2017 NUTRITION SYMPOSIUM

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Nutritional Sciences Graduate Student Association

University of Illinois
at Urbana-Champaign
Division of
Nutritional Sciences

ILLINOIS 150
1867-2017

April 19, 2017

Welcome

On behalf of the Nutritional Sciences Graduate Student Association (NSGSA), Division of Nutritional Sciences (DNS), and all participating presenters, we would like to welcome you to the 2017 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 the NSGSA, the symposium offers students within the DNS and related disciplines on campus an opportunity to present their nutrition research. This symposium offers a first glance at exciting research in the areas of metabolic regulation, cancer, gastrointestinal physiology, immunology, physical activity, public health, and bioactive plant compounds. Students will be traveling and presenting at a variety of conferences, including Experimental Biology and meetings of the American Society of Animal Sciences.

This year, the NSGSA is honored to have Dr. Teresa Davis deliver the keynote address, "Role of Nutrition in the Regulation of Muscle Protein Synthesis and Lean Growth in the Neonate." Dr. Davis will discuss the current understandings of protein synthesis. Particularly, she will focus on the stimulatory effect of feeding on protein synthesis and how timing of nutrient delivery can modulate this. Further, she will discuss her use of the young pig as an animal model to elucidate these underlying mechanisms.

Additionally, the NSGSA is proud to highlight the work of world-class faculty members through a mini-symposium. This year's presentations address protein and its dynamic role in modern nutrition, and will feature Drs. Juan Andrade, Hans Stein, Nicholas Burd, and Yuan-Xiang Pan.

We are grateful to the many people involved with this meeting and program. We would like to first thank our keynote speaker, Dr. Teresa Davis. Thank you to our sponsors – their support is essential to the success and quality of the program. The NSGSA executive board and the symposium program committee have worked long and hard to organize an excellent program. We also thank the many others who contributed to this undertaking, including DNS staff and College of ACES Advancement Office staff. Most of all, we would like to thank our session chairs, judges, presenters and attendees for participating in this year's events and making them a success.

The Nutritional Sciences Graduate Student Association Board

www.nutritionalsciences.illinois.edu

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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 purpose 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.

The NSGSA serves as a forum for student opinion and input to the DNS as well as giving students the opportunity to expand their experiences as graduate students. Our activities reflect our desire to enrich our experiences as graduate students and to 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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Dr. Hong Chen
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Dr. Elvira de Mejia
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Dr. Juan Loor
Dr. Manabu Nakamura
Dr. Andrew Steelman
Dr. Hans Stein

Contact Information

2017 Symposium Contact

John K. Mathai
234 Animal Sciences Laboratory
University of Illinois
1207 W. Gregory Ave
Urbana, IL 61801
(847) 404-3746
jmathai2@illinois.edu

2018 Symposium Contact

Jan Lumibao
2136J Carl R. Woese Institute for Genomic Biology
University of Illinois
1206 W. Gregory Ave
Urbana, IL 61801
(708) 745-1398
jlumib2@illinois.edu

Division of Nutritional Sciences

Dr. Jessica Hartke
Associate Director
445 Bevier Hall
University of Illinois
Urbana, IL 61801
(217) 333-4177
nutritionalsciences@illinois.edu

Nutritional Sciences Graduate Student Association

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Schedule of Events

APRIL 19, 2017

***8:15 a.m. – 9:15 a.m. .....Breakfast**
Sims Executive Conference Room, ACES Library

Sponsors, presenters, DNS students, faculty, and staff are invited

***9:15 a.m. – 10:15 a.m. ....Graduate Student Oral Presentations 1**
Monsanto Room, ACES Library

9:15 a.m. Jennifer L. Kaczmarek

9:30 a.m. Sharon V. Thompson

9:45 a.m. Kristy Du

10:00 a.m. Patricia G. Wolf

10:15 a.m. – 10:30 a.m.....Break

***10:30 a.m. – 11:30 a.m.....Graduate Student Oral Presentations 2**
Monsanto Room, ACES Library

10:30 a.m. Caitlyn G. Edwards

10:45 a.m. Laura Moody

11:00 a.m. Brett R. Loman

11:15 a.m. Sookyoung Jeon

11:30 a.m. – 12:30 p.m. ....Lunch
Heritage Room, ACES Library

DNS students, presenters, and sponsors are invited, RSVP required

12:30 p.m. – 12:45 p.m. ....Break

***12:45 p.m. – 2:45 p.m. ....Faculty Mini-Symposium**
Monsanto Room, ACES Library

Protein in the Modern World

12:45 p.m. Dr. Juan Andrade
Addressing global protein issues: an overview

1:15 p.m. Dr. Hans Stein
Protein quality in human foods determined based on digestible indispensable amino acid score (DIAAS)

1:45 p.m. Dr. Nicholas Burd
Maximizing protein in the diet with exercise

2:15 p.m. Dr. Yuan-Xiang Pan
Impact of dietary protein in early life on the development of both mother and offspring

2:45 p.m. – 4:00 p.m. .....Industry Panel and Discussion
249 Bevier Commons

Sponsors, presenters, DNS students, faculty, and staff are invited

***4:00 p.m. – 5:00 p.m. .....Keynote Address by Dr. Teresa Davis, Baylor College of Medicine**
180 Bevier Hall

Role of Nutrition in the Regulation of Muscle Protein Synthesis and Lean Growth in the Neonate

5:00 p.m. – 5:15 p.m. .....Break

***5:15 p.m. – 6:40 p.m. .....Graduate Student Poster Session**
Heritage Room, ACES Library

Evening Reception, Award Announcements
Sponsors, presenters, DNS students, faculty, and staff are invited

** Open to the general public*

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Keynote Speaker: Dr. Teresa A. Davis

Teresa Ann Davis, Ph.D. is a Professor of Pediatrics at the Children's Nutrition Research Center at Baylor College of Medicine in Houston, Texas. She received her doctorate from the University of Tennessee and her postdoctoral training from Washington University School of Medicine. Dr. Davis is a pediatric nutrition scientist who is internationally recognized for her studies on the nutritional regulation of protein metabolism and growth. Dr. Davis has extensive experience in protein metabolism, amino acid and insulin signaling, and isotopic approaches to study the metabolic effects of nutrients, hormones, and growth factors. Dr. Davis' research is supported by the National Institutes of Health, the United States Department of Agriculture, and other sources. Dr. Davis is the Editor-in-Chief of The Journal of Nutrition and a Past President of the American Society for Nutrition. Dr. Davis has received the Stockstad Award for outstanding fundamental research in nutrition from the American Society for Nutrition, the Animal Growth and Development Award from the American Society of Animal Science, the Centennial Leader Award from the University of Tennessee, and the Research Mentor Award from Baylor College of Medicine and has been recognized as a Distinguished Foreign Expert by China and a Fulbright U.S. Distinguished American Scholar. She is a member of the Board of Directors of the American Society of Animal Science and a scientific advisor of the International Life Sciences Institute North America.

Role of Nutrition in the Regulation of Muscle Protein Synthesis and Lean Growth in the Neonate

The ingestion of food stimulates the synthesis of protein in skeletal muscle and this response is profound in early life. This feeding-induced stimulation of protein synthesis is crucial to support the rapid muscle growth during early postnatal life and the maintenance of body protein in adulthood. Because ethical considerations limit studies in human infants, we have used the neonatal pig as a model for the human infant. These studies have shown that the sharp increase in muscle protein synthesis after eating is triggered by the rise in amino acids and insulin. Amino acids and insulin stimulate protein synthesis by activating independent signaling pathway that converge at mechanistic target of rapamycin complex 1 (mTORC1), leading to the activation of key regulators of translation. The protein, and particularly leucine, content of the diet impacts the rate of protein synthesis in skeletal muscle. Because many low birth weight infants are fed by gastric tube either on an intermittent bolus schedule or continuously, we recently tested whether timing of nutrient delivery also influences protein synthesis and ultimately, muscle mass. Our studies demonstrated that intermittent bolus feeding, similar to meal feeding, enhances muscle protein synthesis compared to continuous delivery of the same nutrient load. The increase in muscle protein synthesis with intermittent bolus feeding is enabled by the rapid and profound increases in insulin and amino acids that occur following a bolus meal. This pulsatile pattern of insulin and amino acids activates the insulin and amino acid signaling pathways that lead to translation initiation. By contrast, the low and constant hormone and substrate pattern elicited by continuous feeding attenuates translation initiation signaling and resulting in a blunted rate of muscle protein synthesis. The higher muscle protein synthesis rates achieved by the intermittent bolus pattern of nutrient delivery can be sustained long term to promote protein deposition and increase lean body mass and growth. Because some infants must be fed continuously due to feeding intolerance, we tested the effectiveness of leucine supplementation during continuous feeding. We found that pulses of leucine during continuous feeding activates the mTORC1-dependent translation initiation pathway in muscle leading to an increase in protein synthesis and lean growth. Current studies are aimed at determining if prematurity limits the anabolic response to feeding and if this is mitigated by optimizing feeding strategies to enhance the efficiency of nutrient use for anabolic processes.

Dr. Davis' Keynote Address is from 4:00 – 5:00 p.m. in room 180 Bevier Hall.

Graduate Student Oral Presentations Session 1

9:15 a.m. - 10:15 a.m.
Monsanto Room, ACES Library

Graduate Student Oral Presentations Session 2

10:30 a.m. – 11:30 a.m.
Monsanto Room, ACES Library

Faculty Mini-Symposium *Protein in the Modern World*

12:45 p.m. – 2:45 p.m.
Monsanto Room, ACES Library

Graduate Student Poster Session

5:15 p.m. – 6:40 p.m.
Heritage Room, ACES Library

See poster session floor plan on page 41.

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Abstracts

Graduate Student Oral Presentations Session 1

Session 1 Judges
Dr. Elvira de Mejia, Dr. Anna Dilger, and Dr. Brenna Ellison

Broccoli consumption impacts the human gastrointestinal microbiota

Jennifer L. Kaczmarek[1], C.S. Charron[2], J.A. Novotny[2], E.H. Jeffery[1,3], H.E. Seifried[4], S.A. Ross[4], K.S. Swanson[1,5], H.D. Holscher[1,3]
[1]Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL; [2]USDA, ARS, Beltsville Human Nutrition Research Center, Beltsville, MD; [3]Department of Food Science and Human Nutrition, University of Illinois at Urbana-Champaign, Urbana, IL; [4]Division of Cancer Prevention, NCI/NIH, Rockville, MD; [5]Department of Animal Sciences, University of Illinois at Urbana-Champaign, Urbana, IL

The human gastrointestinal (GI) microbiota is increasingly linked to health outcomes; however, our understanding of how specific foods alter the microbiota is limited. Cruciferous vegetables such as broccoli have been associated with cancer prevention as a result of their high levels of glucosinolates, especially glucoraphanin. The activation of glucoraphanin to its isothiocyanate form, sulforaphane, is dependent on the enzyme myrosinase. Myrosinase is naturally found in broccoli, but is degraded by cooking. It has been hypothesized that plasma sulforaphane observed in persons eating cooked broccoli may be related to glucoraphanin hydrolysis by microbial myrosinase. Myrosinase activity is greater in rodents who regularly consume cruciferous vegetables compared to those who do not, suggesting a priming effect on the microbiota. However, it remains to be discovered which members of the microbiota are responsible for this action in clinical populations. We aimed to determine the impact of broccoli consumption on the GI microbiota of healthy adults as a means to understand the role of microbes in glucosinolate hydrolysis. A controlled feeding, randomized, crossover study consisting of two 17-day treatment periods separated by a 24-day washout was conducted in healthy adults (n=18). Participants were fed at weight maintenance, and received a *Brassica*-free control diet or the same diet with 200 g of cooked broccoli and 20 g of fresh daikon radish (as a source of plant myrosinase) per day. Fecal samples were collected at baseline and at the end of each treatment period. Following fecal DNA isolation, bacterial, archaeal, and fungal barcoded amplicon pools were generated using a Fluidigm Access Array system prior to high-throughput sequencing on an Illumina MiSeq. Data were analyzed using QIIME 1.8.0 and 1.9.1 and SAS 9.4. Beta diversity analysis based on 97% operational taxonomic unit composition and abundances indicated that bacterial communities were impacted by treatment (p=0.03). Broccoli consumption resulted in a significant change in the proportion of Bacteroidetes relative to Firmicutes, whereby participants consuming broccoli increased this ratio by 37% from baseline to end, compared to a 5% reduction during the control period (p=0.02). *Bacteroides* increased by 6% following broccoli consumption and decreased by 2% in the control group, but the difference between these two groups was not statistically significant (p=0.15). These novel results reveal that broccoli consumption affects the diversity and composition of the GI microbiota of healthy adults. These data help fill the gap in knowledge related to the role of bacterial hydrolysis of phytonutrients. The increase in *Bacteroides* spp. is particularly relevant because *Bacteroides thetaiotaomicron* has been shown *in vitro* to utilize glucosinolates.

