2016 NUTRITION SYMPOSIUM

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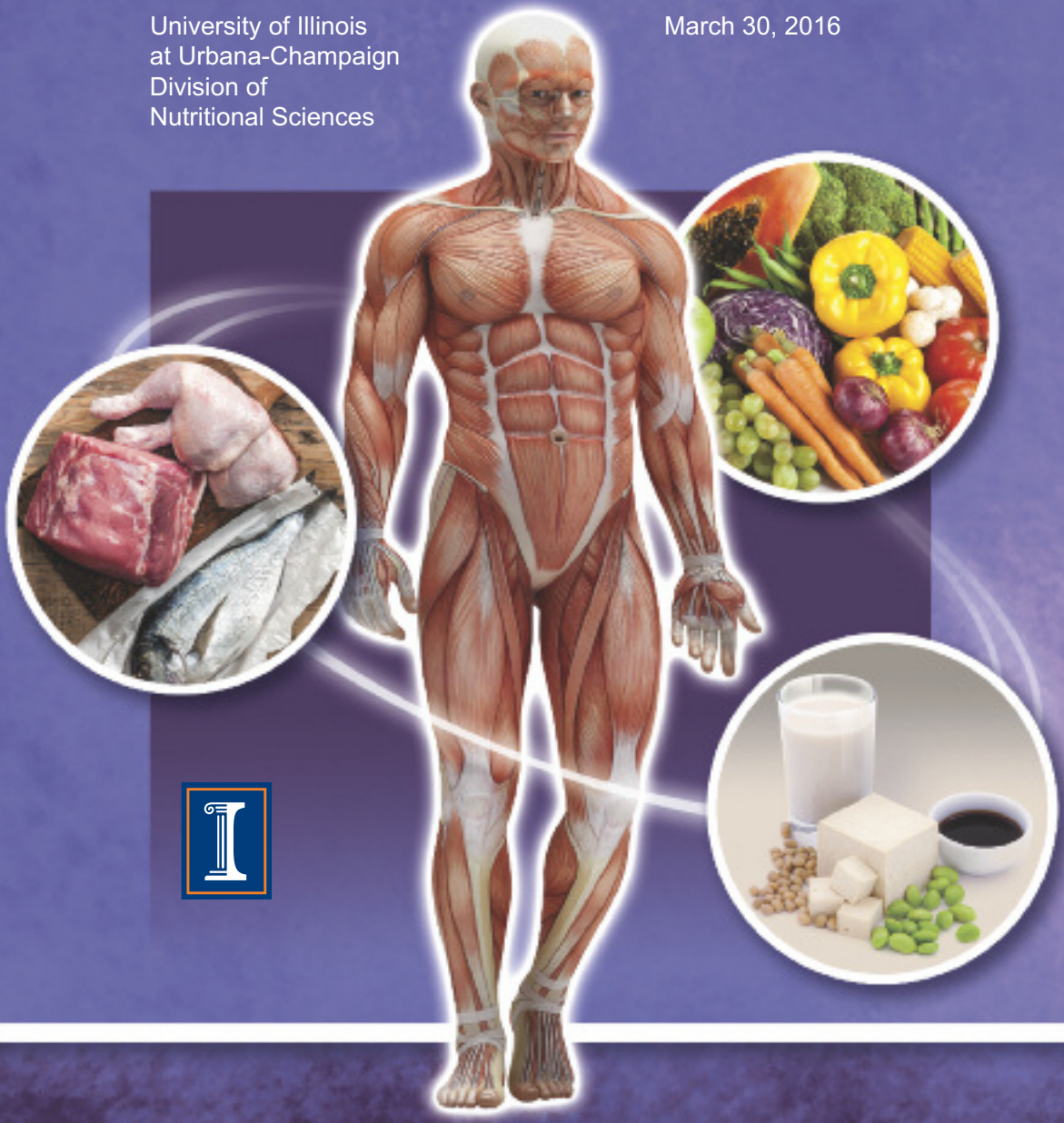
Nutritional Sciences Graduate Student Association

University of Illinois
at Urbana-Champaign
Division of
Nutritional Sciences

March 30, 2016



Welcome

On behalf of the Nutritional Sciences Graduate Student Association (NSGSA), the Division of Nutritional Sciences (DNS), and all participating presenters, we would like to welcome you to the 2016 Nutrition Symposium at the University of Illinois! The Nutrition Symposium is an important event for sharing ideas across disciplines and with the community.

Started in 1994 by NSGSA, the symposium offers students within DNS and related disciplines on campus an opportunity to present their nutrition research prior to the national meetings held annually in the spring. 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 American Society of Animal Sciences Joint Annual Meeting.

This year, NSGSA is honored to have Dr. Paul S. MacLean deliver the keynote address, "Physiological and Behavioral Challenges to Successful Weight Loss Maintenance." Dr. MacLean will discuss the primary barriers to successful weight loss maintenance, strategies for obesity treatment as well as physiological and metabolic adaptations in response to dieting and weight loss. Further, he will address the impact of exercise on these biological adaptations and will show that a comprehensive approach may be the gold standard to successful weight loss maintenance.

Additionally, NSGSA is proud to highlight the work of world-class faculty members through a mini-symposium. This year's presentations address soybeans and health, and will feature Drs. Hong Chen, Elvira de Mejia, John Erdman, and William Helferich.

