by spread plating on MRS agar and incubated for 5 h at 37°C under anaerobic conditions to allow *Bifidus* cells to recover. Then, plates were overlaid with MRS supplemented with lithium chloride and sodium propionate and incubated at 37°C for an additional 67 h prior to quantification of the probiotic colony forming units (CFU).

RESULTS: Similar probiotic counts were observed in yogurt samples with honey, regardless of varieties, and controls after exposure to oral and gastric simulated fluids (<1 Log CFU/g of probiotic reduction after gastric phase). There was comparable probiotic survival after the simulated intestinal phase for yogurt with the alfalfa, buckwheat, and orange honey varieties relative to control yogurt treatments. However, significantly higher *Bifidus* survivability was observed in yogurt with clover honey after exposure to simulated intestinal fluids (~3.5 Log CFU/g reduction) compared to undiluted yogurt, sucrose added yogurt, and water added yogurt (~5.5 Log CFU/g reduction, $P < 0.05$).

CONCLUSIONS: These results demonstrated that clover honey increased *Bifidus* survivability in commercial yogurt during *in vitro* digestion. Further study is needed to determine the optimal dose of clover honey *in vitro*, as well as to determine if these effects translate *in vivo*.

SNAPSHOT FROM THE PAST

Dr. Jessica Hartke at the 2003 Nutrition Symposium at the University of Illinois



Diet quality and the fecal microbiota in healthy adults in the American Gut Project

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INTRODUCTION: The human gastrointestinal microbiota contributes to the relationship between diet and health via microbial metabolism of undigested food components. Thus, it is valuable to understand the relations between gut microorganisms and diet quality. Herein, we examined the associations between compliance to the Dietary Guidelines for Americans, as measured by the Healthy Eating Index (HEI) 2010 scores, and the fecal microbiota in a subset of healthy adults in the American Gut Project cohort.

METHODS: This was a cross-sectional observational study of healthy adults ($n=1,573$ (984 females); BMI: 18.5-29.9 kg/m²; 20-90 years of age) from the American Gut Project cohort who provided a stool sample and completed a Food Frequency Questionnaire (FFQ; VioScreen). Fecal samples were processed using Earth Microbiome Project protocols. Briefly, DNA was extracted from the stool samples and the V4 region of the 16S rRNA gene was amplified and sequenced. Taxonomies were determined using Greengenes 13_8. HEI-2010 scores were calculated by VioScreen, and for the purposes of this study, further divided into tertiles. Bacterial genera that were present in at least 50% of the cohort were assessed. Bacterial relative abundances between high and low tertiles of HEI total score were compared using the Mann-Whitney test. Corrections for multiple comparisons were made using a false discovery rate of 5%.

RESULTS: Greater abundances of the genera *Faecalibacterium*, *Coprococcus*, and *Lachnospira* were detected among participants within the highest HEI total score tertile ($q<0.03$). Alternatively, the relative abundances of *Bacteroides*, *Alistipes*, *Bilophila*, and *Collinsella* were greatest among those with the lowest HEI total score ($q<0.03$).

CONCLUSIONS: These results reveal that higher HEI-2010 total scores were associated with greater abundances of SCFA-producing microorganisms but inversely associated with bile-tolerant taxa. Ongoing analyses include further examination of relations between the 12 different components of the HEI-2010, as well as examining differences among demographic groups.

Gardening and the human gut microbiota

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INTRODUCTION: Urbanization has reduced environmental microorganism exposure, with most Americans spending over 90% of their time indoors. However, gardening remains a viable means of exposure to soil microorganisms and harvesting of edible produce. Accordingly, we aimed to determine relations between gardening, dietary habits, and gut microbiota.

METHODS: Gardening families (GDN; N=10) and non-gardening families (CON; N=9) were enrolled in a case-controlled cohort study. Families included two adults (one adult gardener in the GDN families) and one child (5-18 yr) for a total of 54 participants. Fecal samples were collected prior to (PRE) and at the end of the gardening season (POST). PRE and POST soil samples (N=9) were collected from where the gardening families planted and harvested produce. PRE and POST Healthy Eating Index (HEI) scores were calculated from diet history questionnaires. Fecal and soil DNA were extracted, sequenced (V4 region of 16S rDNA gene), and analyzed using DADA2 and QIIME2.