Bacterial fermentation end-products are related to hepatic steatosis among overweight and obese adults

Sharon V. Thompson[1], J. Berndt[2], C.G. Edwards[1], J.W. Erdman Jr. [1,3], N.A. Khan[1,4,5], W.D. O'Brien, Jr.[1,2], H.D. Holscher[1,3]

[1]Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL; [2]Department of Electrical and Computer Engineering, University of Illinois at Urbana-Champaign, Urbana, IL; [3]Department of Food Science and Human Nutrition, University of Illinois at Urbana-Champaign, Urbana, IL; [4]Department of Kinesiology and Community Health, University of Illinois at Urbana-Champaign, Urbana, IL; [5]Neuroscience Program, University of Illinois at Urbana-Champaign, Urbana, IL

Background: Nonalcoholic fatty liver disease (NAFLD) is an increasingly prevalent manifestation of metabolic dysfunction characterized by elevated hepatic fat accumulation and elevated liver enzymes. Currently it is estimated that NAFLD may affect up to half of the US population. Although previous work has linked excess adiposity with NAFLD, there is a paucity of data examining whether hepatic steatosis is also related to gut microbiota fermentation end-products, particularly among humans. Discovering this knowledge stands to benefit future dietary approaches to preventing the development of NAFLD in the increasingly overweight and obese US population. Methods: Accordingly, this study aimed to characterize the relationships between hepatic steatosis and markers of liver function, fat mass, and gut microbiota fermentation end-products. We conducted correlational analyses concerning adiposity (%Fat), volatile fatty acid (VFA) concentrations, and measures of hepatic health within a sample of overweight/obese (BMI ≥ 27.5 kg/m^2) adults (N=57, 64.9% females). Whole body and total, visceral, and subcutaneous abdominal adiposity (% Fat Mass) were measured using DXA. Gas chromatography mass spectroscopy was used to assess VFA concentrations, including short-chain fatty acids (SCFAs; acetate, propionate, butyrate) and branched-chain fatty acids (BCFAs; isovalerate, valerate, and isobutryate). Hepatic enzyme concentrations (whole blood) were assessed using an automated chemical analyzer. Hepatic steatosis (fat fraction [FF]) was measured using quantitative ultrasound in a subset of participants (n=21). Initial bivariate correlations were conducted to examine relationships between hepatic health measures, adiposity, and bacterial fermentation end products. Subsequently, a partial correlation was conducted to determine whether the relationships between bacterial fermentation end-products and hepatic measures persisted following the adjustment of adiposity. Results: Elevated alanine aminotransferase (ALT), aspartate aminotransferase (AST), and hepatic FF were present in 16.7%, 13.0%, and 5.1% of participants, respectively. Whole body %Fat was negatively correlated with butyrate concentrations (r=-0.29, p=0.03, n=57). Hepatic FF was positively related to isovalerate (r=0.48, p=0.03, n=21) and tended to correlate with isobutyrate (r=0.40, p=0.07, n=21). Partial correlational analyses revealed that the relationships between hepatic FF and BCFA concentrations may be mediated by BMI and whole body, visceral, and subcutaneous adiposity. Conclusions: Results of the present study indicate that VFA concentrations differ by hepatic health and adiposity status. Further research is needed to determine if these observed relationships are mediated by dietary factors or gastrointestinal microbial abundances. Funding:
Partial funding support was provided by the Hass Avocado Board and the USDA National Institute of Food and Agriculture, Hatch project ILLU-668-902.

Graduate Student Oral Presentations Session 1 *(continued)*

Egg white protein meals induce greater satiety and plasma amino acids compared to wheat gluten protein meals

Kristy Du[1,2], E. Markus[3], M. Fecych[3], J. L. Beverly[3], J. Rhodes[1,2], M. J. Dailey[1,4]

[1]Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL; [2]Beckman Institute for Advanced Science and Technology, University of Illinois at Urbana-Champaign, Urbana, IL; [3]Department of Nutrition, University of North Carolina Greensboro; [4]Department of Animal Sciences, University of Illinois at Urbana-Champaign, Urbana, IL

While dietary protein is known to induce greater satiety than fats and carbohydrates, the extent to which the source of protein matters and the mechanisms involved are less certain. This study examined the effect of the level and source of protein on subsequent food intake, metabolism, and changes in plasma amino acids in adult Sprague-Dawley rats. Rats were entrained to a meal-feeding schedule consisting of a 30-minute treatment meal, equivalent to 10-20% of average daily intake, one hour into the dark phase followed by ad libitum access to a control diet for 5.5 hours later in the dark phase. Treatments were 1) 20% wheat gluten, 2) 35% wheat gluten, 3) 20% egg white, and 4) 35% egg white and provided in a randomized crossover design. Energy expenditure and food intake patterns were measured using indirect calorimetry housing system. Rats provided meals containing egg white protein had decreased food intake at the subsequent meal compared to wheat gluten fed rats, regardless of protein level ($P<0.005$). While energy expenditure did not differ among treatments, respiratory exchange ratio following ingestion of the 35% egg white protein meal was lower than the other treatment meals for several hours following ingestion ($P<0.001$). In a separate cohort of rats, blood plasma was collected at 30 minute intervals for 2 hours following ingestion of the treatment meals. Analysis of plasma amino acid concentrations revealed greater increases in measured amino acids following ingestion of meals containing egg white protein. Specifically, concentrations of valine and lysine were the largest contributors to the difference observed in plasma amino acids. Overall, these results suggest protein-induced satiety depends on the protein source. Egg white protein caused greater satiety than wheat gluten protein, corresponding to greater postprandial increases of plasma amino acids. These results collectively highlight the importance of the consideration of protein sources as it relates to controlling appetite.

Race-dependent association of sulfidogenic bacteria with colorectal cancer

Patricia G. Wolf[1], C. Yazici[2], H. Kim[2], T.L. Cross[1], T. Carroll[2], G.J. Augustus[3], E. Mutlu[4], L. Tussing-Humphreys[1,2], C. Braunschweig[2], R.M. Xicola[5], B. Jung[2], X. Llor[5], N.A. Ellis[3], H.R. Gaskins[1,6]

[1]Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana IL; [2]University of Illinois at Chicago, Chicago, IL; [3]University of Arizona, Tucson, AZ; [4]Rush University Medical Center, Chicago, IL; [5]Yale University, New Haven, CT; [6]Department of Animal Sciences,University of Illinois at Urbana-Champaign, Urbana, IL

In the US, there is a higher incidence of colorectal cancer (CRC) in African Americans (AAs) compared to non-Hispanic whites (NHWs). Recent evidence links consumption of a diet high in animal protein and fat as an environmental risk factor for CRC development, and the intestinal microbiota modulates the tumor promoting or protective effects of diet. Hydrogen sulfide, produced by resident sulfidogenic bacteria, triggers pro-inflammatory pathways and

hyper-proliferation, and is genotoxic. We hypothesized that sulfidogenic bacterial abundance in colonic mucosa may be an environmental CRC risk factor that distinguishes AA and NHWs, and may be correlated with differences in dietary composition. Colonic biopsies from uninvolved or healthy mucosa from CRC cases and controls were collected from five medical centers through the Chicago Colorectal Cancer Consortium. Using quantitative PCR, sulfidogenic bacterial abundance was measured in uninvolved colonic mucosa of 97 AA and 56 NHW CRC cases, and 100 AA and 76 NHW controls. In addition, 16S rRNA sequencing was performed in AA cases and AA controls. A Block Brief 2000 Food Frequency Questionnaire was collected from a subset of subjects of 50 AA and 31 NHW CRC cases and 30 AA and 24 NHW controls. Differences were examined among bacterial targets, race, disease status, and dietary intake. AAs harbored a greater abundance ($p<0.001$) of sulfidogenic bacteria compared to NHWs regardless of disease status, including the functional gene for H_2S production in sulfate reducing bacteria, dissimilatory sulfate reductase (pan-*dsrA*), as well as *Bilophila wadsworthia*-specific *dsrA*, and 16S rRNA genes for *Desulfobacter* spp., *Desulfovibrio* spp., and *Desulfotomaculum* spp. *Bilophila wadsworthia*-specific *dsrA* was significantly more abundant in AA cases compared to AA controls ($p<0.001$). Linear discriminant analysis of 16S rRNA gene sequences highlighted the sulfidogenic *Bilophila*, *Lactococcus*, *Odoribacter*, *Porphyromonas* and *Pyramidobacter* genera as significant in AA cases. Fat intake and daily servings of meat were significantly higher ($p<0.01$) in AAs compared with NHWs, and dietary fat intake correlated positively with pan-*dsrA* abundance ($p=0.011$). Additionally, intake of dairy and calcium was lower ($p<0.001$) in AA, and servings of dairy correlated negatively with pan-*dsrA* abundance ($p=0.007$). Together, these results implicate sulfidogenic bacteria as an environmental risk factor contributing to CRC development in AAs.

Abstracts

Graduate Student Oral Presentations Session 2

Session 2 Judges
Dr. Ruopeng An, Dr. Megan Dailey, and Dr. Hannah Holscher

Domain-specific relationships between cognitive control and disordered eating attitudes

Caitlyn G. Edwards[1], A.M. Walk[2], S.V. Thompson[1], S. Mullen[2], H.D. Holscher[1,3], N.A. Khan[1,2,4]
[1]Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL [2]Department of Kinesiology and Community Health, University of Illinois at Urbana-Champaign, Urbana, IL [3]Department of Food Science and Human Nutrition, University of Illinois at Urbana-Champaign, Urbana, IL [4]Neuroscience Program, University of Illinois at Urbana-Champaign, Urbana, IL

Introduction: Cognitive control comprises a set of mental operations vital for regulation of eating behaviors. Previous work indicates that impairment in cognitive control, particularly cognitive flexibility, is a trait characteristic among patients with diagnosed eating disorders. However, this work has remained limited to clinical populations. This is concerning because disordered eating attitudes and behaviors are evident among the general/nonclinical population and are often underdiagnosed in non-underweight and male individuals. Elucidating the relationship between eating attitudes and cognitive control processes may provide information on the cognitive underpinnings of eating behavior regulation and inform future therapeutic approaches to improving adherence to healthful diet habits in the general population. Methods: Data was collected from 85 adults (Age= 34.0 ± 5.8 years, 35 males, BMI= 30.7 ± 6.5 kg/m2). Disordered eating Attitudes were assessed using the Eating Attitudes Test-26 (EAT-26). Components of cognitive control including selective attention, inhibitory control, and cognitive flexibility were assessed through a modified flanker, Go/NoGo task, and switch tasks, respectively. Covariate assessment included age, sex, intellectual ability (IQ) via the Kaufman Brief Intelligence Test, diet quality, and BMI (kg/m2). Habitual diet intake was measured using the National Cancer Institute's Food Frequency Questionnaire and overall diet quality was assessed using the Healthy Eating Index (HEI-2010). Results: No significant differences in Eat-26 score or cognitive performance were observed between males and females. Following adjustment of age, sex, IQ, HE-2010, and BMI, higher EAT-26 scores were positively associated with reaction time during the homogenous conditions (r= .317, p= .005) and reaction time during switch trials in the heterogeneous condition (r= .244, p= .034) suggesting that increasing risk for disordered eating was related to poorer cognitive flexibility. Further, EAT-26 scores were related to reaction time during the congruent trials of the flanker task (r=.247, p=.038). However, no significant correlations were observed for incongruent trials during the flanker task nor the Go/NoGo task (all ps>0.85). Conclusion: These findings are consistent with previous work relating disordered eating attitudes to cognitive flexibility. However, this study is among the first to reveal that this selective relationship extends to the non-clinical population and is independent of general intellectual abilities, sex, diet quality, and weight status. These findings are important since deficits in cognitive flexibility may contribute to behavioral rigidity which leads to maintenance of abnormal eating patterns and difficulty to follow a healthful diet pattern. Ongoing work is examining the specific EAT-26 subscales (dieting, oral control, and bulimia/food preoccupation) contributing to the results.

Epigenetic regulation of carnitine palmitoyltransferase 1 (Cpt1a) in response to high fat diet

Laura Moody[1], P.M. Jung [2], A. Kriska [2], H. Chen[1,2], Y-X. Pan[1,2,3]
[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]Illinois Informatics Institute, University of Illinois at Urbana-Champaign, Urbana, IL

Carnitine palmitoyltransferase 1 (Cpt1a) is a rate-limiting enzyme that mediates the transport of fatty acids into the mitochondria for subsequent beta oxidation. Cpt1a is highly regulated at the transcriptional, translational, and substrate level. Epigenetic mechanisms regulating Cpt1a expression were investigated in the liver of rats fed a high fat diet. Hepatic Cpt1a mRNA was increased in response to high fat. High fat diet reduced DNA methylation and increased histone 3 lysine residue 4 dimethylation (H3K4Me2) both upstream of and within the promoter region of Cpt1a. This was accompanied by increased binding of C/EBP directly downstream of the Cpt1a transcription start site within the first intron. In addition to the transcriptional regulation of Cpt1a, expression of miR-499, a predicted repressor of both Cpt1a and C/EBP , was also reduced. Treatment of rat hepatoma H4IIEC3 cells with non-esterified fatty acid (NEFA) confirmed the correlation between the upregulation of Cpt1a gene expression and cellular fat accumulation. While H4IIEC3 cells transfected with non-specific microRNA upregulated Cpt1a expression at high NEFA concentrations, exogenous overexpression of miR-499 abolished this increase, resulting in suppressed beta oxidation and elevated lipid accumulation. We conclude that hepatic fat increases Cpt1a expression through a highly coordinated epigenetic mechanism involving an early reduction in miR-499 expression, followed by transcriptional regulation by histone tail modifications at specific chromatin locations, and finally C/EBP transcription factor recruitment.