We are grateful to the many people involved with this meeting and program. We would like to first thank our keynote speaker, Dr. Paul S. MacLean. 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.

NSGSA serves as a forum for student opinion and input and gives 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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Nutritional Sciences Graduate Student Association

http://nutrsci.illinois.edu/current_students/nutritional_sciences_graduate_student_association

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Schedule of Events

MARCH 30, 2016

***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. Joshua W. Smith

9:30 a.m. Renae R. Geier

9:45 a.m. Sharon V. Thompson

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. Hanna Erickson

10:45 a.m. Annabel Biruete

11:00 a.m. Joseph W. Beals

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

Soybeans and Health: What Have We Learned?

12:45 p.m. Dr. Hong Chen
Generations of Continuous Intake of Dietary Soy Reduced Preneoplastic Lesion Formation by Epigenetic Regulation of Gene Expression in the Colon of Rats

1:15 p.m. Dr. Elvira de Mejia
Role of Soybean Proteins and Peptides on Health

1:45 p.m. Dr. John W. Erdman Jr.
Soy and the Prevention of Prostate Cancer

2:15 p.m. Dr. Bill Helferich
Soy and Breast Cancer – a Double-Edged Sword

2:45 p.m. – 4:00 p.m. .....Networking Session
Conference Room 104, ACES Library

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

***4:00 p.m. – 5:00 p.m. .....Keynote Address by Dr. Paul S. MacLean, University of Colorado**
180 Bevier Hall

Physiological and Behavioral Challenges to Successful Weight Loss Maintenance

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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The University of Illinois Division of Nutritional Sciences and the Nutritional Sciences Graduate Student Association would like to acknowledge the generosity of the sponsors and friends of our 2016 Nutrition Symposium.

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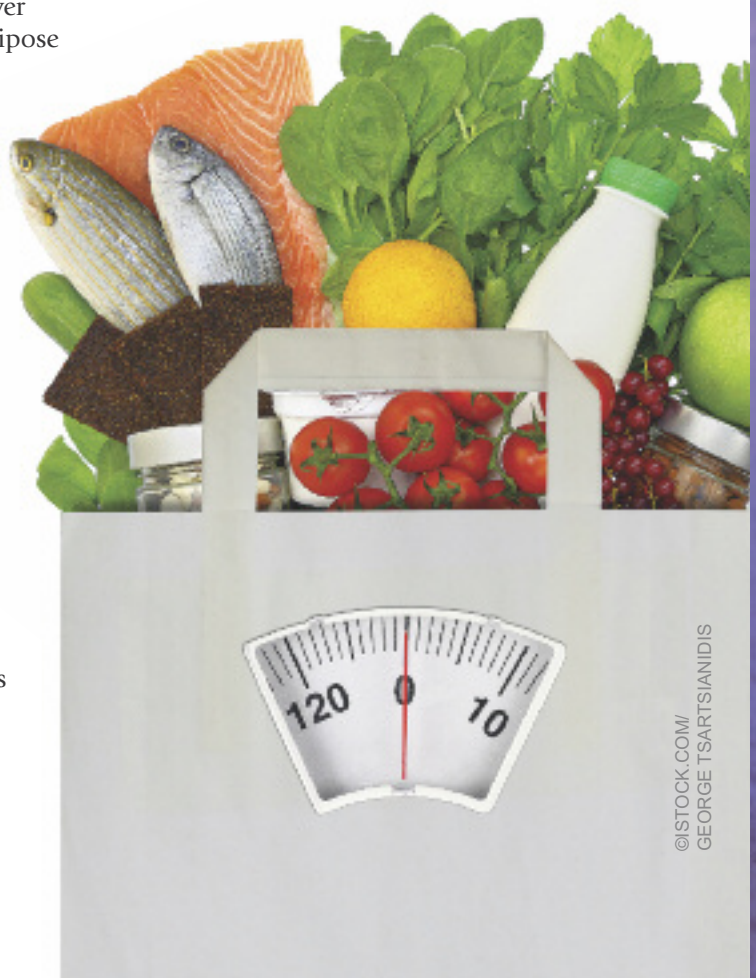
Keynote Speaker: Dr. Paul S. MacLean

Dr. MacLean joined the faculty at the University of Colorado Anschutz Medical Campus in 2001 after receiving his B.S. and M.S. from Brigham Young University and a Ph.D. from East Carolina University. He is now Professor of Medicine and Pathology and serves as the Associate Director of the Colorado Nutrition Obesity Research Center (NORC), as Research Director of his Division, and as the Director of the Energy Metabolism Program affiliated with the Colorado Obesity Research Initiative (CORI). Over the past decade, Dr. MacLean has applied state-of-the-art tools used for measuring energy balance and nutrient metabolism to study obesity, its metabolic consequences, and therapeutic strategies that can lead to long term weight reduction. He has a particular interest in understanding the biological drive to regain weight after weight loss. More recently, he has turned his efforts to understand how obesity and weight loss affect certain aspects of women's health, including the development of the mammary gland during gestation, lactation performance, parturition, the menopausal transition, and postmenopausal breast cancer. His research program is supported by the National Institutes of Health, with grants from NIDDK, NICHD, and NCI. Dr. MacLean's overarching objective is to translate the wealth of knowledge generated from mechanistic basic science studies of energy balance to clinically relevant concepts and applications in obesity therapeutics.