RESULTS: Fecal observed operational taxonomic units (OTUs) were highest in GDN POST participants, followed by GDN PRE, CON POST, and CON PRE; however, differences were not statistically significant ($P = 0.2$). Collapsing PRE and POST timepoints together to test differences between GDN and CON revealed that GDN had more observed OTUs than CON ($160 + 38.9$ vs. $148 + 52.6$, $P = 0.04$); unweighted UniFrac distances also differed between GDN and CON ($t=2.2$; $P=0.003$). Bifurcating GDN into those that gardened for > 5 yr or < 5 yr revealed differences in observed OTUs ($P = 0.03$) and unweighted UniFrac distances ($P = 0.002$). Prior to the gardening season, GDN participants had greater HEI scores than CON ($57 + 9.1$ vs. $49 + 8.8$, $P = 0.03$). HEI scores were not different between GDN and CON groups at the end of the study.

CONCLUSIONS: Alpha- and beta-diversity measures of the gut microbiota differed between GDN participants and CON participants. Differences were also observed between GDN participants that had a longer versus shorter history of gardening. These results suggest that environmental influences on the gut microbiota may occur over multiple gardening seasons. Further research is required to understand the role of diet and if soil microbes can be found within the gastrointestinal tract.

Understanding the sex-specific role of Farnesoid X Receptor in heme biosynthesis

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INTRODUCTION: Dysregulation of heme biosynthesis can result in porphyrin accumulation, as well as buildup of the micronutrient iron. Heme is a vital prosthetic group for hemoglobin, myoglobin, and cytochromes. Nuclear receptor, Farnesoid X Receptor (FXR), regulates bile acid homeostasis, glucose and lipid metabolism, and has been shown to promote a liver regenerative response. With FXR having many metabolic roles, we wanted to understand its role in heme biosynthesis in both males and females.

METHODS: Male and female WT and Farnesoid X Receptor knockout (*Fxr*KO) mice were treated with 3,5-diethoxycarbonyl-1,4-dihydrocollidine (DDC, a heme biosynthesis disruptor) for two weeks to examine the role FXR plays in heme metabolism. Mice were fasted prior to tissue collection. The liver and serum were analyzed for signs of tissue damage and changes in expression of genes associated with heme biosynthesis and liver proliferation.

RESULTS: The DDC diet led to liver injury as measured by elevated serum ALT and AST levels in both control and *Fxr*KO mice. Furthermore, accumulation of bile plugs and ductular reaction was visible in the WT mice, whereas both histological hallmarks were dramatically reduced in *Fxr*KO mice. Despite similar histology, the proliferative response in the hepatocytes were different between both the sexes of *Fxr*KO animals. Loss of *Fxr* resulted in increased hepatocyte size and low-grade Ki-67 positive hepatocyte nuclei even under basal conditions. But upon DDC challenge, *Fxr*KO female livers displayed a dramatic induction of Ki-67 positive staining even though minimal bile duct injury was visible. This finding correlated well with increased expression of cyclins. On the contrary, Ki-67 staining was comparable between male *Fxr*KO livers fed either chow or DDC diet, which matches with lower injury. We are actively investigating the crosstalk of estrogen signaling with FXR in controlling liver proliferation. At the molecular level, genes regulating the cell cycle (*Ccnd1*, *Ccna*, *Ccnb1*) were induced upon injury in the male livers in an *Fxr*-dependent manner, whereas this response was not observed in female livers. To test if the absence of bile plugs in *Fxr*KO mice is secondary to reduced heme synthesis in these livers, we examined the heme biosynthetic pathway. In collaboration with Dr. Martin Wagner's lab, we found strong *Fxr* occupancy and binding to genes involved in the heme synthesis pathway including *Alas1*, which is the rate-limiting step in heme biosynthesis.

CONCLUSIONS: In summary, FXR may regulate heme metabolism and modulate hepatocyte proliferation in a sex-specific manner.

Early life factors predictive of weight status in 2 year-olds

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OBJECTIVES: The extent to which early life factors predict weight status by age two is unclear. This study elucidated early life factors predictive of BMI-for-age z-score (MN24 BMI) in 2-year-olds in the ongoing STRONG Kids 2 longitudinal study.