Prebiotic enhancement of intestinal adaptation in piglets with short bowel syndrome is associated with microbial and enteroendocrine modifications

Brett R. Loman[1], K.A. Tappenden[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

Background: Short bowel syndrome is a costly condition affecting very low birth weight, premature infants and is associated with microbial dysbiosis. Microbially derived short chain fatty acids (SCFA) stimulate enteroendocrine secretion of glucagon-like peptide 2 (GLP-2), an intestinotrophic hormone. Hence, leverage of the intestinal microbiota to stimulate enteroendocrine driven intestinal adaptation requires investigation. Objective: The aim of this study was to determine the mechanism by which prebiotic (short chain fructooligosaccharides, scFOS), probiotic (Lactobacillus rhamnosus GG, LGG), and synbiotic modify microbial stimulation of the enteroendocrine system to enhance intestinal adaptation in a neonatal piglet model of intestinal failure. Methods: Neonatal piglets (48 hours old, n = 38) underwent 80% jejunoileal resection and jugular catheter placement. Piglets received 80% parenteral and 20% enteral nutrition (EN) for 7 days and received 1 of 4 treatments: (1) control (CON), unsupplemented EN; (2) prebiotic (PRE), 10g scFOS/L EN; (3) probiotic (PRO), 10^9 CFU LGG/L EN, or (4) synbiotic (SYN), scFOS + LGG. Bacterial 16s rRNA genes (V3-V5 region) were amplified from the distal ileum

Graduate Student Oral Presentations Session 2 *(continued)*

and proximal colon and sequenced on the Illumina MiSeq system. qPCR was used to quantify expression of genes associated with enteroendocrine function. Multiple regression analysis was performed to assess the relationship of data to markers of intestinal adaptation. Statistical significance was determined at $p < 0.05$. Results: In the ileum, SYN increased expression of the SCFA transporters monocarboxylate transporter 1 (MCT1) and sodium monocarboxylate transporter 1 (SMCT1). In the colon, SYN increased MCT1, but PRE and PRO decreased SMCT1. SYN increased expression of SCFA-responsive free fatty acid receptors 2 and 3 (FFAR2, FFAR3) in the ileum while PRO decreased FFAR2 in the colon. PRE and PRO decreased expression of dipeptidyl peptidase-4 (DPP-IV, the enzyme that inactivates GLP-2) in the ileum but PRO decreased expression of GLP-2 receptor (GLP-2R) in both ileum and colon. PRO decreased expression of trophic hormone insulin-like growth factor 1 (IGF-1) and IGF-1 receptor (IGF-1R) in the colon. PRO also decreased expression of caudal-type homeobox transcription factor 2 (CDX2, a marker of intestinal differentiation) in both ileum and colon. Multiple regression was conducted to identify factors that contributed to markers of intestinal adaptation. Three models were generated to explain ileal villus height, with enteroendocrine factors (adj $R^2 = 0.998$, $P < 0.001$), microbial factors (adj $R^2 = 0.793$, $P = 0.01$), and barrier function factors (adj $R^2 = 0.753$, $P = 0.001$) explaining the most variation respectively. The colonic electrogenic glutamine transport model was explained by factors related to SCFA transport, IGF signaling, and amino acid transport (adj $R^2 = 0.655$, $P < 0.001$). Conclusions: These data demonstrate that intestinal adaptation is associated with a complex interaction between the intestinal microbiota and enteroendocrine system in a segment-dependent fashion. Interestingly, SYN induced changes in enteroendocrine regulation that were unique from PRE and PRO. Microbial activity may contribute both positively (butyrate producing bacteria enhancing proliferation) and negatively (E. faecalis diminishing villus height). Future research should determine how various microbial products impact each step of enteroendocrine regulation specifically.

Lutein-supplemented formula enhances lutein accumulation in brain and other tissues in infant rhesus macaques

Sookyoung Jeon[1], K.M. Ranard[1], M. Neuringer[3], E.E. Johnson[3], M. Kuchan[4], E.J. Johnson[5], J.W. Erdman Jr.[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]Oregon National Primate Research Center, Oregon Health and Science University, Beaverton, OR; [4]Abbott Nutrition, Columbus, OH; [5]Jean Mayer USDA HNRCA, Tufts University, Boston, MA

Lutein, a yellow xanthophyll, is well known for its critical role in eye health, and several recent studies also showed associations of lutein intake with improved cognitive function in adults. In addition, it has been suggested that lutein's presence as the most abundant carotenoid in brain may contribute to neural development. However, there is limited data on the effect of lutein bioaccumulation in early life. The purpose of this pilot study was to investigate if a lutein-supplemented infant formula can increase lutein deposition in brain regions and other tissues using a nonhuman primate model. Infant rhesus macaques (1-3 months old) were fed either a control formula containing a basal level of lutein (10 nmol/L) (n=2) or a formula with a higher level of lutein (100 nmol/L) (n=2) to mimic the breast milk composition from mothers consuming a healthy vegetable-rich diet. Serum

carotenoids were measured monthly, and retina, brain, and other tissues were collected after 4 months of feeding. The levels of carotenoids in serum and tissues were analyzed by high-performance liquid chromatography. Final serum lutein level in the supplemented group was 5 times higher than in the unsupplemented group (104 nmol/L and 21 nmol/L, respectively). Lutein accumulated differentially across brain areas. Occipital cortex exhibited the highest lutein level among brain areas regardless of the formula type, and was 3-fold higher in the supplemented group (64 pmol/g versus 21 pmol/g). The other brain areas, including prefrontal and superior temporal cortex, striatum, hippocampus and cerebellum, all showed increased lutein concentrations in supplemented group; indeed, in the unsupplemented group, lutein was undetectable in prefrontal and superior temporal cortex and cerebellum. Lutein was two times higher in mesenteric and thigh subcutaneous adipose tissues, three times higher in abdominal adipose tissue and six times higher in brown adipose tissue in the supplemented group compared with the unsupplemented group. In addition, higher lutein deposition was found in liver, lung, kidney, heart, and other tissues. In conclusion, infant rhesus macaques showed enhanced lutein levels in serum, brain and other tissues in response to formula lutein supplementation, and lutein was preferentially deposited in the occipital cortex. This pilot study demonstrates that increased early exposure to dietary lutein substantially enhances lutein tissue deposition. Supported by Abbott Nutrition through the Center for Nutrition, Learning and Memory, University of Illinois, Urbana-Champaign, and NIH grant P51OD011092.

Abstracts and Biographies

Faculty Mini-Symposium
Protein in the Modern World

Addressing global protein issues: an overview

Juan E. Andrade, Ph.D.
Division of Nutritional Sciences, Department of Food Science and Human Nutrition, University of Illinois at Urbana-Champaign, Urbana, IL

ABSTRACT: In 2015, the Food and Agriculture Organization (FAO) estimated that 793 million people, or almost 1 in 7 people worldwide, were chronically hungry; with a greater number afflicted by micronutrient deficiencies and inadequate access to quality protein. Despite significant strides to address the basic, underlying, and immediate causes of malnutrition over the past 25 years, there is still more work ahead. Facing the grand challenge of preventing hunger and malnutrition in a World that aches with increased pressures over its natural resources, due to population growth and climate change, will be the story of our generation.

The benefits of economic development include access to education, healthcare, water and sanitation, and food and nutrition security. A "sustainable" diet is one that addresses the nutrient needs of today in terms of quantity and quality of water, macro and micronutrients and sufficient energy, without jeopardizing the needs of tomorrow. Nonetheless, economic and population growth elicits a higher demand for animal-source food and, if no complementary policies on nutrition and physical activity present, an increased risk for obesity and chronic disease.

Adequate protein consumption is fundamental to human growth and health. Despite our efforts to increase protein intake, a staggering one billion people do not have access to adequate protein amounts and quality. Protein needs can be satisfied with the current diversity present in our food supply from either plant- or animal-source foods. Disparate wealth distribution has led to those living in low-income countries to depend on food staples, most of which offer lower protein quantity and quality, along with limited micronutrients. Therefore, the charge is to revamp our current food supply chain to improve the quality, availability, accessibility and utilization of protein, in particular among those living in low-resource settings. In this presentation, a discussion will revolve around current statistics on protein malnutrition worldwide, existing programs, and innovative protein sources aimed at addressing this global health problem.

BIOGRAPHY: Juan E. Andrade is an assistant professor of global food and nutrition from the University of Illinois, Urbana. He holds a Ph.D. in Human Nutrition from Purdue University. Dr. Andrade's long-term goal is to develop sustainable strategies that can be used to deliver adequate nutrition, especially micronutrients, to residents of low-resource countries and thereby help to promote human health and economic development. His research interests are focused on innovative concepts for food fortification, lipid-based nutrition supplements, point-of-care technologies for assessment of micronutrient deficiencies, functional food aid products, and service, experiential learning education programs. Technologies are low-cost, use local foods and rely on the participation of beneficiaries in a bottom-up approach. Dr. Andrade is an affiliated faculty in the Department of Food Science and Human Nutrition, the Division of Nutritional Sciences, the Center for Latin American and Caribbean Studies, and the Food Security Initiative at Illinois. He is also a faculty research affiliate with the Integrating Gender and Nutrition into Agricultural Extension Services (INGENAES) program and the PI of the nutrition team at the Soybean Innovation Lab (SIL), which are US Agency for International Development projects.

Protein quality in human foods determined based on digestible indispensable amino acid score (DIAAS)

Hans H. Stein, Ph.D.
Division of Nutritional Science, Department of Animal Sciences, University of Illinois at Urbana-Champaign, Urbana IL

ABSTRACT: In a report published in 2013, FAO introduced the term "Digestible Indispensable Amino Acid Scores" (DIAAS) to evaluate amino acid quality in human foods. Values for DIAAS are calculated from values for true or standardized ileal digestibility of amino acids, and unless these values can be determined in humans, values obtained in growing pigs or rats can be used, but the report specifically points out that the pig is considered a better model than the rat. Indeed, in a 2014 report, FAO specified details on how to determine DIAAS values using the pig as the model. Since publication of these reports, DIAAS values for 16 different foods have been reported in 2 peer-reviewed publications. Conclusions from this work indicate that dehulled oats has a DIAAS value of 77 whereas sorghum has a DIAAS value of 29, with wheat, rye, pearled barley, two varieties of maize, and polished rice being intermediate having DIAAS values of 43, 47, 51, 48, 54, and 64, respectively. However, DIAAS values in milk protein concentrate, skim milk powder, whey protein concentrate, and whey protein isolate are between 125 and 139 and DIAAS values close to 100% were obtained for soy flour and soy protein isolate and the DIAAS value for pea protein concentrate is 73. Results from this work confirm that the pig can be used as a model to generate DIAAS values for human foods and results are repeatable among experiments. There is, however, a need to determine DIAAS values in a large number of food ingredients to make it possible to formulate diets for humans based on values for digestible indispensable amino acids and thereby making sure that amino acids are provided in sufficient quantities to support growth and development in children, adolescents, and adults. There is also a need to determine effects of processing on DIAAS values because most foods are consumed after some kind of processing. It is also important to establish the additivity of DIAAS values calculated in individual foods when they are mixed together in balanced diets consumed by humans. In such mixed diets, complementary effects of individual food proteins may overcome limitations in DIAAS values in an individual food and thus make the best use of all amino acids provided in the combined diet.

BIOGRAPHY: Hans H. Stein is a professor of nutrition at the University of Illinois. He directs 9 PhD students, a post-doctoral research fellow, four research technicians, and three visiting scholars. His research focusses on energy and nutrient digestibility in humans and pigs. Dr. Stein has published 186 peer-reviewed manuscripts and he has delivered invited presentations in 35 countries around the world. He has also served as the external examiner on Graduate Student Defense committees in Canada, Australia, Spain, The Netherlands, The Philippines, and Denmark and he has been an outside evaluator of the undergraduate Animal Science Program at the National University of Colombia in Bogota, Colombia, and of the Graduate Animal Science Program at the University of Sao Paolo, Pirassununga, SP, Brazil. He was also a member of the committee that was invited by the National Academies to write the 11th revised edition of Nutrient Requirements of Swine.

Maximizing protein in the diet with exercise

Nicholas A. Burd, Ph.D.
Division of Nutritional Sciences, Department of Kinesiology and Community Health, University of Illinois at Urbana-Champaign, Urbana IL

ABSTRACT: An adequate quantity and quality of skeletal muscle is important to optimize health and physical performance across the lifespan. Dietary protein intake is essential for stimulating skeletal muscle protein synthesis and remodeling, which ultimately contributes to the maintenance of skeletal muscle mass and health throughout adult life. The current Recommended Dietary Allowance (RDA) for protein is placed at 0.8 g/kg per day for men and women aged 19 years or older; however, the RDA is not set as an 'optimal' dietary target to maximize muscle mass or health. Instead, the protein RDA represents an average intake that would be *sufficient* to meet the protein needs of practically all healthy persons. Thus, the RDA only represents the minimal daily amount of protein required to consume on a daily basis to prevent net nitrogen (protein) loss. The current protein RDA is important as it provides the obligatory frame-work, or starting point, to provide guidance towards a more optimal dietary allowance (ODA) for protein. The use of sensitive stable isotope amino acid methods allow for the definition of protein requirements that target the optimization of whole body and muscle protein synthesis as opposed to merely achieving nitrogen balance. Thus, direct incorporation tracer methods provide insight into a protein ODA that can maximize skeletal muscle remodeling and help develop guidelines that optimize the quantity and quality of vital tissues. The ingested protein amount for younger adults at which postprandial muscle protein synthetic responses are maximally stimulated is ~0.25 g protein/kg per meal. Accounting for potential inter-individual differences (+2 SD) the estimated protein requirements to maximize skeletal muscle remodeling of healthy adults may be closer to ~0.4 g protein/kg per meal or 1.2 g protein/kg per day (assuming 3 daily meal times), which is ~1.5-fold higher than the current protein RDA. Meal planning, however, may become problematic from an economic and societal cost standpoint with this muscle-centric protein ODA. Thus, adjunct strategies are warranted to improve the use of protein in the diet for optimal muscle health. Exercise is fundamentally an anabolic stimulus that increases the sensitivity of muscle to dietary protein-derived amino acids that under some circumstances can persist for up to 2 days. As such, increasing habitual physical activity levels by the incorporation of daily exercise is a safe, healthy, cost-effective strategy to improve the use of protein in the diet. Current approaches that compartmentalize physical activity and nutrition guidelines discount the interactive nature of these two stimuli. Instead, physical activity and protein guidelines are inextricably linked and should be considered together in order to provide the most effective lifestyle recommendations to optimize (muscle) health across the lifespan.