Physiological and Behavioral Challenges to Successful Weight Loss Maintenance

Weight regain after weight loss represents the most significant challenge in obesity therapeutics. In the summer of 2014, NIH hosted a Working Group of an interdisciplinary panel entitled "Innovative Research to Improve Maintenance of Weight Loss", to summarize the primary barriers to successful weight loss maintenance and how we might utilize this knowledge to pursue better strategies for obesity treatment. Front and foremost in this discussion was the collection of integrated biological adaptations that occur in response to dieting and weight loss. An extensive body of literature from both animal and clinical studies indicates that dieting leads to an elevated appetite and a reduction in metabolic requirements. Accompanying this drive to overeat are comprehensive changes in nutrient metabolism in the gut (increased absorption efficiency), muscle (reduced fat oxidation, enhanced work efficiency), liver (enhanced metabolic efficiency), and adipose tissues (enhanced lipogenic potential). These adaptations allow the body to absorb, clear, and deposit ingested energy in rapid and efficient manner. Key neuroendocrine signals from the periphery, in turn, convey a message of "energy depletion" and "low nutrient availability" to the brain. This message is received by critical regulatory circuits, which respond with a strong drive to overeat. At the same time that these adaptive responses develop and strengthen, the behavioral, pharmaceutical, and lifestyle strategies employed to lose weight wane. The transient nature of obesity treatments andprograms is plainly juxtaposed to the persistence of biology's drive to regain what weight was lost. Regular exercise provides the best example strategy of this juxtaposition between biology and behavior in the context of weight loss maintenance. Exercise appears to be an important part of a weight loss maintenance program for those who are successful, and a number of studies have shown that exercise may counter the biological adaptations that are driving weight regain. However, this intervention has proven disappointing in randomized clinical trials because adherence is so poor and/or variable. The emerging themes from this NIH panel and within the broader scientific community are: 1) we must acknowledge and address the aforementioned biological and behavioral challenges; 2) there is no "one-size-fits-all" strategy; and 3) a comprehensive approach that combines dietary, exercise, pharmacotherapy, devices, and surgery, in an intuitive, personalized manner, is likely the only path to success.

Dr. MacLean's Keynote Address
4:00 – 5:00 p.m. in 180 Bevier Hall



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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 *Soybeans and Health: What Have We Learned?*

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. Michael Miller, Dr. Nicholas Burd, and Dr. Zeynep Madak-Erdogan

Dietary tomato reduces castration-resistant prostate cancer burden in the TRAMP model

Joshua W. Smith[1], J.L. Rowles III[1], R.J. Miller[2], S.K. Clinton[4], W.D. O'Brien Jr.[1,2], J.W. Erdman Jr.[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]The James Cancer Hospital and Comprehensive Cancer Center, The Ohio State University, Columbus, OH

Epidemiological evidence supports the hypothesis that consumption of diets rich in tomato products are associated with a reduced risk of prostate cancer. Castration-resistant prostate cancer (CRPC) represents the late and lethal phase of human prostate carcinogenesis, and is defined as cancer progression after surgical castration or pharmacologic reduction of serum testosterone through androgen deprivation therapy (ADT). One mechanism involved in the transition to CRPC is cancer cells' acquired capacity for androgen synthesis. We have previously shown that dietary tomato reduces primary cancer incidence and inhibits tumoral expression of androgen biosynthetic genes in the transgenic adenocarcinoma of the mouse prostate (TRAMP) model. Therefore, we questioned whether dietary tomato might be an effective inhibitor of CRPC progression in mice. We hypothesized that lifelong dietary intake of tomato, as well as dietary tomato intervention following castration, would reduce tumor burden and growth rate in a mouse model of CRPC. TRAMP mice (3 wks old) were fed an AIN-93G diet (CON) for one week and then randomized to the CON diet (n=27) or a similar diet with 10% w/w lyophilized tomato paste (TP; n=28) from 4 wks of age until euthanization. A third group, modeling dietary intervention, consumed CON from 4 to 12 wks of age, and the 10% w/w lyophilized tomato paste diet from wk 12 until euthanization (TP-I; n=26). All animals were castrated at 12-13 wks of age. Beginning at 10 wks of age, mice were monitored longitudinally with ultrasound for tumor detection, tumor volume estimation, and calculation of tumor growth rate. Serial 2D tumor image slices were used to generate 3D volume measurements. Mice were euthanized after 5 consecutive tumor scans or if no tumor had been detected by 30 weeks of age. As determined by non-linear regression, TP-I significantly ($p<0.001$) reduced tumor growth rate, compared to CON and TP groups. Accordingly, longitudinal tumor volume area under the curve (AUC) was reduced 49% ($p=0.05$) by TP-I, compared to CON. At euthanization, TP-I reduced tumor weight by 37% ($p=0.03$). Additionally, gross lung metastasis at necropsy was completely prevented by TP-I, compared to CON (0% and 25%, respectively, $p=0.05$). Observational studies have shown that the lycopene content of the tomato diets in the present study, in human equivalent dose (approximately 17 mg lycopene/day), is both achievable and protective against prostate cancer. Future work should address efficacy of adjuvant dietary tomato with pharmacologic ADT to assess the potential for this approach to translate into clinical benefits for men with CRPC.