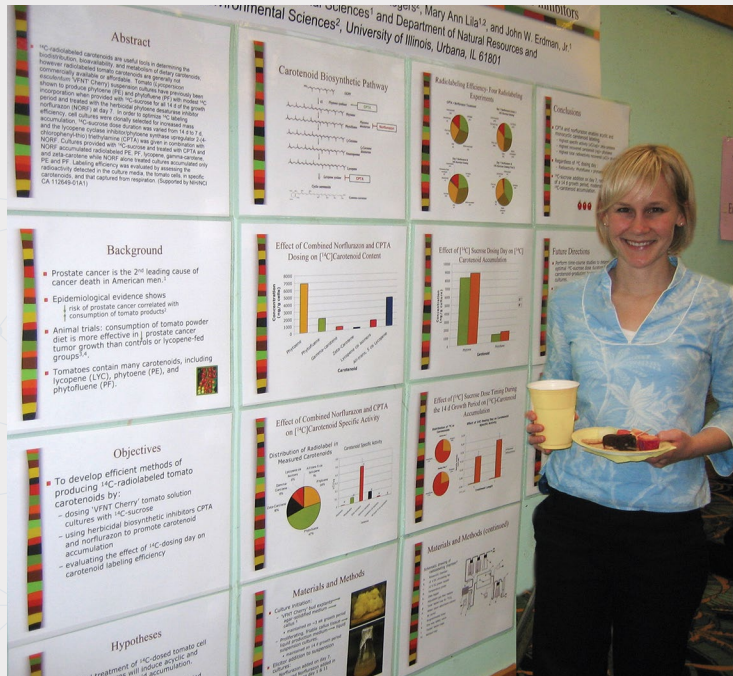
METHODS: At registration, 6 weeks, 3, 12, 18, and 24 months, parents (N=126) completed online surveys (questions derived from CDC Infant Feeding Practices questionnaire, Short Form of the MOS Health survey, and Block Kids Food Frequency Questionnaire (Ages 2-7; Nutrition Quest) for diet MN21-24). Height and weight were collected at home visits. Child BMI-for age z-scores were based on WHO growth standards, and dietary patterns at MN24 were derived by principal component analysis (PCA). Mode of delivery (i.e., vaginal or caesarean), timing of introduction to solids, dietary patterns, child's BMI z-score and feeding methods (i.e., exclusive formula or breastfeeding, or both), and maternal weight were obtained. Multiple regression modelling determined the explanatory power of these factors on MN24 BMI.

RESULTS: Modelling revealed a significant regression equation ($p < .001$), with an R^2 of .359. MN12 BMI-for-age z-score (MN12 BMI) ($\beta = .555$, $p < .001$) explained 31.2% of the variance in MN24 BMI. Child feeding method at MN3 ($\beta = -.218$, $p = .003$) accounted for 4.7% of the variance in MN24 BMI.

CONCLUSIONS: Children with a greater MN12 BMI have a higher MN24 BMI, while those who undergo breastfeeding at MN3 have a lower MN24 BMI. Future studies will expand on these findings by examining if the predictive power of these early life factors on BMI persists in later life.

SNAPSHOT FROM THE PAST

Dr. Nancy Engelmann at the 2007 Nutrition Symposium at the University of Illinois



Endocannabinoid dysregulation in multiple sclerosis

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INTRODUCTION: Multiple Sclerosis (MS) is a neurological disease that results in the damage of the protective myelin sheath surrounding neurons in the central nervous system (CNS). Patients with MS often develop symptoms such as optic neuritis, spasticity, and neuropathic pain due to the relapse-remitting nature of the disease. While increased consumption of omega-3 fatty acids are associated with reduced instance and progression of multiple sclerosis, there is a lack of knowledge of how levels of omega-3 derived endocannabinoids change during disease progression, and their mechanism of action. Therefore, we investigated the changes of all omega-3 derived metabolites through each stage of disease progression (onset, peak, remission, relapse) in relevant *in vivo* model of MS in mice, and the mechanism by which these omega-3 metabolites act on immune cells to reduce neurodegenerative inflammation.

METHODS: We induced a relapse-remitting model of MS in SJL mice (N=30). Recently, our group showed that downstream metabolites of omega-3 polyunsaturated fatty acid, docosahexaenoic acid, increases anti-inflammatory cytokines while decreasing pro-inflammatory cytokines. Therefore, we administered vehicle and docosahexaenoyl ethanolamide via daily intraperitoneal injections. Daily monitoring of weight and clinical scores were assessed in a double blinded manner. Upon termination of the experiment, splenocytes were cultured for stimulation and treatment with downstream metabolites of DHA. Moreover, as T-cells play a critical role in progression of multiple sclerosis, we conducted stimulations and treatments on splenocytes overexpressing T-cell receptors. To determine the effect of DHA metabolites on inhibiting activation of splenocyte cultures, we measured IFN γ production by ELISA, and conducted flow cytometry to assess the specific mechanisms by which DHA metabolites inhibit activation of splenocytes, similar to that of MS.