BIOGRAPHY: Nicholas Burd received graduate degrees in Exercise Physiology (MSc) and Kinesiology (PhD) from Ball State University and McMaster University in Canada, respectively. He trained as a post-doctoral research fellow at Maastricht University Medical Center in the Netherlands. He joined the University of Illinois faculty in 2013 as an Assistant Professor in the Department of Kinesiology and Community Health and is also a member of the Division of Nutritional Sciences. Research in his group regularly uses substrate or non-substrate specific stable isotope tracers to provide a window into the intricacies of human metabolism and its responses to nutrition, exercise, and disease. He has authored more than 70 peer-reviewed research, review articles, and book chapters related to dietary protein and its application in sports and/or clinical nutrition. He is a member of the American College of Sports Medicine (ACSM) and American Society for Nutrition. He has received grant funding from the National Pork Board, Egg Nutrition Center, ACSM, and the National Cattlemen's Beef Association.

Impact of dietary protein in early life on the development of both mother and offspring

Yuan-Xiang Pan, Ph.D.
Division of Nutritional Sciences, Department of Food Science and Human Nutrition, University of Illinois at Urbana-Champaign, Urbana, IL

ABSTRACT: Early life protein diet has been used as an experimental model to examine and understand early life influences on fetal programming. Many research teams have published extensively the physiological, epigenetic, as well as pathological consequences of this early nutritional distress in the offspring. However, very little is known regarding the effects of protein deficiency on the maternal body and its physiology and metabolism. Maternal metabolism is altered drastically during pregnancy and lactation, and maternal nutrition is essential to support these changes. The low-protein (LP) rodent model, one of the best-characterized developmental programming models, suggests that inadequate protein intake during pregnancy activates the amino acid response (AAR) pathway, triggering cell destruction – a process called autophagy, which in turn affects pregnant rats and their offspring differently. Our study brings insight into the molecular mechanisms of early life protein diet, underscoring the importance of women consuming diets with adequate amounts of protein during pregnancy to protect the health of their children.

BIOGRAPHY: Yuan-Xiang 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), where he has been a faculty member since 2006. He graduated with a B.S. degree in cell biology from Lanzhou University and received both his M.S. and Ph.D. in Animal Nutrition from Virginia Tech where he studied protein metabolism. He completed his postdoctoral training in nutritional control of mammalian gene expression in the Department of Biochemistry and Molecular Biology in College of Medicine at the University of Florida. Over the past decade, Dr. Pan's research is focused on molecular mechanisms of developmental origins of chronic diseases. 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. Dr. Pan has over 50 peer-reviewed publications and book chapters (h-index 23) and receives grant support from the National Institutes of Health (NIH), the United States Department of Agriculture, and industry. Dr. Pan is an investigator in the Children's Environmental Health Research Center at Illinois.

Abstracts

Graduate Student Poster Session

Effects of prebiotic inulin-type fructans on blood metabolite and hormone concentrations and fecal microbiota and bile acids in overweight dogs

Celeste Alexander[1], T.W. Liu[1], S. Devendran[2], S. Theis[3], J.M. Ridlon[1,2], J.S. Suchodolski[4], M.R.C. de Godoy[1,2], K.S. Swanson[1,2]
[1]*Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL;* [2]*Department of Animal Sciences, University of Illinois at Urbana-Champaign, Urbana, IL;* [3]*Beneo GmbH, Mannheim, Germany;* [4]*Gastrointestinal Laboratory, Texas A&M University, College Station, TX*

Obesity commonly affects both humans and companion animals, and is often associated with altered blood glucose and hormone responses. Many studies have shown the ability of dietary fibers or prebiotics to curb postprandial glycemic responses, but some have suggested that certain prebiotics, when consumed at an early meal, can even curb the responses after a second meal consumed hours later. This response has been coined the 'second-meal effect'. Although it is known that dietary prebiotics can elicit shifts in the fecal microbiota composition, little research has been performed in dogs using modern high-throughput DNA-sequencing. In this study, our objective was to evaluate the (1) second-meal effect of a commercial prebiotic blend of inulin-type fructans, and (2) effects of the prebiotic on fecal microbiota, metabolites, and bile acids (BA). We hypothesized that the prebiotic would elicit a second-meal effect in response to an oral glucose challenge, beneficially shift fecal microbiota by increasing *Bifidobacterium, Faecalibacterium, and Lachnospira* and decreasing *Fusobacterium and Desulfovibrio*, and shifting the fecal BA composition. Nine overweight dogs (4.2 ± 0.7 yr, 12.7 ± 2.4 kg, 7.8 ± 1.4 BCS) were used in a replicated 3x3 Latin Square design to test a non-prebiotic control (cellulose) against low- (0.5% of diet) and high-dose (1.0% of diet) prebiotic treatments. The study included three 14-d treatment periods separated by 14-d washouts. All dogs were fed the same experimental diet formulated to meet all nutrient needs as defined by AAFCO, with treatments provided orally via gelatin capsules prior to each meal. Dogs were fed twice daily (8 am; 4 pm) to maintain BW. At the end of each period, fresh fecal samples were collected for microbiota, metabolite, and BA analysis. On d13 or d14 of each period, dogs were fed at 8 am as usual, then dosed with 1 g/kg BW of maltodextrin as a 50% solution in place of the 4 pm meal. Blood samples were collected at baseline and 10, 20, 30, 45, 60, 90, 120, and 180 min after dosing, and analyzed for glucose, insulin, and active glucagon-like peptide-1 (GLP-1) concentrations. Baseline and postprandial incremental area under the curve (IAUC) data were analyzed statistically. The prebiotic tended to attenuate postprandial blood glucose response to the oral glucose challenge ($p=0.089$), but did not affect ($p>0.10$) baseline glucose or baseline and postprandial active GLP-1. The prebiotic also tended to increase the relative abundance of fecal *Erysipelotrichi* ($p=0.089$), particularly in the genus *Eubacterium* ($p=0.075$), the order *Turicibacterales* ($p=0.066$), the family *Veillonellaceae* ($p=0.051$), and the genus *Megamonas* ($p=0.054$). Fecal lithocholic acid, a secondary BA, tended to decrease ($p=0.083$) in dogs fed the prebiotic. Our results indicate that inulin-type prebiotics may elicit a second-meal effect and serve as a modulator of the gut microbiota in overweight dogs.

Soy consumption and the risk of prostate cancer in men: an updated systematic review and meta-analysis

Catherine C. Applegate[1], J.L. Rowles III[1], K.M. Ranard[1], S. Jeon[1], J.W. Erdman Jr.[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*

Background: Prostate cancer (PCa) is the second most commonly diagnosed cancer and the fifth leading cause of cancer-related deaths worldwide. PCa incidence is higher in more developed countries, with Australia/New Zealand and North America having the highest rates, while rates remain lowest in Asian countries. The lower incidence of PCa in Asian populations has been associated with the consumption of soy foods. Soy has been under scrutiny in recent years for its potential role in the prevention of hormone-driven cancers. The purpose of this study was to provide an updated systematic review and meta-analysis focused on the association of soy foods on the risk of PCa in men. **Methods:** A systematic review and meta-analysis to determine the influence of soy food consumption on the risk of PCa in men was conducted. Eligible studies were published before October 10, 2016 and were identified from PubMed, Web of Science, and the Cochrane Library. Articles were identified using the following key words and their variants: prostate cancer, prostate neoplasm, soy, soymilk, soy milk, isoflavone, bean curd, tofu, soy protein, daidzein, and genistein. For studies to have been included in this meta-analysis, they must have met the following criteria: (a) evaluated the association between soy food consumption and PCa risk by using randomized control trials and cohort, cross-sectional, retrospective, prospective, or case-control studies; (b) methodology was documented in replicable detail; (c) evaluated the relationship between soy and prostate cancer risk; (d) included relative risk ratio with 95% confidence intervals for exposure categories; (e) were written in English; and (f) peer-reviewed publications or theses. We estimated pooled relative risk ratios (RR) and 95% confidence intervals (CI) using random and fixed effects models. **Results:** Twenty-six articles met the inclusion criteria and were included in this meta-analysis. Of these 26 studies, 21 reported data regarding total soy food and/or soy isoflavone intake, while 8 studies reported circulating isoflavone (genistein and daidzein) plasma levels. Dietary total soy food (RR=0.84, 95% CI: 0.76-0.92, p=0.044), genistein (RR=0.82, 95% CI: 0.70-0.95, p=0.008), and diadzein (RR=0.96, 95% CI: 0.65-0.96, p=0.019) intakes were significantly associated with a decreased risk of PCa. In contrast, circulating genistein (RR=0.78, 95% CI: 0.54-1.12, p=0.171) and diadzein (RR=0.84, 95% CI: 0.63-1.13, p=0.248) plasma levels showed no association with PCa risk. **Conclusions:** Our data demonstrate that dietary soy intake is inversely associated with risk of PCa, while circulating plasma isoflavone levels are not associated with PCa risk.

Investigating the links between habitual diet, the gastrointestinal microbiota, and cardiovascular disease risk factors in healthy weight, overweight, and obese men and women

Melisa A. Bailey[1], J.W. Beals[1], S.K. Skinner[2], S.A. Paluska[3], N.A. Burd[1,2], H.D. Holscher[1,4]

[1]Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL; [2]Department of Kinesiology and Community Health, University of Illinois at Urbana-Champaign, Urbana, IL, Urbana, IL; [3]Department of Family Medicine, University of Illinois at Urbana-Champaign, Urbana, IL; [4]Department of Food Science and Human Nutrition, University of Illinois at Urbana-Champaign, Urbana, IL

Background: The connection between diet and the gastrointestinal (GI) microbiota is an area of intense interest as the microbiota is increasingly linked to a growing list of metabolic diseases. Dietary factors including saturated fat, added sugars, and dietary fiber are all related to cardiometabolic health. However, the relationship between the human GI microbiota, blood lipids, and habitual diet remains under-investigated. Objective: We aimed to determine the relationships among bacterial taxa, blood lipids, and dietary intake patterns in healthy weight, overweight, and obese men and women. Methods: Blood and fecal samples were collected from adults (n=68, 31 males; 25-45 years of age) without physician diagnosed metabolic or gastrointestinal diseases. Dietary intake patterns were assessed using the Diet History Questionnaires (DHQII, Past Year and Past Month with

Portion Size) and Healthy Eating Index (HEI-2010) scores were calculated to assess diet quality. Following DNA isolation, bacterial (V4 region of 16S rRNA), fungal (ITS1-4), and archaeal amplicons were generated using a Fluidigm Access Array followed by high-throughput sequencing on an Illumina MiSeq. Sequences were quality filtered, then operational taxonomic units (OTUs) were picked against the Greengenes 13-8 reference database using QIIME versions 1.8 and 1.9. Total cholesterol (TC), low density lipoprotein (LDL) cholesterol, very low density lipoprotein (VLDL) cholesterol, high density lipoprotein (HDL) cholesterol, non-HDL-cholesterol (nHDLc), and triglycerides were measured using a chemical analyzer. Body composition was assessed using dual energy x-ray absorptometry. Data were analyzed using SAS 9.4. Results: Bivariate correlations revealed positive associations between *Phascolarctobacterium* and nHDLc (r=0.28, p=0.03) and refined grains (r=0.34, p=0.01). However, these relationships were mitigated by age and whole body percent fat. *Dorea spp* were positively related to nHDLc (r=0.38, p=0.003), TC (r=0.40, P=0.001), LDL-cholesterol (r=0.34, p=0.007), and total dairy intake (p=0.35, p=0.01). The positive association between *Dorea spp*. and TC remained significant after controlling for whole body percent fat, age, total HEI-2010 score and dietary intake of saturated fat/kcal and total dairy. Total dairy intake tended to positively relate to nHDLc (r=0.26, p=0.07). Conclusions: These results suggest potential relationships between microbial, metabolic, and dietary factors. Specifically, *Dorea* is independently related to increased cardiometabolic disease markers and dietary components such as total dairy intake in US adults. Future directions include assessments of additional dietary factors, bile acids, and inflammatory markers to better define the interconnections between the gut microbiota composition, diet, and health. Supported in part by the Hass Avocado Board and USDA National Institute of Food and Agriculture, Hatch project ILLU-668-902.