Interspecies hydrogen transfer and its effects on global transcript abundance in *Ruminococcus albus*, a predominant fiber-degrading species in the rumen

Renae R. Geier[1,2], I.H. Kwon[3], I.K. Cann[2,3,4], R.I. Mackie[1,2,3]
[1]*Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL;*
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[4]*Department of Microbiology, University of Illinois at Urbana-Champaign, Urbana, IL*

The mutually-beneficial interdependence of hydrogen-producing and hydrogen-utilizing bacteria was discovered by M.P. Bryant, M. J. Wolin and R.S. Wolfe at the University of Illinois in 1967. Based on thermodynamic principles, interspecies hydrogen transfer is a central process in anaerobic environments, such as gastrointestinal tracts of animals, linking transfer of reducing power from fermentation of organic molecules to inorganic electron acceptors via hydrogen. *R. albus* 7 is a hydrogen-producing, fermentative bacterium with two known hydrogenase complexes (HydABC and HydA2) as well as a putative hydrogen-sensing protein, HydS. HydABC is the only chromosomal hydrogenase, while HydA2 and HydS form a transcriptional unit in *R. albus* 7 on its plasmid pRumal01. The electron-bifurcating ferredoxin- and NAD-dependent [FeFe]-hydrogenase, HydABC, couples proton reduction using nicotinamide adenine dinucleotide (NADH) to proton reduction using reduced ferredoxin, producing molecular hydrogen: $3H^+ + NADH + Fd_{red} \rightarrow 2H_2 + NAD^+ + Fd_{ox}$. HydA2, a ferredoxin-dependent [FeFe]-hydrogenase, reduces protons to molecular hydrogen using only reduced ferredoxin: $2H^+ + Fd_{red} \rightarrow H_2 + Fd_{ox}$. HydS contains a C-terminal PAS domain, which often are present on sensory proteins. In addition, HydS contains a putative redox-sensing [4Fe:4S] cluster. We hypothesized that HydS transcriptionally regulates HydA2 in a manner dependent on the presence of a hydrogen-utilizing syntroph. To test this hypothesis, we grew *R. albus* 7 and a hydrogen-utilizing bacterium, *W. succinogenes* DSM-1740, in mono- and bi-culture. We monitored cell growth by optical density (OD_{600}) and quantitative polymerase chain reaction (qPCR), as well as gas and fermentation product production. Lastly, based on qPCR growth data, we determined mid-log phase ($\Delta OD \sim 0.20$ for *R. albus*, 0.14 for *W. succinogenes*, and 0.35 for the bi-culture) and extracted RNA for sequencing to compare whole genome transcriptomic profiles. In bi-culture with the hydrogen-utilizing bacterium, *R. albus* produced 1.11 moles acetate and 0.03 moles ethanol per mole available glucose. In monoculture, *R. albus* produced 0.75 moles acetate and 0.30 moles ethanol per mole available glucose. We confirmed that hydrogen accumulated in the *R. albus* monoculture, but not in the bi-culture. From RNA-Seq analysis, we identified that *R. albus*, in bi-culture, had a lowered transcript abundance of HydA2 (90-fold), relative to monoculture. Interestingly, the electron-bifurcating hydrogenase, HydABC, had a similar transcript abundance in bi-culture to monoculture (1.2-1.3-fold change). This suggests that HydS might be sensing hydrogen levels and regulating the transcription of HydA2. These results also suggest the electron-bifurcating hydrogenase (HydABC) functions in central metabolism regardless of external hydrogen concentration.

Graduate Student Oral Presentations Session 1 *(continued)*

Gastrointestinal microbiota changes following whole grain barley and oat consumption in healthy men and women

Sharon V. Thompson[1], K. S. Swanson[1,2], J. A. Novotny[4], D. J. Baer[4], H. D. Holscher[1,3]
[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]*Department of Food Science and Human Nutrition, University of Illinois at Urbana-Champaign, Urbana, IL;* [4]*USDA, ARS, Beltsville Human Nutrition Research Center, Beltsville, MD*