RESULTS: We have identified an inverse correlation of anti-inflammatory omega-3 derived metabolites in the central nervous system with each stage of disease progression (onset, peak, remission, relapse). Furthermore, we have identified that precursor to omega-3 metabolites including omega-3 endocannabinoids, can inhibit severity of MS at peak disease. Of note, certain moieties present on endocannabinoids appear critical for inhibition of IFN γ production by splenocytes, a pro-inflammatory cytokine produced as a result of T and B-cell activation. Since splenocytes contain a mixture of immune cells, we have profiled the effects of endocannabinoid epoxides on individual immune cells, including antigen-presentation, and inhibition of cytokine and chemokine production.

CONCLUSIONS: This study helps identify how DHA elicits its beneficial health effects. Furthermore, we unearth a potential mechanism by which omega-3 fatty acids and metabolites reduce inflammation and neurodegenerative disease progression.

Advising based on self-experimentation assignments increases the magnitude of weight loss**Mindy H. Lee**¹, A.L. Shaffer¹, N. Alfouzan², C.C. Applegate¹, J. Hsu-Lumetta^{1,3}, J.W. Erdman Jr.^{1,2}, M.T. Nakamura^{1,2}¹ *Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL*² *Department of Food Science and Human Nutrition, University of Illinois at Urbana-Champaign, Urbana, IL*³ *Carle Illinois College of Medicine, Urbana, IL*

INTRODUCTION: Individualized Diet Improvement Program (iDip) has been developed to help participants develop a sustainable diet for weight loss and maintenance through self-experimentation with a primary focus on increasing protein and fiber and reducing calorie intake. Upon a successful feasibility test with the first study completed in 2018 (iDip 1), we hypothesized that assigning homework at each session and providing advice based on their submitted homework would improve weight loss along with the dietary changes.

METHODS: Thirty adults (BMI>25 kg/m²) were enrolled in a 1-year before and after study design with an additional 12 months follow up (iDip 2). The study comprised of 19 diet improvement group sessions and 3 individual counseling sessions over 12 months, identical to iDip 1. In iDip 2, participants were assigned to complete a self-experimentation homework after each session and received advising based on responses. Visual feedbacks were provided including weekly weight charts and dietary analyses in the form of Protein-Fiber (PF) plot. Daily weights were collected via WiFi scale, body composition and waist circumference were measured at baseline and 6 months, and 24-hour dietary records were obtained periodically. An unpaired t-test was used for statistical analysis.

RESULTS: During the first 8 months, 6 participants dropped out, leaving 24 participants (80%) in the study. Mean body weight change (n=24) in iDip 2 at 8 months was $-6.2 \pm 1.5\%$ while mean body weight change (n=12) in iDip 1 was $-5.2 \pm 1.1\%$. Among the 24 participants in iDip 2, 9 (38%) achieved clinically meaningful weight loss (>5% of initial body weight) with a mean body weight change of $-12.9 \pm 2.8\%$. Out of these 9 participants, 2 reached their healthy target weights (BMI<25 kg/m²). The magnitude of weight loss of the successful group in iDip 2 was significantly greater ($p<0.05$) than that of the successful group in iDip 1 where 5 out of 12 participants (42%) achieved >5% weight loss with a mean body weight change of $-8.9 \pm 1.3\%$. Skeletal muscle mass was well-maintained with a mean change (n=18) of $-0.7 \pm 0.2\%$ at 6 months. Waist circumference (n=18) was significantly decreased ($p<0.05$) from baseline by $-6.5 \pm 1.3\text{cm}$ (n=18). 24-hr records showed improvements in protein and fiber intake throughout the study. Although no significant differences were found in protein and fiber intake between iDip 1 and iDip 2, higher mean protein and fiber intake was observed at 6 months in iDip 2.

CONCLUSIONS: Incorporating self-experimentation assignments at each session followed by individualized feedback significantly increased the magnitude of weight loss over the previous study with sufficient protein intake to prevent skeletal muscle mass loss as evidenced by its minimal loss. The success rate of participants achieving >5% weight loss did not improve in this study.