Impact of long-term dietary patterns and short-term nutrient intake on the gut microbiota of children 4 to 8 years of age

Kirsten Berding[1], S.M. Donovan[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*

The gut microbiota is undergoing rapid changes in the first few years of life and diet plays a fundamental role in shaping the gut microbiota. It is commonly believed that by age 3 years, the microbiota composition resembles that of an adult. However, recent research shows differences in the microbiota composition between pre-adolescence children and adults. Little is known about how diet influences the gut microbiota composition in young, healthy children. Herein, the effect of long-term dietary patterns and short-term dietary intake on longitudinal changes in microbiota composition were studied in children aged 4-8 years. A food frequency questionnaire, 3-day food record and stool sample were collected for each participant (n=24) at baseline, 6-weeks and 6-months post-baseline. Nutrient intake was analyzed using Nutrition Data System for Research (NDSR). Dietary patterns based on food groups were identified using principal component analysis. Bacterial genomic DNA was analyzed for total bacteria, *Prevotella*, *Lactobacillus*, and *Roseburia* by quantitative real-time qPCR. Distinct microbial profiles were identified for three long-term dietary patterns. Compared to the other two dietary patterns, a diet pattern characterized by a higher intake of fruits, vegetables, meat, fish, legumes, nuts and seeds, but also sugary drinks and desserts showed higher abundance of total bacteria. A diet pattern defined by a higher intake of whole grains and starchy vegetables was characterized by lower density of *Lactobacillus* and *Roseburia*, but higher density of *Prevotella*. Lastly, a diet pattern characterized by higher intake of refined grains, French fries and a lower intake in salty snacks was associated with lower abundance of total bacteria. Short-term dietary fiber intake was not significantly correlated with bacterial abundance. Overall, there was no significant difference in the mean of the bacteria concentration between

baseline and 6 weeks. However, bacterial abundance differed for some individuals between the two time points. In conclusion, long-term dietary patterns influence the fecal microbiota of children aged 4 to 8 years. Analysis of 6 month samples will inform findings relative to the longitudinal stability of the gut microbiota. Future analysis includes microbiome analyses using next generation sequencing and assessment of short chain fatty acid concentrations.

Effects of inulin supplementation on mineral metabolism and fecal short-chain fatty acid excretion in hemodialysis patients

Annabel Biruete[1,4], B.M. Kistler[5], J.M. Allen[2,4], L.L. Bauer[3,4], G.C. Fahey[1,3,4], K.S. Swanson[1,3,4], K.R. Wilund[1,2,4]
[1]Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL; [2]Department of Kinesiology and Community Health, University of Illinois at Urbana-Champaign, Urbana, IL; [3]Department of Animal Sciences, University of Illinois at Urbana-Champaign, Urbana, IL; [4]Department of Nutrition and Health Sciences, Ball State University

Background: Mineral and bone disorder (MBD) is highly prevalent among hemodialysis (HD) patients and is associated with increased morbidity and mortality. Despite the pharmacological treatment for MBD, its prevalence remains high. The supplementation of fermentable dietary fiber may lead to an enhanced absorption of minerals mediated by the production of short-chain fatty acids (SCFA) by the gut microbiota, which has benefited other populations with MBD. However, this mechanism remains unexplored in HD patients. Our objective was to examine the effect of a 4-week supplementation of inulin on blood minerals and fecal SCFA in HD patients. Methods: Twelve HD patients were recruited (56±10 y, 50% M, 58% AA, 31.2±9.2kg/m2). In a randomized, double-blind, placebo-controlled, crossover design subjects consumed inulin (IN) [10g/d for females; 15g/d for males] or maltodextrin (CON) [6g/d for females; 9g/d for males] providing the same amount of energy per day with a 4-week washout period between periods. Plasma and fecal samples were obtained before and after each supplementation period. Blood minerals were assessed through an auto-analyzer, while SCFA by gas-chromatography. Dietary recalls of the 48h before the fecal sample collection were obtained as well as gastrointestinal (GI) symptoms in a 4-point Likert scale (1=no discomfort, 4=severe discomfort). A within-subjects analysis was performed with treatment (IN, CON), time (Pre, Post), and the variables of interest. Results: IN did not produce any changes in blood minerals ($p>0.05$ for all). There was a time effect for fecal excretion of acetate and propionate, but not butyrate (acetate pre 219.48±39.31 vs. post 298.47±47.41 umol/g of dry matter (DM), $p=0.032$; propionate pre 70.29±13.27 vs. post 89.74±15.33 umol/g DM $p=0.027$; butyrate pre 40.89±8.05 vs. post 54.58±11.36 umol/g DM, $p=0.12$) and a trend towards a group effect for butyrate (IN 43.10±9.19 umol/g DM vs. CON 52.37±9.34 umol/g DM, $p=0.075$), but no treatment by time interactions. Total SCFA fecal excretion was not different between treatments, but there was a time effect (pre 330.67±58.54umol/g DM vs. post 442.79±68.18umol/g DM; $p=0.03$), with no carryover effect for those that were randomized to IN first ($p=0.141$). Flatulence was the only GI symptom different between treatments, being higher in the IN group (IN 1.69±0.85 to 2.53±1.12 vs. CON 1.75±1.05 to 1.66±0.78, p interaction=0.026). There was no difference in total macronutrients, but IN corrected dietary fiber intake (IN 7.9±5.3 to 15.4±2.7g/1000kcal vs. CON 6.7±2.5 to 7.8±5.2g/1000kcal; p interaction= 0.024). Conclusion: A 4-week supplementation of IN did not produce significant changes in plasma levels of blood minerals ($p>0.05$). Contrary to our hypothesis, there was also no increase in fecal excretion of SCFA with IN supplementation and both, IN and CON, had a higher excretion of acetate and propionate after supplementation. More studies are needed to examine the effects of IN on SCFA utilization and other markers of BMD including those related to bone formation and resorption in HD patients.

Bazedoxifene and conjugated estrogen combination improves gut-liver axis health

Karen L. Chen[1], Y.C Zhao[2], G. Rossi[3], K. Hieronymi[2], X. Liu[2], M.J. Miller[1,2], L.S. Auvil[4,5], M.E. Welge[4,5,6,7], C.B. Bushell[4,5,6,7], R.L. Smith[3,6,7], Z. Madak-Erdogan[1,2,6,]
[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]Department of Pathobiology, University of Illinois at Urbana-Champaign, Urbana, IL; [4]Illinois Informatics Institute, University of Illinois at Urbana-Champaign, Urbana, IL; [5]Applied Research Institute, University of Illinois at Urbana-Champaign, Urbana, IL; [6]Institute for Genomic Biology, University of Illinois at Urbana-Champaign, Urbana, IL; [7]National Center for Supercomputing Applications, University of Illinois at Urbana-Champaign, Urbana, IL

Bazedoxifene and conjugated estrogens (CE+BZA) combination has been shown to prevent visceral adiposity and weight gain after menopause. However, its interaction with the microbiota has yet to be examined. In the present study, we use several genomics and postgenomics technologies to characterize the effects of various estrogens on the health of gut-liver axis. As reported in previous studies, CE+BZA combination is very effective at preventing ovariectomy-induced weight gain in mice fed a high-fat diet. Additionally, CE+BZA induces unique liver transcriptomic and blood metabolite profiles compared to estradiol, conjugated estrogens alone, and bazedoxifene alone. Several pathways and serum metabolites influenced are associated with lower rates of inflammation and overall benefits to gut and liver health. Finally, microbiome analysis shows that several bacterial species that potentially metabolize estrogens and affect their half-life in the body were significantly changed in CE+BZA treated mice. Our findings indicate a possible link between certain estrogens and gut microbiome and suggest a metabolic benefit of estrogens through manipulation of the gut-liver axis.

Weight status and visceral adiposity are related to intraindividual variability in cognitive function

Morgan R. Chojnacki[1], C.G. Edwards[1], N.W. Baumgartner[2], A.M. Walk[2], A.R. Covello[2], G.E. Reeser[2], H.D. Holscher[1,3], N.A. Khan[1,2]
[1]Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL; [2]Department of Kinesiology and Community Health, University of Illinois at Urbana-Champaign, Urbana, IL; [3]Department of Food Science and Human Nutrition, University of Illinois at Urbana-Champaign, Urbana, IL

Although the metabolic consequences of obesity are well studied, less is known regarding the cognitive implications of obese weight status and fat distribution. We investigated the relationship between weight status and adiposity (whole body and visceral) and intraindividual variability (IIV) during a cognitive control task. Adults (34.2 ± 5.9 years [N=82, 45 females]) underwent DXA to determine %fat mass and visceral adipose tissue (VAT). Cognitive control was assessed using a modified Eriksen Flanker task. IIV was assessed as standard deviation of reaction time (SDRT) and coefficient of variation of reaction time (CVRT). Covariates assessed included intelligence quotient (IQ) measured using the Kaufman Brief Intelligence Test and demographic factors. Following adjustment of covariates, regression analyses using BMI as a predictor yielded marginally significant changes in R^2 for congruent accuracy (β=-0.22, P=0.07), congruent SDRT (β=0.22, P=0.10), congruent CVRT (β=0.22, P=0.09), and incongruent SDRT (β=0.21, P=0.07). VAT predicted significant changes in R^2 for incongruent accuracy (β=-0.27, P=0.03). %Fat mass predicted marginally significant changes in R^2 for incongruent accuracy (β=-0.32, P=0.09) and incongruent CVRT (β=0.31, P=0.06). Relative to their healthy weight counterparts, obese participants exhibited lower accuracy in the incongruent condition (2.96%; 95% CI 0.36 to 5.55) and higher SDRT in the incongruent condition (-13.96; 95% CI -27.43 to -0.49). In conclusion, weight status and visceral adiposity were negatively

associated with cognitive function, particularly during the task condition requiring greater modulation of attentional control. These findings provide further support that the negative implications of obesity and visceral adiposity extend to cognitive health as well. Funded by the Department of Kinesiology and Community Health at the University of Illinois and the Hass Avocado Board.

Relationship between solid food introduction and picky eating in the STRONG Kids 2 cohort

Natasha Chong Cole[1], S.Y. Lee[1,2], S.M. Donovan[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

Picky eating behavior is prevalent in toddlers and has been linked to infant feeding practices, such as complementary feeding. However, few studies have explored how the introduction of solid food affects picky eating in early childhood. The objective of this study was to examine associations between types of solid food introduced during infancy and picky eating behavior in children 18-months of age. Participants were drawn from an ongoing STRONG Kids 2 birth cohort of mother-infant dyads (current study n = 259, full sample n = 440). Mothers responded to survey questions about the amount and type of complementary food given to their infants during the introduction to solids, their child's picky eating behavior at 18-months (Oregon Research Institute Child Eating Behavior Inventory), and whether they breastfed their child during the introduction to solids. Ordinal logistic regression (i.e., proportional odds model) was used to determine associations between the introduction of solid foods and children's picky eating behavior. All analyses controlled for child sex, age of introduction to solids, breastfed status, and parent education level. Children who were introduced to pureed meat, pureed fish, and pureed vegetables during complementary feeding were more likely to be perceived as a picky eater at 18 months. Whereas, children who were introduced to regular fish and vegetables eaten by the rest of the family were less likely to be perceived as a picky eater at 18 months. There was no association between picky eating and the introduction of fruit, juice, cereal, sweets, eggs, or dairy. Overall, our findings suggest that early exposure to various tastes and textures may influence the development of picky eating later in childhood. Further research is needed to determine the influence of the timing and type of solid food introduction on children's long-term dietary variety and eating behavior. This material is based upon work that is supported by the National Institute of Food and Agriculture, U.S. Department of Agriculture, under award number 2011-67001-30101, and the Dairy Research Institute.

Early life milk intake among infants of different feeding modes

Erin C. Davis[1], S.M. Donovan[1,2], P. Dong[3]
[1]Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL; [2]Food Science and Human Nutrition, University of Illinois at Urbana-Champaign, Urbana, IL; [3]Department of Children's Healthcare, Children's Hospital of Fudan University, Shanghai, China

Feeding mode is known to impact an infant's growth pattern throughout the first year of life, which can be an important factor in the risk of childhood obesity. While breastfeeding has been shown to be protective against later overweight and obesity, the underlying mechanisms involved remain unclear. Feeding practices of young infants are hard to measure, but may provide valuable information for clinicians and researchers studying the long-term implications of early life growth trajectories. It is hypothesized that feeding mode affects self-regulation and infant satiety; however, few studies have investigated whether intake characteristics differ among infants who are exclusively breastfed (EBF), mixed-fed (MF), or exclusively formula-fed (EFF). The objective was to assess whether feeding frequency, average intake per feeding, and overall daily intake differ among infants of different feeding regimes, and whether these characteristics may be related to the

infant's weight-for-length (WFL) Z-score and maternal BMI. Intake data was collected for 191 healthy, 6-week old infants, enrolled in the STRONG Kids 2 cohort at the University of Illinois at Urbana-Champaign. Mothers weighed infants, before and after each feeding, over an average of 23.38 ± 2.26 hours, in order to measure intake volume. Feeding mode was assessed from a questionnaire completed by the mother. The overall intake weight (ml/kg BW) consumed across the entire weighing period was not significantly different between the 3 feeding methods. Average intake per feeding, across all feeding modes, was positively associated with overall ml/kg intake ($P<0.0001$) and negatively associated with feeding frequency ($P<0.0001$). Feeding frequency tended to differ by feeding mode ($P=0.056$). EBF infants (n = 151) fed on average 9.17 ± 1.87 times across the entire weighing period, which was significantly greater than the number of feeds of 7.92 ± 1.31 recorded for the EFF infants (n = 12). The feeding frequency of MF infants (n = 28) did not differ from that of EBF or EFF infants. Average intake per feeding was significantly higher among EFF infants (102.2 ± 34.0) compared to both EBF infants (84.4 ± 25.5) and MF infants (74.8 ± 29.4), which did not differ from each other. Further analysis was completed to evaluate differences among 132 EBF infants based on whether or not mothers indicated regular breast milk pumping. While the overall intake (ml/kg) and total number of feeds per day did not differ among the two groups of EBF infants, average intake per feeding tended to be greater ($P=0.06$) in infants whose mothers regularly pump breast milk. While none of the reported feeding characteristics were associated with infant WFL Z-score, feeding frequency was negatively associated with maternal BMI at 6 weeks postpartum. Average intake per feeding and overall intake (ml/kg) were not associated with maternal BMI. These findings suggest that intake characteristics of infants differ based on feeding mode and may provide context regarding differences in growth trajectories observed during later infancy. Supported by the National Dairy Council (NDC).