Background: Whole grain fiber consumption is a promising approach to positively alter the human gastrointestinal (GI) microbiome. The Dietary Guidelines for Americans recommends half of all grain servings be consumed as whole grains to minimize chronic disease risk. However, little is known about the effects of whole grain barley and oat consumption in their whole food forms on GI microbial profiles in healthy individuals. Objective: We aimed to assess the impact of whole grain barley and oat consumption on the GI microbiota in healthy men and women and determine whether effects of whole grain consumption on the GI microbiota are associated with metabolic and immunological improvements. Methods: A 6-week randomized, double-blinded, parallel-arm, controlled-feeding intervention was undertaken in healthy adults (n=68) fed at weight maintenance. Male and female participants were randomly assigned to 1 of 3 treatments: 1) a control diet containing 0.8 daily servings of whole grain/1800 kcal, 2) a diet containing 4.4 daily servings of whole grain barley/1800 kcal or 3) a diet containing 4.4 daily servings of whole grain oats/1800 kcal. Blood, urine, and fecal samples were collected at baseline and at the end of the intervention period for metabolic, immunologic, and microbial analyses. Bacterial, fungal, and archaeal sequences were generated using an Illumina MiSeq and analyzed with QIIME 1.8. Data were analyzed using SAS 9.4. Results: Prior to treatments, associations between bacterial taxa and host metabolism were observed. The Bacteriodes:Firmicutes ratio was negatively correlated with BMI (r=-0.31, p=0.009). The abundance of *Bifidobacterium* was negatively correlated with age (r=-0.40, p=0.0008). Alternatively, *Collinsella* was positively correlated with age (r=0.26, p=0.03), LDL cholesterol (r=0.21, p=0.09), and triglycerides (r=0.23, p=0.06). Microbial community structure was affected by whole grain barley and oat consumption. Total species richness was higher in participants consuming oats compared with control (p=0.01). Principal coordinates analysis (PCoA) of UniFrac distances between samples based on their 97% OTU composition and abundances indicated that the microbiota of participants within a treatment were more similar than between treatments (p=0.03). Conclusions: Our findings are congruent with previous research demonstrating associations between the GI microbiota, weight status, age, and serum lipids. Ecological analyses revealed that whole grain barley and oats induced changes in the microbial community structure of the Gl microbiota. Additional study is ongoing to delineate the microbial taxa driving these shifts and the interrelationships among changes in the GI microbiota and metabolic improvements.
Supported by USDA and Kellogg Company.

Exploring microbial interactions between 7α-dehydroxylating and sulfidogenic bacteria

Patricia G. Wolf, H. R. Gaskins
Division of Nutritional Sciences, University of Illinois at Urbana-Champaign, Urbana, IL

Intestinal microbiota has garnered substantial attention as a factor in disease etiology, yet much remains unknown. It stands to reason microbial metabolites may have a significant impact on colonic mucosa and in turn trigger or perpetuate colonic disease. Abundant evidence indicates a diet high in red meat and animal fat poses significant risk for the development of colorectal cancer (CRC), but mechanisms remain uncertain. This implicates steps in protein and fat absorption as potential causative factors in CRC, specifically colonic microbiota and secondary bile acids. Secondary bile acids are produced by anaerobic 7α-dehydroxylating bacteria from taurine and glycine derivatives of primary bile acids. The secondary bile acid deoxycholic acid (DCA), which activates proinflammatory pathways leading to increased cell proliferation and oxidative stress, is in higher abundance in patients with adenomatous polyps or CRC. A study recently published by Dr. Gaskins and coworkers observed significantly higher levels of both primary and secondary bile acids in high CRC risk African Americans (AA) consuming a high fat and animal protein western type diet as compared to low risk native Africans consuming a low fat and protein diet. In addition, rapid reciprocal changes were seen in levels of DCA producing bacteria and DCA in stool. Reciprocal changes were also seen in levels of sulfidogenic bacteria to protective butyrate producing bacteria. Additionally, we have intriguing new data from a recent collaborative study with researchers associated with the Chicago Colorectal Cancer Consortium, which demonstrate that mucosal abundance of *Bilophila wadsworthia* distinguished AA CRC patients from non-Hispanic white CRC patients and controls. *Bilophila wadsworthia* produces the genotoxic gas H_2S through taurine respiration. A diet rich in animal protein and fat, increases both dietary taurine and the taurine conjugated primary bile acid taurocholic acid. Deconjugation by microbial bile salt hydrolase liberates taurine and cholic acid, utilized by *B. wadswothia* and 7α-dehydroxylating bacteria, producing H_2S and DCA respectively. Our next step is to utilize FISH techniques to explore microbial interactions in colonic mucosa in the context or CRC. Specifically we aim to examine location and proximity of 7α-dehydroxylating and sulfidogenic bacteria in involved and non-involved mucosa at varying stages of colorectal carcinogenesis. This work can provide novel information, which would lead to a greater understanding of our proposed mechanisms.

Abstracts

Graduate Student Oral Presentations Session 2

Session 2 Judges
Dr. Rex Gaskins, Dr. Michael De Lisio, and Dr. Hannah Holscher

A scaffolding protein for fat metabolism

Hanna Erickson[1], K. Wendt, S. Anakk[1]
[1]*Department of Molecular and Integrative Physiology, University of Illinois at Urbana-Champaign, Urbana, IL*