Dietary cholesterol affects the pathogenesis of influenza A virus infection in mice**Allison Louie**¹, L. Wetzel², K. Soto-Diaz³, E. Dray², D. McKim^{1,2,3}, A. Steelman^{1,2,3}¹ *Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, Illinois*² *Department of Animal Sciences, University of Illinois at Urbana-Champaign, Urbana, Illinois*³ *Neuroscience Program, University of Illinois at Urbana-Champaign, Urbana, Illinois*

INTRODUCTION: Influenza is one of the most prevalent and devastating infectious diseases in the world. But it is unclear how host factors may function to increase disease susceptibility or severity. Here, we sought to determine the role of dietary cholesterol in modulating the immune response or altering viral activity during influenza A infection.

METHODS: A pilot experiment indicated mice fed a 2% cholesterol diet prior to inoculation with mouse-adapted human influenza A virus (Puerto Rico/8/1934 H1N1; 1 HAU) exhibit greater morbidity compared to controls fed an energy density-matched diet. To confirm these data, 5-week-

old C57Bl/6 mice were fed either standard rodent diet or matched diet with 2% cholesterol for 5 weeks, then inoculated intranasally with either saline or flu (0.7 HAU). The effect of diet on circulating leukocytes was determined by flow cytometry. Serum cholesterol was measured by ELISA. Viral load and pathology were quantified by RTqPCR and immunohistochemistry. Finally, serum virus-neutralizing antibody levels were evaluated by haemagglutination inhibition.

RESULTS: As observed previously, infected cholesterol-fed mice exhibited greater weight loss than diet matched controls. Total plasma cholesterol did not differ between diet groups. Infection increased the percentage of circulating granulocytes and decreased that of B cells at day 4 post-infection (p.i.). In contrast, diet did not affect circulating leukocytes. The amount of viral RNA at day 8 p.i. as well as serum neutralizing antibody levels were not affected by diet.

CONCLUSIONS: Taken together, these data suggest dietary cholesterol affects the pathogenesis of influenza infection but prompt further study into better understanding the mechanism.

Screen time is related to dietary intake in children at 24-months-of-age

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INTRODUCTION: Screen time throughout childhood is positively related to anthropometric measures, mediated partially through its impact on diet quality. Existing literature lacks specific data for 24 months (24MN) children and focuses primarily on television screen time rather than all sources of screen time (smart phones, tablets, and video streaming services). Thus, we explored the relationship between screen device usage and diet quality at this early age.

METHODS: Parents and 24MN children ($N= 396$) were recruited from the STRONGKids 2 cohort study. Data included parent and child anthropometric measurements, physical activity time (Sports, Play, and Active Recreation for Kids Survey), dietary intake (Block Food Frequency Questionnaires), and the types and duration of screen time usage by the child (Common Sense Media Survey). Calories from macronutrients, sweets, added sugar, dietary fiber, and fruit and vegetable consumption were used to assess diet quality.

RESULTS: 26% of children exceeded the Academy of Pediatrics Guidelines of <2h screen time per day. TV, DVDs, and shows on cellphones accounted for 79% of child screen time. 26% of children were overweight or obese, although BMI z-score at 24 MN was not related to screen time, physical activity time, or diet factors. Parent and child diet quality were related. However, independent of parent diet, education, ethnicity, gender, and BMI, total screen time was associated with kcal consumed through sweets ($r=0.147$, $p=0.014$), added sugar intake in grams ($r=0.137$, $p=0.023$), and fruit consumption ($r= -0.235$, $p<0.001$). Passive screen use (TV, DVDs, shows on a cell phone or computer) was associated with total kcals ($r= 0.127$, $p=0.036$), kcals from sweets ($r=0.137$, $p=0.023$) and added sugar intake ($r=0.138$, $p=0.022$), and fruit ($r=-0.260$, $p<0.001$) and vegetable consumption ($r= -0.119$, $p=0.049$). Active screen use (playing games on a console, computer, cell phone, or other handheld device) was related to percent fat intake ($r=-0.119$, $p=0.048$).

CONCLUSION: Total and passive screen time at 24 MN are associated with factors indicative of poor diet quality, which could negatively impact child health.



SNAPSHOT FROM THE PAST

Winners of the 2011 University of Illinois Nutrition Symposium poster and oral competitions with keynote speaker, Dr. Brian Wansink

Dietary supplementation with a low dose of finasteride does not alter the lipid profile of *Ldlr*-deficient mice

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INTRODUCTION: Androgenic alopecia is characterized by a receding hairline and hair loss from the frontal scalp. This genetic condition affects approximately 80% of men and 42% of women. Finasteride is the only oral treatment currently approved by the FDA to prevent and treat androgenic alopecia, and it is currently prescribed to over nine million males in the US. Recent claims suggest that long-term use of finasteride could have detrimental health effects by affecting the lipid profile in people. Finasteride prevents the conversion of testosterone to its active metabolite dihydrotestosterone by inhibiting the type II 5 α -reductase, which is predominantly present in the hair follicle and the prostate. As a result, finasteride alters the systemic levels of testosterone and its derivative estradiol. Hormone homeostasis affects plasma lipid levels, therefore we hypothesize that supplementation with finasteride will affect systemic lipid profile in atheroprone low-density lipoprotein receptor (*Ldlr*^{-/-}) mice fed a Western diet (high cholesterol, high fat).