Assessment of dietary intervention compliance of subjects participating in an ongoing randomized-controlled trial

Jessica R. Dietrich[1], J.L. Kaczmarek[2], G.E. Reeser[3], N.A. Khan[2,3], H.D. Holscher[1,2]
[1]Department of Food Science and Human Nutrition, University of Illinois at Urbana-Champaign, Urbana, IL; [2]Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL; [3]Department of Kinesiology and Community Health, University of Illinois at Urbana-Champaign, Urbana, IL

Background: When conducting human subject research, outcomes vitally depend upon how well participants follow instructions provided by the research team. Assessing compliance to interventions enables participant classification as per protocol or intention to treat for outcome assessments. It also provides insight into participant characteristics that may be related to study compliance, with relevance to future dietary intervention studies. Objective: Herein we aimed to determine overall self-reported compliance of study participants to a dietary intervention during an ongoing randomized, controlled trial. Our secondary objectives were to determine whether factors such as age, sex, income, or education are related to study compliance. Methods: All study participants were counseled to consume the entire study meal daily throughout a 12-week intervention. Daily compliance records were provided throughout the study. Participants were instructed to indicate the percentage of the meal consumed each day. Consumption was computed on a per-week basis for each participant. Statistical analyses was performed in SAS 9.4, accepting a p-value of 0.05 as statistically significant. A general linear mixed model was created for each demographic variable using compliance as the outcome measure and including week of the study as a repeated measure predictor. Week was included in order to examine not only what variables were associated with compliance, but also how compliance changed over the duration of the study. Results: The average overall consumption of the control group (n=31) was 87%, and the average overall consumption of the intervention

group (n=27) was 90%. The average meal consumption for females was 86% (n=36) and 92% (n=22) for males. The analysis of the entire participant pool (n=58) showed no significant relationships between meal compliance and group, age, sex, income, or education level. Conclusion: These results reveal that overall study compliance is high with no differences between groups or over time. Even when other variables such as age, sex, income, and education were considered, there still were no significant associations with compliance, nor did compliance decrease significantly over the course of the study.

Mobile multimedia effects on cognitive engagement: association between app format, learning and cognitive load

Kristen N. DiFilippo[1], K.E. Mathewson[2], W. Huang[3], J.E. Andrade[1,4], K.M. Chapman-Novakofski[1,4]
[1]Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL; [2]Department of Psychology, University of Alberta, Edmonton, AB, Canada; [3]Department of Education Policy, Organization & Leadership, University of Illinois at Urbana-Champaign, Champaign, IL; [4]Department of Food Science and Human Nutrition, University of Illinois at Urbana-Champaign, Urbana, IL

Diet-related mobile applications (apps) are being used by clients and practitioners. In any form of mobile learning environment (MLE), there is limited evidence to support that multimedia improves learning efficiency. This lack of understanding could lead to MLE development that overloads learners' cognitive and motivational processing capacities, compromising desired learning engagement. The objective of this study was to compare participants' cognitive load from learning declarative knowledge on food concepts delivered via a multimedia-intensive gaming app or a passive app with the same content using electroencephalogram (EEG) measurements. Participants (n=20) completed first one app, then the other a month later, counter-balanced in order, with knowledge tested one week after each session. Most participants had correct declarative knowledge measured during app use (median 97.7%, both apps) and at post-testing (median 100%, both apps). There were no significant knowledge differences between the gaming and passive app during use, post-testing, or from app use to post-test. For passive, 63% improved knowledge while in gaming 42% improved. At baseline, 6 scored 100% (range 81.4-100%) in passive compared to 7 in gaming (range 95.3-100%). 15 and 14 scored 100% at post-testing respectively. EEG spectra (the power of different oscillations in the brain) were recorded from participants while they used each app. More power in the 8 -10 Hz range (alpha waves) in the gaming app was found, associated with reduced cognitive load. The decreased cognitive load in the gaming app corroborate with the principle that MLEs support a more efficient, focused learning process.

Relationship between whole grain consumption and selective attention

Jackson Evensen[1], Caitlyn G. Edwards[2], S.V. Thompson[2], H. Holscher[2,3], N.A. Khan[1,2,4]
[1]Department of Kinesiology and Community Health, University of Illinois at Urbana-Champaign, Urbana, IL; [2]Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL; [3]Department of Food Science and Human Nutrition, University of Illinois at Urbana-Champaign, Urbana, IL; [4]Neuroscience Program, University of Illinois at Urbana-Champaign, Urbana, IL

Introduction: Greater habitual diet quality has been associated with weight regulation and reduced risk for chronic diseases including Cardiovascular Disease and Type-2 Diabetes. However, the role of markers of diet quality – wholegrain consumption in particular – in cognitive function remains unclear. Studying these relationships would bring to light the importance of whole grain consumption for both physical and mental health. Methods: Adults between 25-45 years (N=76, 32 males) reported their dietary intake using the National Cancer Institute's Food Frequency Questionnaire. Overall diet quality was assessed using the Healthy Eating Index (HEI-2010) and whole grain consumption was measured using the whole

grain component of the HEI-2010. Selective attention was assessed using a modified Eriksen flanker task. Overall intellectual ability (IQ) and whole body adiposity (%Fat) was measured using the Kaufman Brief Intelligence Test and dual energy x-ray absorptiometry, respectively. Results: Partial correlations were conducted to examine the relationship between whole grain consumption and flanker task variables following adjustment of age, sex, IQ, and total HEI-2010. Whole grain consumption correlated with several task measures including accuracy in the both the congruent ($r=0.37$, $P<0.01$) and incongruent task conditions ($r=0.28$, $P=0.02$). Further, although no significant relationships were observed for mean response time (all $Ps> 0.26$), greater whole grain subcomponent scores were related to lower intraindividual variability (coefficient of variation) in reaction time during the incongruent ($r=-0.33$, $P<0.01$) but not congruent condition ($r=-0.18$, $P=0.13$). Conclusion: These data indicate that individuals with greater whole grain intake exhibited superior selective attention, as indicated by higher response accuracy and reduced variability in response time. Given that these relationships persisted even after adjusting for overall diet quality and important health and demographic factors provides support for the selective importance of whole grain intake for cognitive function. Future experimental studies are necessary to determine the impact of changes in whole grain intake on changes in cognitive function. Funded by the Department of Kinesiology and Community Health at the University of Illinois and the Hass Avocado Board.

The *2015 Dietary Guidelines for Americans*: adherence to key recommendations in Hispanic females

Bridget Hannon[1], E. Villegas[2], A. Wiley[2], M. Teran-Garcia[1,2,3]
[1]*Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL;* [2]*Department of Human Development and Family Studies, University of Illinois at Urbana-Champaign, Urbana, IL;* [3]*University of Illinois Extension, University of Illinois at Urbana-Champaign, Urbana, IL*

The Dietary Guidelines for Americans (DGAs) are released by the United States Department of Agriculture and Department of Health and Human Services to encourage consumption of a healthy eating pattern. Key recommendations of the 2015 DGAs include limiting saturated fats and sugars, and increasing consumption of a variety of fruits and vegetables, low-fat dairy, and whole grains. The Healthy Eating Index (HEI) is commonly used as a measure of adherence, but the current HEI does not reflect the newest DGAs. Here, we propose a new HEI to assess adherence (HEI-A) to the 2015 DGAs in a cohort of Hispanic females, a group disproportionately affected by obesity and related comorbidities. Fifty Hispanic females completed a semi-quantitative food frequency questionnaire. Anthropometric measurements were also taken. Key recommendations from the 2015 DGAs for women were reviewed and an adherence index was derived from ten categories, each with a maximum score of ten. Total adherence was the sum of these 10 categories (max = 100). The HEI-A is similar to the 2010 HEI, but reflects changes made in the 2015 DGAs.The average adherence score was 44.49 (SD: 14.47, 95% CI: 40.14-48.83). High fruit and vegetable intake was significantly associated with high adherence score ($p=0.001$). Low intake of saturated fat was significantly correlated with higher HEI-A ($r=0.71$, $p=0.03$). The category with the greatest adherence was reduction of added sugars, with a mean score of 5.81 (SD: 2.94) out of 10. Adequate consumption of fruits and vegetables had the lowest mean of 2.89 (SD: 3.53). HEI-A was not correlated with body mass index or waist circumference, and there were no significant differences between normal weight, overweight, or obese individuals. On average, participants were meeting fewer than half the recommendations of the 2015 Dietary Guidelines for Americans, regardless of weight status. Of note, the lowest adherence was in consumption of fruits and vegetables, but those individuals meeting this recommendation had overall greater HEI-A scores. The DGAs are released to encourage healthy eating to prevent disease, and nutrition education tailored to Hispanics

should continue to focus on emphasizing adherence to prevent obesity and related disease in this at-risk population.

Dietary fiber and the human gastrointestinal microbiota as predictors of bone health

Anne Y. Hou[1], J.L. Kaczmarek[2], N.A. Khan[2,3], H.D. Holscher[1,2]
[1]Department of Food Science and Human Nutrition, University of Illinois at Urbana-Champaign, Urbana, IL, [2]Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL, [3]Department of Kinesiology and Community Health, University of Illinois at Urbana-Champaign, Urbana, IL

Background: Increasingly, the gastrointestinal (GI) microbiota is emerging as a factor relevant to bone health. Proposed mechanisms of the inter-relationships among dietary fiber, the GI microbiota, and bone health include increased availability of absorbable calcium because of lowered gut pH related to bacterial fermentation of fiber; short-chain fatty acid (SCFA) signaling from bacterial metabolism of dietary fibers that regulates mineral absorption and cell proliferation, thereby increasing surface area for absorption; and suppression of systemic inflammation, a risk factor for osteoporosis, by the microbiota. However, these relationships are under-investigated in human populations. Objective: We aimed to determine the relationship among bone health, dietary fiber consumption, and the GI microbiota and their metabolites (i.e., SCFAs) in adults. Methods: Cross-sectional analyses were conducted on 25-46-year-old adults (n=64, 36 females). Dietary fiber, calcium, and vitamin D intake were assessed using a 7-day diet record. Body composition and bone density were assessed using dual-energy X-ray absorptiometry (DXA). Fecal samples were utilized to assess bacterial composition, SCFA concentrations, and pH. Barcoded amplicon pools of bacterial sequences were generated using high-throughput sequencing followed by analysis using QIIME 1.9.0. SCFAs were quantified on a dry matter basis using gas chromatography. Fecal pH was measured using a pH meter. Relationships between bacterial relative abundances, SCFA concentrations, and pH were first assessed using Pearson (for normally distributed variables) and Spearman (for non-normally distributed variables) correlations, with partial correlation for normalized dietary fiber intake (fiber/kcal). Then, a regression model was conducted to assess the relationship between fiber and bone density after adjusting for covariates including age, sex, and BMI. Results: Bivariate analyses revealed that greater bone mineral density tended to be correlated with higher intakes of fiber (r=0.24, p=0.03). Bone mineral density was inversely related to Blautia (r=-0.28, p=0.03) and Clostridiaceae (rho= -0.31, p=0.01). Greater bone mineral density tended to be related to higher fecal butyrate concentration (r=0.31, p=0.08) and lower fecal pH (r=-0.30, p=0.06). Similar to bone mineral density, bone mineral content was inversely related to Blautia (r=-0.26, p=0.04) and Clostridiaceae (rho=-0.27, p=0.03); and greater bone mineral content tended to be positively related to fecal butyrate concentration (r=0.30, p=0.09) and negatively related to fecal pH (r=-0.30, p=0.06). Interestingly, Blautia and Clostridiaceae were not related to fecal pH or butyrate. The linear regression model revealed a positive relationship between greater bone mineral density and dietary fiber intake (p=0.02) Conclusions: In summary, bone mineral density was associated with greater intakes of fiber, lower fecal pH, and higher fecal concentrations of butyrate, which supports proposed mechanisms. Additional study is necessary to determine the role of specific microbes in this relationship.