IQGAP1 (IQ motif-containing GTPase Activating Protein 1) is a ubiquitously expressed protein that is known to integrate signaling from various cellular processes including cellular motility, adhesion, and proliferation. Furthermore, IQGAP1 has been shown to modulate MTORC1 signaling, indicating an important role for this protein in metabolism. These findings reveal that IQGAP1 may integrate proliferation and metabolism. Since its role in proliferation is characterized, we examined the metabolic impact of IQGAP1. We found that fasting induces IQGAP1 levels in the liver; therefore, we analyzed the fed and fasted response of wild-type and *Iqgap1*$^{-/-}$ mice. During the fed state, excess energy is converted to free fatty acids in the liver and is typically stored in adipose tissue. Compared to wild-type, *Iqgap1*$^{-/-}$ mice exhibit decreased expression of fatty acid synthase. Consequently, the fed *Iqgap1*$^{-/-}$ mice displayed reduced serum triglyceride levels and white adipose tissue compared to wild-type mice. These findings clearly indicate that loss of IQGAP1 results in dysregulation of lipid metabolism. To further characterize the role for IQGAP1 in regulating lipid metabolism, we fasted wild-type and *Iqgap1*$^{-/-}$ mice and examined their response. As expected, fasting resulted in a decrease in the liver to body weight ratio and serum triglycerides in both sets of mice. But surprisingly, *Iqgap1*$^{-/-}$ mice had reduced white adipose tissue and displayed a blunted induction of the beta-oxidation genes. This suggests that *Iqgap1*$^{-/-}$ mice have a putative decrease in fatty acid-derived acetyl-CoA flux into the ketogenic pathway. It is known that in ketogenic conditions, such as fasting, increased expression of beta-oxidation genes is dependent on liver-derived factor FGF21, which is secreted into the serum. Therefore, we analyzed *Fgf21* expression and found that its induction upon fasting in *Iqgap1*$^{-/-}$ mice is significantly blunted compared to wild-type. This was also consistent with the circulating serum FGF21 levels. Next, we examined the response of *Iqgap1*$^{-/-}$ mice to ketogenic diet. After 4 weeks on ketogenic diet, *Iqgap1*$^{-/-}$ mice had a higher liver to body weight ratio but a dramatically lower white adipose tissue to body weight ratio, suggesting an altered distribution in energy and metabolism occurs in the absence of IQGAP1. Moreover, these mice had reduced expression of *Fgf21*, *Acadm*, *Ehhadh*, and the rate-limiting enzyme for ketone body synthesis, *Hmgcs2*. Excitingly, the increase in serum ketone bodies found in wild-type mice on ketogenic diet was completely absent in *Iqgap1*$^{-/-}$ mice. Overall, our findings reveal that IQGAP1 is crucial to regulate lipid metabolism as well as mediating the ketogenic response.

Gut microbiome and clinical risk factors in maintenance hemodialysis patients

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The gut microbiota (GM) is important for human health and has been implicated in the pathogenesis of many chronic diseases. However, little is known about the composition and effects of the GM in patients undergoing maintenance hemodialysis (MHD). The aim of this study was to examine the GM structure and its association with clinical risk factors in MHD patients. **Methods:** Ten MHD patients (7M, 50 ± 4years, 80% African American) were assessed on a non-dialysis day. Assessment included: bone and body composition by DEXA; arterial function by applanation tonometry; and dietary intake through dietary recalls over the 48h prior to the fecal sample collection. Participants were asked to collect one fecal sample; DNA was extracted and the V4 hypervariable region of the bacterial 16S rRNA gene was sequenced using Illumina MiSeq. Sequence data was analyzed using QIIME 1.9.1. Descriptive statistics were reported while Spearman correlations were used to compare GM operational taxonomic units (representative of ≥1% of total bacterial population) and clinical risk factors. **Results:** Taxonomic summary of the GM revealed *Firmicutes*-to-*Bacteroidetes* ratio of 1.40±0.37, which was associated with resting brachial and aortic systolic blood pressures (ρ= 0.648 and 0.636, respectively; p<0.05). Additionally, it was associated with total and saturated fat consumed on non-dialysis days (ρ=0.667 and 0.636, respectively; p<0.05). At the genus level, *Faecalibacterium* was variably represented between patients (median 7.54%; range 0.1 to 23.17% of the total sequences) and was associated with carbohydrate intake (ρ=0.636; p<0.05) and negatively associated with carotid-femoral pulse wave velocity (ρ=-0.867, p=0.001), a surrogate of arterial stiffness. Concurrently, *Akkermansia* was not present in four participants and its concentration ranged from 0.01 to 12.02% of sequences (median 0.008%). Finally, *Prevotella* was only present in one participant, but was not associated with any variable. No associations were found between the gut microbiota and bone and body composition. **Conclusions:** Similar to other metabolic diseases, the GM showed a high *Firmicutes*-to-*Bacteroidetes* ratio at the phyla level. However, at the genus level there was high variability across individuals with some bacteria associated with positive health outcomes. *Akkermansia*, a gram-negative bacteria that preferentially colonizes the mucus layer and is associated with improved metabolic health, was expressed in low concentrations and was not present in some individuals, similar to *Prevotella*, which previously has been associated with higher dietary fiber intake. This association, however, was not found because it was present in only one individual. In addition, dietary fiber intake was less than 50% of the recommendation (6.26±2.48g/1000kcal). Finally, *Faecalibacterium*, which contains the machinery for the production of butyrate, was strongly associated with lower arterial stiffness, which is an independent risk factor for cardiovascular (CV) mortality in this population. Further studies should aim to explore the relationship between the GM and CV health in MHD patients.