METHODS: We fed six-week-old male *Ldlr*^{-/-} mice (10/group) a Western diet (control) or a Western diet supplemented with 10 mg Finasteride/kg diet for 12 weeks. We monitored body weight progression and food intake during the entire experiment. A week before harvesting the tissues, mice were fasted overnight to perform a glucose tolerance test. At the moment of sacrifice, final body weight and several tissues were collected such as the inguinal, retroperitoneal, and gonadal adipose tissues, skeletal muscle (gastrocnemius), and liver. Plasma was harvested to determine total cholesterol and triglyceride levels.

RESULTS: Our data show that 12-week supplementation with a low dose of finasteride does not have a significant impact on food intake, body weight, or adiposity index. We did not observe any significant change in plasma lipids or glucose tolerance.

CONCLUSIONS: A low dose of finasteride supplemented for 12 weeks does not alter the lipid profile in the atheroprone *Ldlr*^{-/-} mouse model, nor alters adiposity index. These data indicate that finasteride does not have detrimental effects on these metabolic parameters.

Food systems, climate change, and food waste: Knowledge, attitudes and beliefs among middle school students

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INTRODUCTION: While the food system is a major contributor to climate change, waste reduction is one of the top three recommendations to keep the food system within environmental limits. Consumers, however, are responsible for the largest share of food waste in developed countries, and their attitudes and beliefs about food and the environment influence their eating and wasting behaviors. Currently, little is known about the knowledge, attitudes, and beliefs of middle school students regarding topics of the food system, climate change, and food waste.

METHODS: The purpose of this research is to establish baseline data on student's knowledge, attitudes, and beliefs about the food system, food waste, climate change, stewardship, and an underpinning of the Self Determination Theory: relatedness. These baseline measures were collected prior to starting a food systems education intervention, Healthy Planet, Healthy Youth (HPHY). Measures were collected in Advancement by Individual Determination (AVID) classes at two public middle schools in central Illinois (n=68, ages 10-12 years) using a validated student survey. The HPHY intervention is a non-randomized cluster-controlled trial designed to inform students of the food system and environment to change beliefs, behaviors, and knowledge related to food, the environment, and waste habits. Descriptive statistics were ran using survey results and participant demographics.

RESULTS: The majority of students find themselves throwing away their uneaten food from school lunch (60%) versus when they eat at a restaurant (8%). Likewise, students are more inclined to share or save unwanted food if it is from a restaurant (75%) than if it is from school lunch (19%). Students who identified as white had significantly higher knowledge scores on climate change and combined knowledge related to farming, natural resources, and food waste, transportation, and processing. They also had significantly higher stewardship scores.

CONCLUSIONS: Students conserve food differently based on their dining setting. Gaps in knowledge and beliefs about the environment and food system exist across student racial groups.



Photos courtesy of Ana Mitchell, Laboratory of Dr. Melissa Pflugh Prescott. Pre and post tray photos taken at a local Champaign middle school as part of Ana Mitchell's project looking at cafeteria plate waste, and student selection and consumption during school lunch.

Effects of salmon ingestion on post-exercise muscle protein synthesis: exploration of whole protein foods versus isolated nutrients

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INTRODUCTION: Healthy eating patterns consist of eating whole foods as opposed to single nutrients. The maintenance of skeletal muscle mass is of particular interest to overall health. As such, there is a need to underpin the role of eating nutrients within their natural whole-food matrix versus isolated nutrients on the regulation of postprandial muscle protein synthesis rates. This study assessed the effects of eating salmon, a potential food within a healthy Mediterranean style eating pattern, on the stimulation of post-exercise muscle protein synthesis rates versus eating these same nutrients in isolation in healthy young adults.