Human gastrointestinal microbes vary throughout the day

Jennifer L. Kaczmarek[1], H.D. Holscher[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

Background: Human health is intricately intertwined with the composition and

function of the trillions of microorganisms that make up the gastrointestinal (GI) microbiota. Habitual diet patterns, rapid changes in dietary fat and fiber composition, and consumption of dietary fibers and prebiotics have all been shown to impact the GI microbiota. Intriguingly, the impact of diet on the microbiota may not only be related to what we eat, but also to when we eat. Emerging research suggests gut microbes experience diurnal rhythms, and that the health effects of eating patterns, such as time-restricted feeding and meal frequency, may also be related to the GI microbiota. **Objective:** We aimed to investigate the relationship between time of day and the composition and function of the gastrointestinal microbiota in healthy adults. **Methods:** Healthy adult male and female participants (n=29) provided up to 9 fecal samples (189 total samples) within 15 minutes of defecation over the course of a 15 week trial. Fecal DNA extracts were subjected to 16S ribosomal RNA amplicon-based high-throughput sequencing to assess the composition of the microbiota. Sequences were clustered into operational taxonomic units (OTUs) using the Greengenes 13-8 reference OTU database (97% similarity). Fecal short-chain fatty acids (SCFA), products of microbial metabolism, were measured by gas chromatography mass spectroscopy. Dietary records were kept throughout the sample collection period and analyzed using the Nutrition Data System for Research (NDSR). Correlations were performed between sample time and bacterial OTUs, and partial correlations between sample time and SCFA concentration were performed with total dietary fiber intake normalized by energy intake as the controlling variable. **Results:** Time of defecation ranged from 07:30 to 22:00, median=10:40. Concentrations of acetate, butyrate, and propionate decreased over the course of the day (r=-0.35, -0.31, -0.33, respectively, $p<0.0001$ for all). The abundance of *Clostridium spp.* also decreased throughout the day (r=-0.20, $p<0.01$). Conversely, *Dorea* (r=0.18, p=0.01), *Oscillospira* (r=0.36, $p<0.0001$), *Ruminococcus* (r=0.19, p=0.01) and *Butyricimonas* (r=0.16, p=0.03) increased over the course of the day. **Conclusions:** These novel results support and expand preclinical research findings—*Oscillospira* and *Ruminococcus*, as well as members of the Lachnospiraceae family and Clostridiales order, have been shown to exhibit diurnal oscillations in rodent models. Our findings also reveal functional changes in the microbiota over the course of the day, as evidenced by reductions in SCFA concentrations with time. In summary, these results suggest that diurnal patterns are also relevant factors for assessments and interventions aimed at modulating the GI microbiota.

Nutritional habits and FODMAPs in relation to gastrointestinal issues of endurance athletes

Lauren Killian[1], S-Y. Lee[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*

Gastrointestinal (GI) issues have been shown to be prevalent among endurance athletes and can significantly impair performance during training and competition. The distribution and characteristics of these symptoms are analogous to those in patients with irritable bowel syndrome (IBS). Recent studies have shown IBS symptom improvement upon implementation of a diet low in fermentable oligosaccharides, disaccharides, monosaccharides, and polyols (FODMAPs). No studies have evaluated the nutritional intake of U.S. endurance athletes for FODMAPs in relation to GI symptoms. **Objective:** The objective of this study was to examine the nutritional habits of endurance athletes from a FODMAP perspective to determine the association between FODMAPs and athletes' GI distress. **Methods:** A 93-item online questionnaire on endurance athlete nutritional habits and lower GI symptom frequency was previously validated. The questionnaire was completed between December 2015 and January 2017 by 417 athletes in the U.S. completing a marathon, ultra-marathon, half-distance triathlon, or full-distance triathlon within the calendar year. **Results:** Only 0.7% of athletes reported following a low FODMAP diet in everyday

life. Of the typical pre-race dinners reported, 87.9% included a potentially high FODMAP source, while 65.7% specifically mentioned a high FODMAP food (e.g. pasta, pizza, bread). For a typical pre-race breakfast, 84.8% of athletes reported potentially high FODMAP foods, with 55.4% reporting a wheat-type breakfast food (e.g. bagel, toast). Potentially high FODMAP food intake at these meals, however, was significantly correlated with the frequency of only two GI symptoms during competition, and the correlations were weak and negative in both cases. Other potentially high FODMAP foods reported were sports nutrition products such as sports drinks, gels, energy bars, or homemade products, which include ingredients like fructose, honey, sugar alcohols, and fruit. The usage frequency of several of these product types was positively correlated with the frequency of various GI symptoms ($p<.05$) during and following training and competition. Of the homemade products reported during training and competition, 64.4% and 62.1% were potentially high in FODMAPs, respectively (e.g. sandwiches or bars with dried fruit or honey). **Conclusions**: Endurance athletes commonly consume potentially high FODMAP foods. While there are some correlations between these foods and GI symptoms, it is likely that, as in the general population and patients with IBS, certain individuals have differing degrees of sensitivity. Testing of FODMAP levels in popular sports nutrition products is recommended to more accurately identify the FODMAP intake of endurance athletes and further examine correlations with GI symptoms.

Acculturation and Hispanic-heritage mothers' perception of child weight as related to child feeding practices

Viridiana Luna[1], E. Villegas[2], B. Hannon[1], A. Hammons[3], M. Cruz-Santiago[2], A. Wiley[2, 4], M. Teran-Garcia[1, 2, 4]
[1]*Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL;*
[2]*Department of Human Development and Family Studies, University of Illinois at Urbana-Champaign, Urbana, IL;*
[3]*Department of Child and Family Sciences, California State University, Fresno, CA;*
[4]*University of Illinois Extension, University of Illinois at Urbana-Champaign, Urbana, IL*

Hispanic children in the United States are disproportionately affected by obesity. Previous analysis revealed that mothers participating in the *Abriendo Caminos* intervention aimed at preventing childhood obesity in Hispanic-heritage families, incorrectly classified their overweight/obese child as normal weight. Effective obesity prevention efforts must consider mothers' roles in child feeding practices and their impact on child weight status over the life course. Acculturation and mother perception of weight may explain some child feeding practices. The aim of this study was to determine whether mothers' acculturation and perception of children's weight was associated with mothers' rationale for offering children snacks. Mother-child dyads (n=71) of Mexican or Puerto Rican descent were recruited as part of the *Abriendo Caminos* randomized control/workshop multi-state intervention. Here we report on the cross-sectional baseline data acquired to date from participating mothers in the Illinois and California cohorts. The Brief Acculturation Rating Scale for Mexican Americans-II (ARSMA-II) was used for assessment of acculturation and a set of questions previously developed by Blaine and colleagues (Nutrients, 2015) was used to assess the rationale behind offering snacks. Anthropometric measures were collected from all participants. One-way ANOVA and Fisher's LSD were used to compare differences in mean times per week that snacks were offered. At baseline, 57.8% of children were overweight or obese, while only 26.8% of mothers categorized their child as such. Over half of the mothers (64.8%) were categorized with low levels of acculturation (very Hispanic oriented). There were no significant associations between child BMI, acculturation, mother perception of child weight and reasons mothers offered snacks. A further understanding of how weight perceptions and acculturation influence health and feeding practices can equip professionals to provide culturally relevant tools for mothers to enact positive changes in their families. This research was supported by the Agriculture and Food Research Initiative Competitive Grant no. 2015-68001-23248 from the USDA National Institute of Food and Agriculture.

Effects of a 6 week aerobic exercise intervention on gut bacterial metabolites in lean and obese adults

Lucy J. Mailing[1], J.M. Allen [2], G. Niemiro[2], J. Cohrs[2], H. Holscher[1,3], M. De Lisio[1,2], J.A. Woods[1,2]
[1]Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL; [2]Department of Kinesiology and Community Health, University of Illinois at Urbana-Champaign, Urbana, IL; [3]Department of Food Science and Human Nutrition, University of Illinois at Urbana-Champaign, Urbana, IL

Introduction: Dietary changes have been shown to significantly alter the composition and metabolic function of the gut microbiota in both mice and humans; however, study of the effects of exercise alone on the gut microbiota and microbial metabolites has been limited to mice. Short chain fatty acids (SCFAs) are bacterial metabolites with numerous downstream effects on the host, influencing satiety, inflammation, and adiposity. Here, we characterized the effects of an aerobic exercise intervention on fecal SCFA output in lean and obese humans. Methods: Previously sedentary but otherwise healthy adults (n=11 lean; n=4 obese) underwent a six week aerobic exercise intervention. Participants performed 3 exercise sessions per week on a bike and/or treadmill, starting with 30 min at 60% HRR and building up to 60 min at 75% HRR by week 6. Fecal samples were collected before and after the intervention, preceded by a 3-day control diet. Approximately 0.1 g of fecal samples was immediately stabilized in metaphosphoric acid until SCFA analysis by gas chromatography/mass spectrometry (GC/MS). Results: Six weeks of exercise caused a significant increase in the fecal concentration of butyrate, acetate, and propionate ($p<0.01$), among lean individuals. The changes in acetate and butyrate concentrations were strongly correlated to changes in lean mass as a result of training, an effect driven by the lean individuals ($r=.633$ $p<0.029$ and $r=0.854$, $p<0.01$, respectively). However, exercise training failed to increase fecal SCFA concentration in our small sample of obese individuals ($p>0.05$). Conclusion: A 6-week aerobic exercise intervention is sufficient to increase fecal SCFA concentrations in lean, adult humans. This effect was not observed in obese individuals, however, and thus suggests that exercise-induced metabolic changes within the gut may be influenced by obesity status.

Designing and evaluating a training protocol for visual estimation of fruits and vegetable intake among K-2nd grade students

Natalie Masis[1], K. Chapman-Novakofski[1,4], J. McCaffrey[2], S. Johnson[3],
[1]Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL; [2]University of Illinois Extension, University of Illinois at Urbana-Champaign, Urbana, IL; [3]University of Colorado at Denver, Denver, CO; [4]Department of Food Science and Human Nutrition, University of Illinois at Urbana-Champaign, Urbana, IL

Objective: To design a replicable training protocol for visual estimation of fruit and vegetable (FV) intake of K-2nd grade students through digital photography of lunch trays that results in trainees recording reliable data for food served and food eaten. **Design, Setting, Participants, and Intervention**: Protocol development through literature and researcher input was followed by 3 trainings of 3 trainees and a practice session at a local elementary school. Data were then collected at 2 elementary schools for K-2nd graders' lunches. School 1 included nutrition education and salad bar; school 2 was control school. **Outcome Measures and Analysis**: Intraclass correlation coefficients (ICC) for trainings and lunchroom data collection. **Results**: By training 3, ICC was substantial for amount of FV served (0.86, $p<.01$); percentage FV consumed (0.954, $p<.01$), amount F served (0.97, $p<.01$); amount V served (0.81, $p<.01$); percentage V consumed (0.98, $p<.01$). In-school estimates for ICCs were all significant for amounts served at 1 school, and amount FV consumed at both schools. Mean percentages consumed differed between the 2 schools (fruit consumed: 76.9% + 38% school 1 vs 42.2% + 40% school 2; vegetable consumed: 67% + 44% school 1 vs 18% +32% school 2).

Conclusions and Implications: The protocol resulted in reliable estimation of FV intake using digital photography. Being able to accurately estimate FV intake will benefit intervention development and evaluation.
Funding: University of Illinois Extension

Outcomes and lessons of a 6-month nutrition and exercise pilot program in hemodialysis patients

Luis Perez[1], L.E. Chan[2], B. Burrows[3], A. Biruete[1], J.L. Barnes[2], K.R. Wilund[1,3]
[1]Division of Nutritional Sciences, University of Illinois, Urbana, IL; [2]Department of Family and Consumer Sciences, Illinois State University, Normal, IL; [3]Department of Kinesiology and Community Health, University of Illinois, Urbana, IL

Background: End-stage renal disease patients on hemodialysis (HD) often have poor nutrition and physical function that contribute to poor health outcomes such as an increased risk of falls, hospitalizations, and mortality. HD patients are also often prescribed highly restrictive diets and provided little support for physical activity. The purpose of this feasibility study was to improve nutritional and exercise knowledge, behaviors, and outcomes in HD patients. A major focus of the nutritional aspect of this intervention was a reduction in blood pressure (BP) primarily driven by reducing dietary sodium (Na). **Methods:** We recruited 32 patients (54 + 14 years, 56% male, 44% AA, 44% DM) from dialysis clinics in central Illinois. At baseline and at 6 months, subjects completed dietary recalls, nutritional and exercise surveys, physical function testing, fluid composition testing, and a standardized BP. After baseline testing, participants were randomly assigned to a volume control group (VC) or the VC protocol combined with an exercise intervention (VCE). The VC protocol was a nutrition intervention focused primarily on limiting dietary salt with BP medication management and progressive reduction of post-dialysis weight. The VCE group focused also on interdialytic cycling and at-home exercise counseling. Subjects received weekly interviews, coaching, handouts, flyers, clinic bulletin boards, and recipes. **Results:** There were no significant changes in BP (160+25 to 156+23 mmHg, p=.56) over time for all patients, but there was a significant reduction in number of BP medications (3+1 to 2+1, p=.003). Sodium intake was reduced for all patients, but was not significant (2.9 to 2.3 grams, p=.09). Meanwhile, energy and protein intake decreased, but was not significant (1618+1066 to 1366+455 kcal, p=.33 & 63+31 to 56+21 g, p=.47). However, total body water, extracellular fluid, and volume overload were decreased for all patients (45.8+10.8 to 44.3+8.8 p=.10, 21.7+5.8 to 20.5+4.5 p=.004, & 3.6+3.9 to 2.5+3.5 p=.01). This was accompanied by a significant decrease in weight (93.6+24.4 to 91.8+22.7 p=.02). Notably, Na knowledge increased in all patients (68+27 to 76+30 p=.06) as well as phosphorus knowledge (66+15 to 74+14 p=.04). **Conclusions:** Maintaining adequate energy and protein intake while limiting dietary Na is important for HD patients to preserve lean body mass and reduce the fluid volume overload that may be associated with poor outcomes such as hospitalizations and mortality. Although the reduction in Na intake was not significant, patients did have increased knowledge related to Na in foods. Furthermore, patients had a significant reduction in BP meds without a significant change in BP. Our further efforts over a longer time-period will continue to refine the study protocol to better support patients in maintaining adequate energy and protein needs while supporting patient confidence to follow a low-Na diet.