Graduate Student Oral Presentations Session 2 *(continued)*

Anabolic sensitivity of postprandial muscle protein synthesis to the ingestion of a protein-dense meal is reduced in overweight and obese young adults

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Background: Excess body fat leads to diminished muscle protein synthesis rates in response to a hyperinsulinemic hyperaminoacidemic clamp. To date, no studies have compared the postprandial muscle protein synthetic response after the ingestion of a single meal containing a protein dense food source across a range of body mass indices and fat masses. **Objective:** We aimed to compare the myofibrillar protein synthetic response (MPS) and underlying nutrient sensing mechanisms after the ingestion of lean pork loin between obese, overweight, and healthy weight adults. **Design:** 10 healthy-weight (HW; Age 24±1 y, BMI 22.7±0.4 kg/m^2, HOMA-IR 1.4±0.2), 10 overweight (OW; Age 26±2 y, BMI 27.1±0.5 kg/m^2, HOMA-IR 1.25±0.11), and 10 obese males and females (OB; Age 27±3 y, BMI 35.9±1.3 kg/m^2, HOMA-IR 5.8±0.8) received a primed continuous L-[*ring*-$^{13}C_6$]phenylalanine infusion. Blood and muscle biopsy samples were collected at rest and after ingestion of 170 g of pork (36 g protein) to assess skeletal muscle anabolic signaling, amino acid transporters (LAT1, CD98, SNAT2), and MPS. **Results:** At baseline, OW and OB showed greater relative amounts of mTORC1 protein compared to the HW group. However, pork ingestion only increased phosphorylation of mTORC1 in the HW group (P=0.001). LAT1 and SNAT2 protein content increased during the postprandial period in all groups (Time effect: P<0.05). Basal MPS were not different between groups (P=0.43). However, postprandial MPS (0-300 min) only increased in the HW group (1.6-fold; P=0.005) after pork ingestion, but not in the OW and OB groups. **Conclusions:** There is a diminished responsiveness of postprandial MPS to the ingestion of protein dense meal in overweight and obese humans as compared to healthy-weight controls. These data indicate that impaired postprandial MPS may be an early defect with greater fat mass and may be dependent on altered anabolic signals leading to poor sensitivity to dietary protein.

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

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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
Soybeans and Health: What Have We Learned?

Generations of Continuous Intake of Dietary Soy Reduced Preneoplastic Lesion Formation by Epigenetic Regulation of Gene Expression in the Colon of Rats

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ABSTRACT: The current study evaluated impacts of generational consumption of soy diets on colon health in both male and female using an azoxymethane (AOM)-induced rat colon cancer model. Rats were maintained for three generations (F0 to F2) and continuously fed diets containing soy protein isolates (SPI), soy isoflavone genistein (GEN), or the AIN-93G control diet (CTL). We focused on the dietary influences on the histopathological changes, gene regulation, and histone modifications. Soy protein isolates (SPI) in the diet reduced the formation of aberrant crypts in F2 male and female rat colon. Male rats fed SPI had the least number of aberrant crypts developed in the colon. Genistein (GEN)-fed F2 female rats had fewer aberrant crypts compared to control group. SPI and GEN suppressed the formation of later-stage aberrant crypt foci formation (N≥3) in both males and females. Male rats fed SPI had highest serum level of total isoflavones. Serum level of total isoflavones inversely correlated with the number of total aberrant crypts in F2 male rats. Expression of Wnt5a was reduced by SPI and GEN in both F2 male and female rat colons. F2 male and female rats had different expression alterations of several Wnt signaling genes in respond to soy diets. GEN reduced the expression of Sfp2 and Sfrp5 in F2 male colons. GEN induced the upregulation of Sfrp5, Esr2, Wnt1, Wnt6 and Wnt8 expression in F2 female colons. GEN elevated the association of Pol II, acetylation of histone H3 within the promoter of Sfrp5 in female. SPI and GEN repressed the phosphorylation of histone H3S10 within the promoter of Wnt5a, Sfrp2 and Sfrp5 in male rats, and GEN reduced abundance of pH3S10 at promoters of the three genes in female rats. GEN increased the binding of estrogen receptor β (ERβ) at the promoter of Sfrp5, Wnt1 and Wnt8. In conclusion, our results suggest an epigenetic mechanism by which dietary genistein differentially affects the Wnt genes and Wnt signaling in male and female during colon cancer development. This study may facilitate establishment of a gender-based and lifelong recommendation on dietary genistein intake in maintaining colon health.

BIOGRAPHY: Dr. Hong Chen is an Associate Professor in the Department of Food Science and Human Nutrition (FSHN) and a member of the Division of Nutritional Sciences at the University of Illinois at Urbana-Champaign. Dr. Chen received her B.S. degree in Cell Biology from Lanzhou University in China and both her M.S. degree and Ph.D. degree in Nutrition from Virginia Tech. She completed her postdoctoral training in Biochemistry and Molecular Biology at University of Florida. Her research focuses on epigenetic regulations of signaling pathways related to diet and cancer development.