METHODS: In a crossover design, 10 recreationally active adults (24±4 y; 5 M, 5 F) performed an acute bout of resistance exercise followed by the ingestion of salmon (SAL) (20.5 g protein and 7.5 g fat) or its matched constituents in the form of crystalline amino acids and fish oil (ISO). Blood and muscle biopsies were collected at rest and after exercise at 2 and 5 h during primed continuous infusions of L-[ring-²H₅]phenylalanine for the measurement of myofibrillar protein synthesis and plasma amino acid profiles. Data were analyzed by using a 2-factor (time × condition) repeated-measures ANOVA with Tukey's post hoc test.

RESULTS: Plasma essential amino acid concentrations increased to a similar extent in both SAL and ISO during the postprandial period ($P>0.05$). Likewise, postprandial plasma leucine concentrations did not differ between nutrient condition ($P>0.05$). The post-exercise myofibrillar protein synthetic responses were similarly stimulated in both nutrition conditions early (0-2 h; 0.079±0.039 %/h (SAL) compared to 0.071±0.078 %/h (ISO); $P=0.64$) and returned to baseline later (2-5 h; 0.046±0.020 %/h (SAL) compared to 0.038±0.025 %/h (ISO); $P=0.90$). Similarly, there were no differences in the stimulation of myofibrillar protein synthesis rates between SAL and ISO during the entire 0-5 h recovery period (0.058±0.024 %/h compared to 0.045±0.027 %/h, respectively; $P=0.66$).

CONCLUSION: We show that the ingestion of salmon or its isolated nutrients increases plasma amino acid concentration and enhances the stimulation of post-exercise muscle protein synthesis rates with no differences in the temporal or cumulative responses in healthy young adults.

SNAPSHOT FROM
THE PAST

Winners of the 2014 University of Illinois Nutrition Symposium poster and oral competitions with keynote speaker, Dr. David Levitsky



Retinoic acid induces catabolic pathways in M2-like macrophages

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INTRODUCTION: Macrophages are the primary cell type involved in atherosclerosis, an inflammatory condition that leads to cardiovascular disease. The plasticity and diversity of these cells upon certain cytokine stimulation has led to its characterization as M1-like and M2-like macrophages. It has been hypothesized that M1 macrophages are pro-atherogenic, whereas M2 are considered anti-inflammatory and contribute to resolving atherosclerosis. Therefore, strategies to increase the balance of M2 macrophages entails promising candidates to promote atherosclerosis regression. Retinoic acid, the active form of vitamin A, modulates lipid metabolism and inflammation, which are hallmarks in the onset of atherosclerosis. We hypothesize that macrophages differentially respond to retinoic acid exposure depending on their polarization status, impacting their phenotype.

METHODS: Bone marrow-derived macrophages were polarized to M1 and M2 phenotypes after 24 hours incubation with LPS and INF γ or IL-4, respectively. Unstimulated macrophages (M0) were included as a control of the polarization status. After polarization, macrophages were incubated with 1 μ M retinoic acid for 6 hours or DMSO (vehicle control) before RNA isolation and sequencing.

RESULTS: Transcriptome analysis revealed that retinoic acid exposure significantly regulated ~6 times more genes in M2 macrophages compared to the M1 phenotype. Over 950 genes were exclusively regulated by retinoic acid in M2-polarized macrophages. We performed unbiased pathway analyses of the genes regulated by retinoic acid on each polarization status using the Metascape website. These results showed that retinoic acid preferentially regulates catabolic pathways in M2 macrophages, but not in M0 and M1, suggesting a polarization-specific effect of retinoic acid on macrophages.

CONCLUSION: Based on our preliminary data, M2 macrophages are more susceptible to retinoic acid than those polarized towards M0 and M1. Pathway analyses indicate that retinoic acid presumably increases the ability of M2-macrophages to degrade intracellular material, which could have a positive impact in atherosclerosis resolution. To confirm our hypothesis, we will perform functional assays both *in vitro* and *in vivo* to determine whether retinoic acid enhances the M2 phenotype, which would be contributing to restore the M1/M2 balance and delays atherosclerosis progression.

Increased protein density during weight loss is correlated with reduced abdominal obesity and body mass index and improved body composition

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OBJECTIVES: There is a clear link between abdominal obesity and chronic diseases. Dietary changes leading to substantial weight loss reduce obesity and improve health; however, no viable dietary treatment program exists that produces clinically significant, cost-effective, and sustainable weight loss. To test the hypothesis that a diet dense in lean proteins and fiber is inversely associated with abdominal obesity while maintaining skeletal muscle mass (SMM), we evaluated the correlation between mean protein and fiber density and changes in BMI, waist circumference and SMM during weight loss.