Differential uptake of RRR -tocopherol, *All-racemic* -tocopherol, and RRR -tocopherol into primary human aortic smooth muscle cells

Katherine M. Ranard[1], M. Kuchan[2], C. Lai[2], J.W. Erdman Jr[1,3]
[1]Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL; [2]Abbott Nutrition, Columbus, OH; [3]Department of Food Science and Human Nutrition, University of Illinois at Urbana-Champaign, Urbana, IL

Alpha-tocopherol (α-toc), one of the eight compounds constituting vitamin E, may play a role in preventing atherosclerosis in

humans. Previous studies have shown that severe α-toc deficiency promotes atherosclerosis in mice and that α-toc is anti-inflammatory. In contrast, another vitamin E vitamer, γ-tocopherol (γ-toc), may be pro-inflammatory. The properties of the synthetic (*all-racemic*) form of α-toc, which is commonplace in our food supply, should also be assessed; humans may have a biological preference for natural (*RRR*) α-toc. Consuming foods with differing forms of tocopherols could impact the vitamin E profile in human tissues. Our *in vitro* study aimed to compare these three human disease-relevant tocopherol forms (RRR α-toc, *all-racemic* α-toc, and *RRR* -toc), by first focusing on uptake of the vitamers into human vascular aortic smooth muscle cells (HVASMC). Primary HVASMC (pass <8) were grown to 70% confluency in 6-well plates. *RRR* α-toc, *all-racemic* α-toc, and *RRR* γ-toc were added to the media in DMSO (0.2% v/v) at 25uM to simulate physiological conditions of human serum. DMSO vehicle was also added to cells alone to serve as a control. After 24, 48, and 72 hours of incubation, cells from each treatment well (n=3 per group) were trypsinized and pelleted. Tocopherols were extracted from the HVASMC and analyzed via high-performance liquid chromatography. After 48 hours, there was an approximately 5-fold higher cell uptake of γ-toc than *all-racemic* α-toc and a 6-fold higher γ-toc uptake compared to *RRR* α-toc. After 72 hours, there was an approximately 6.5-fold higher and 7.5-fold higher cell uptake of γ-toc than *all-racemic* α-toc and *RRR* -toc, respectively. We will also report the impact of these vitamers on the transcription of atherosclerosis-related genes in this cell line, as well as how stimulation by a pro-inflammatory cytokine (TNF-α) following a dose of tocopherol impacts the gene expression profiles. Differential changes in gene expression between the three tocopherol forms could support the suggested non-antioxidative functions of *RRR* α-toc, as well as distinguish the impact of the individual tocopherol isomers. Funding provided by Abbott Nutrition through the Center for Nutrition, Learning and Memory, University of Illinois, Urbana-Champaign, and NIH grant P51OD011092.

Impact of isolated soy protein in non-alcoholic fatty liver disease progression: monitored by a novel quantitative ultrasound (QUS) method

Joe L. Rowles[1], J. Kelly[3], R.J. Miller[3], J. Berndt[3], C.C. Applegate[1], A. Han[3], M.A. Wallig[1,4], W.D. O'Brien Jr.[1,3], J.W. Erdman Jr.[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]Department of Electrical and Computer Engineering, University of Illinois at Urbana-Champaign, Urbana, IL; [4]Department of Pathobiology, University of Illinois at Urbana-Champaign, Urbana, IL

BACKGROUND: Non-alcoholic fatty liver disease (NAFLD) is the most common liver disease in the Western world, affecting 20% of the population. If left untreated, NAFLD may progress into non-alcoholic steatohepatitis (NASH), end-stage liver disease or hepatocellular carcinoma. Emerging evidence indicates that soy protein may protect the liver from steatosis, which may improve health outcomes. We hypothesized that a soy protein intervention would be effective in protecting against further steatosis and disease progression in mice fed a high fat diet. METHODS: Eight-week-old male C57BL/6J mice (n=70) were randomized onto an AIN-93G control diet (CON, n=20) or a high-fat atherogenic diet with a casein protein source (CAS, n=50). After 4 weeks on the CAS diet, when animals were expected to develop NAFLD, animals were randomized onto one of three diets: an atherogenic diet with a soy protein source (SOY, n=15), CAS (n=20) or the control diet (CAS-CON, n=15). We utilized a novel non-invasive QUS method to monitor stages of steatosis. Each animal received liver ultrasound scans at baseline (*in vivo*) and at euthanasia (*in vivo and ex vivo*). At 4, 9 and 12 weeks on study, animals from each group were euthanized. At euthanasia, serum was collected and the liver was harvested. Half of the liver's left lateral lobe underwent hematoxylin and eosin (H&E) staining (3- m

section). The right cranial lateral liver lobe was removed for ex vivo QUS scanning. The remainder of each liver was frozen for further analysis. RESULTS: Liver weight, as a percentage of body weight, was significantly increased with both atherogenic diets (CAS and SOY). CAS animals had significantly higher accumulation of lipids in the liver at each respective time point ($p<0.05$) compared to either dietary control group (CON or CAS-CON). CAS also had significantly higher serum cholesterol by week 12 compared to CON and CAS-CON. Ex vivo ($p<0.0001$) and in vivo ($p=0.047$) ultrasound attenuation was positively correlated with liver lipids concentrations. Serum alanine aminotransferase (ALT) and histology will be analyzed to determine hepatic damage and disease status. QUS attenuation and backscatter will be further correlated to histological measures of steatosis, fibrosis and inflammation in the liver. Total hepatic cholesterol will also be measured. CONCLUSIONS: Atherogenic diets were associated with an increase in liver weight, liver lipids and ultrasound attenuation. Replacing casein with soy as the protein source after four weeks of feeding failed to significantly reverse hepatic lipid accumulation or liver weight. The development of a QUS method to identify early stages of NAFLD and NASH would provide the capability to noninvasively quantify and monitor liver status and evaluate methods for intervention.

- **Gastrointestinal microbiota and cognitive function in adult females**

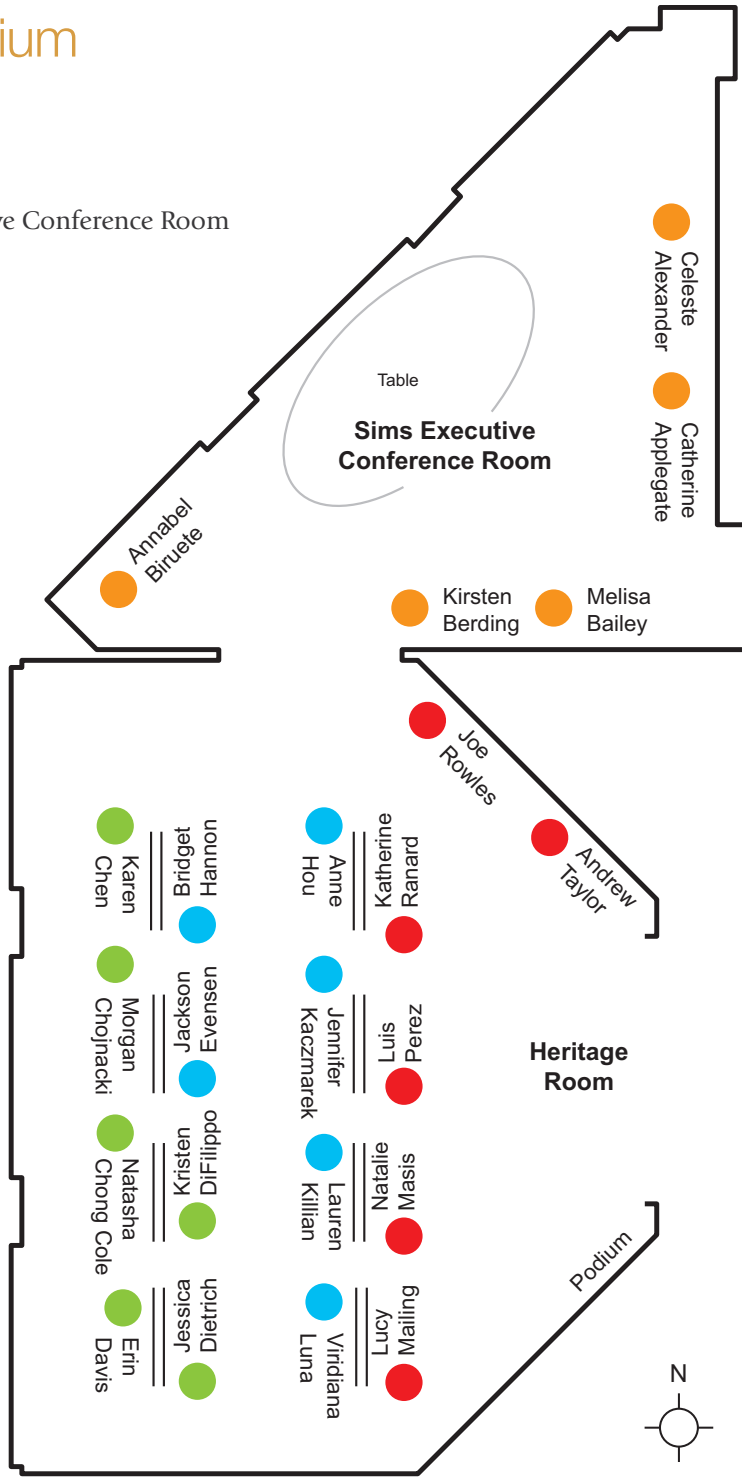
Andrew M. Taylor[1], C.G. Edwards[2], N.A. Khan[2,3], H.D. Holscher[1,2]
[1]*Department of Food Science and Human Nutrition, University of Illinois at Urbana-Champaign, Urbana, IL;* [2]*Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL;* [3]*Department of Kinesiology and Community Health, University of Illinois at Urbana-Champaign, Urbana, IL*

A converging body of literature demonstrates that the gastrointestinal microbiota are implicated in multiple aspects of health including cognitive function and brain health. However, this evidence is largely based on rodent models and there is a paucity of data linking characteristics of the gastrointestinal microbiota profiles and cognitive function in humans. Objective: We aimed to determine the relationship between the human gastrointestinal microbiota and cognition among adult females. Cross-sectional analyses were conducted to determine relationships between cognitive control and gastrointestinal microbiota of adult 25-45-year-old females (n=34, BMI=32.2 kg/m2). Executive function, specifically, interference control, was assessed using a modified flanker task. Interference scores were calculated for accuracy (congruent – incongruent) and reaction time (incongruent – congruent) with greater interference signifying poor ability to maintain task performance when faced with greater cognitive demand. Gastrointestinal microbiota taxonomy was obtained using a fecal sample. Following fecal DNA isolation, a Fluidigm Access Array was utilized to generate barcoded amplicon pools of archaeal, bacterial, and fungal sequences. High-throughput sequencing was conducted on a MiSeq using version 3 chemistry. Sequence data were analyzed using QIIME 1.9.0 and SAS 9.4. Whole body adiposity (% Fat) was assessed using DXA. Covariates assessed included habitual dietary fiber intake (National Cancer Institute's Diet History Questionnaire) and IQ (Kaufman Brief Intelligence Test). According to bivariate correlations, the Bacteroidetes:Firmicutes ratio was not related to %Fat ($r=0.15$, $p=0.38$) or dietary fiber ($r=-0.11$, $p=0.53$). Bacteroidetes and Firmicutes were differentially associated with interference control measures. Accuracy interference was inversely associated with Bacteroidetes ($r=-0.37$, $p=0.03$) and the Bacteroidetes: Firmicutes ratio ($r=-0.39$, $p=0.02$). Reaction time interference was also negatively correlated with Bacteroidetes ($r=-0.37$, $p=0.02$) and the Bacteroidetes:Firmicutes ratio ($r=-0.34$, $p=0.047$). Further, accuracy interference was correlated with Firmicutes ($r=0.34$, $p=0.043$). According to partial correlations, the relationship between accuracy interference and microbiota was mediated by IQ and dietary fiber/kcal (all

p's>0.07). However, the relationship between reaction interference and Bacteroidetes (r=-0.35, p=0.048) persisted even after adjusting for covariates. These results indicate that women with greater relative abundances of Bacteroidetes exhibited greater ability to maintain cognitive performance when faced with greater task demands. These findings are among the first to relate bacterial phylogenetic characteristics to executive function among adult humans. Further study is required to elucidate a causal relationship between dietary manipulation of microbiota composition and changes in selective aspects of cognitive performance.

Nutrition Symposium Poster Session

ACES Library, 1st Floor
Heritage Room and Sims Executive Conference Room
Wednesday, April 19, 2017
5:15 p.m. – 6:40 p.m.



Poster Judges

Orange Team
Dr. Rex Gaskins
Dr. Naiman Khan
Dr. Hans Stein

Green Team
Dr. Maria Cattai de Godoy
Dr. Tzu-Wen Liu Cross
Dr. Juan Loor

Blue Team
Dr. Laia Blavi
Dr. Hong Chen
Dr. Andrew Steelman

Red Team
Dr. Sayee Anakk
Dr. Ryan Dilger
Dr. Manabu Nakamura

Presenting Author Index

Winners of the 2016 University of Illinois Nutrition Symposium poster and oral competitions with keynote speaker, Dr. Paul S. MacLean

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