METHODS: Thirty adult males and females participated in this ongoing, 2-year dietary weight loss program. The Individualized Dietary Improvement Program focused on reducing caloric intake and increasing protein (7-11 g/100kcal) and fiber (1.8-3.2 g/100kcal) density to desired ranges. Participants attended 19 group educational sessions, 3 individual counseling appointments, self-weighed daily, and submitted monthly 24-hour dietary recalls. BMI, waist circumference and body composition (InBody) measurements were collected at baseline and after 6 months.

RESULTS: At 6 months, 25 participants (24-70y) remained in the study with 18 completing all body measurements. Mean weight loss (n=25) was -2.2 ± 0.5 BMI points ($-5.2 \pm 1.3\%$ of initial body weight) and mean waist circumference reduction (n=18) was -6.5 ± 1.3 cm from baseline. Significant increases in protein and fiber density were seen from baseline to month 2 ($p < 0.05$). There were direct inverse associations between mean protein density and both reduced waist circumference ($p < 0.01$) and reduced BMI ($p < 0.01$). Fiber intake had no significant impact on weight loss, and maintenance of SMM did not significantly correlate with mean protein density. However, only $11.0 \pm 3.2\%$ of weight lost was due to the loss of SMM, supporting the efficacy of the program. A significant positive correlation ($p < 0.01$) existed between fat mass loss and protein density, with $74.3 \pm 4.7\%$ of excess body fat accounting for total weight lost.

CONCLUSIONS: Increased protein density correlates with accelerated loss of fat mass, greater reductions in abdominal adiposity, and may protect SMM from degradation during weight loss.



SNAPSHOT FROM THE PAST

Dr. Bridget Hannon (right) at the 2017 Nutrition Symposium at the University of Illinois

The impact of almond and walnut consumption on the human fecal metabolomeLeila M. Shinn¹, A. Mansharamani², Y. Li^{3,4}, R. Zhu^{3,4}, J.A. Novotny⁵, D.J. Baer⁵, H.D. Holscher^{1,4,6}¹ *Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL*² *Department of Computer Science, University of Illinois at Urbana-Champaign, Urbana, IL*³ *Department of Statistics, University of Illinois at Urbana-Champaign, Urbana, IL*⁴ *National Center for Supercomputing Applications, University of Illinois at Urbana-Champaign, Urbana, IL*⁵ *United States Department of Agriculture - Agricultural Research Service, Beltsville Human Nutrition Research Center, Beltsville, MD*⁶ *Department of Food Science and Human Nutrition, University of Illinois at Urbana-Champaign, Urbana, IL*

INTRODUCTION: Metabolomic studies can be utilized to generate biomarkers of food intake. Undigested food components affect the gut microbiota, including the fecal metabolome. Accordingly, we aimed to identify fecal metabolites unique to almond and walnut consumption.

METHODS: Untargeted metabolomic analyses were completed on 66 endpoint fecal samples from two separate 3-week randomized, controlled-feeding, crossover studies examining almond (n=30) and walnut (n=36) consumption in adults (25-75 yr). Control diets were fed at weight maintenance, consisting of an identical base diet representative of the typical American diet with 0 g/day of nuts. During the treatment conditions, the base diet was scaled down to allow isocaloric inclusion of 42 g/day of almonds or walnuts. The Kruskal-Wallis H test was used to determine statistically significant metabolites between treatment and control groups. Type I errors were accounted for using Benjamini-Hochberg false discovery rate adjustments.

RESULTS: Fecal metabolomic analyses revealed 318 quantifiable metabolites. Of the 318 metabolites, 42 were significantly different when comparing the treatment groups to their respective controls after adjustment ($q < 0.05$). Of these 42 metabolites, 9 were significantly different in both the almond and walnut treatment samples. Two metabolites, palmitoleic acid and p-cresol, were unique to almonds—the relative concentration of palmitoleic acid was higher in the almond group compared to control, whereas p-cresol was lower in almond compared to control. Walnut treatment samples contained 31 unique metabolites, including 15 fatty acyls, the majority of which were higher in the walnut group compared to control.

CONCLUSIONS: Higher concentrations of fecal fatty acyls in the almond and walnut groups compared to their respective controls are supportive of previous findings that the plant cell walls of nuts reduce digestibility, therefore, limiting accessibility of intact lipids. Overall, these results reveal promise in identifying fecal biomarkers of food intake for eventual use in microbiota-tailored dietary recommendations. Ongoing analyses include utilizing machine learning models to further biomarker panel development.