Role of Soybean Proteins and Peptides on Health

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ABSTRACT: Soybean is an important source of food proteins and has received increasing interest from the public because of its reported health benefits. Bowman-Birk inhibitor, β-conglycinin, Kunitz trypsin inhibitor, lectins, and lunasin are some of the biologically active proteins and peptides found in soybean. Bowman-Birk protease inhibitor is one of the most widely studied bioactive component that inhibits the protease responsible for carcinogenesis. Lunasin, credited with prevention of cancer and cardiac disease is a unique 43-amino acid peptide, also an effectual antioxidant and anti-inflammatory agent present in human plasma (50.2 to 110.6 ng/ml). Analyses of 838 genes unique to lunasin in microphages were associated with RNA processing, apoptosis, protein kinase activity, cellular growth, proliferation, cellular function and maintenance, cell to cell signaling and interaction. Lunasin prevented carcinogenesis through suppression of NF-kappaB, increased caspase-3 activity, and increased expression of pro-apoptotic nuclear clusterin. The objective of the study was to evaluate the capability of intraperitoneally and orally-administered soybean-derived peptide lunasin to inhibit KM12L4 human colon cancer cell metastasis in a mouse model. Lunasin (4 mg/kg bw) inhibited metastasis and potentiated the effect of oxaliplatin by reducing expression of proliferating cell nuclear antigen. Liver metastatic nodules were reduced from 28 (PBS) to 14 (lunasin, P=0.047) while combination of lunasin and oxaliplatin to 5 (P=0.004). The tumor burden was reduced from 0.13 (PBS) to 0.10 (lunasin, P=0.039) to 0.04 (lunasin+oxaliplatin, P<0.0001). Lunasin potentiated the effect of oxaliplatin modifying expression of proteins involved in apoptosis and metastasis. Lunasin inhibited metastasis of human colon cancer cells by direct binding with α 5β 1 integrin suppressing FAK/ERK/NF-κB signaling, and potentiated the effect of oxaliplatin in preventing the outgrowth of metastasis. Intraperitoneal injection of lunasin (4 mg/kg bw/day) reduced the number of liver metastasis by 50% (P = 0.047) and the liver weight/body weight ratio by 23% (P = 0.039). Oral administration of lunasin reduced the number of liver metastasis by 56% (8 mg/kg bw/day, P = 0.293) and 94% (20 mg/kg bw/day, P = 0.247). Soybean provides proteins and peptides with potential health benefits.

BIOGRAPHY: Dr. Elvira de Mejia is a Professor and University Scholar who joined the University of Illinois in 2002. Professor de Mejia has published over 180 peer-reviewed scientific publications, given over 120 scientific presentations and written 25 chapters in books in the areas of Food Science and Human Nutrition. The long-range goal of her research is to enhance the health of individuals by the identification and evaluation of the benefits of bioactive compounds in plant foods. Her research is focused on plant food components with health benefitsthrough analysis, chemical and biological characterization and the determination of the mechanisms of these actions. Her research has made both fundamental and applied contributions to the development of bioactive compounds from soybean foods. Mentor of students and promoter of science among the general public for the National Academy of Science, she is a fellow of the Mexican Academy of Sciences and the United Nations University. Dr. de Mejia received the 2012 McCormick Award from the American Society of Nutrition. She is currently working on the molecular mechanisms of bioactive food components from legumes, cereals and fruits and their effect on prevention of chronic diseases.

Soy and the Prevention of Prostate Cancer

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ABSTRACT: Prostate cancer (PCa) is the leading cause of cancer cases and second cause of cancer deaths in U.S. men. Epidemiological studies suggest a reduced risk of PCa in men who consume soy products. Many Asian populations consume considerably more soy than populations of European descent and those same populations also have lower PCa risk. Mean serum isoflavone concentrations are higher in men from Asia than men from the Europe or the U.S. suggesting that soy isoflavones may be at least partially responsible for differential PCa risk. A 2009 meta-analysis of 6 cohort and 8 case-control studies described a decreased risk of PCa (RR/OR of 0.74) with total soy consumption. Soy products contain an array of bioactive compounds including saponins, lignans, and isoflavones, yet much of the research in cancer prevention has focused on the predominant isoflavone found in soy foods, genistein. Genistein has been investigated for its anti-proliferative, antioxidant, and chemopreventive properties in cell, animal, and human models of PCa. For example, dietary genistein reduced the incidence of poorly differentiated (PD) lesions in TRAMP mice in a dose-dependent manner. In addition, Lobund-Wistar rats fed an isoflavone-rich diet had a significant reduction in tumor growth compared to control rats. Unfermented soy products are highest in genistein followed by daidzein. However, the commercially-available supplement, soy germ, contains 50% of isoflavones from daidzein, 39% from glycitein, and only 11% from genistein. Our laboratory demonstrated that 2% dietary soy germ resulted in a 34% decreased incidence of PD PCa in the TRAMP model verses the control diet. Despite the growing body of evidence that soy products are protective against PCa, the mechanisms of protection by soy isoflavones and/or their metabolites are still under evaluation.

BIOGRAPHY: Dr. Erdman is an Emeritus Professor of Food Science and Human Nutrition. He has authored over 200 original research articles and has over 350 total publications including other articles and chapters. His H-Index in the Web of Science is 50. He is a member of several professional organizations including the American Society for Nutrition (ASN), the Institute of Food Technologists (IFT), and the American Heart Association (AHA). He is past President of ASN, and has been elected Fellow by ASN, AHA and IFT. He has served on 27 committees for the Institute of Medicine, National Academy of Sciences (NAS). He served on the Food and Nutrition Board for 9 years, 6 as Vice Chair and as Chair of the Standing Committee on the Scientific Evaluation of DRIs and Chair of the Committee on Military Nutrition Research. This committee published the report "Nutrition and Traumatic Brain Injury" in 2011. For his extensive contributions to the NAS, he was elected as a Member of the Institute of Medicine (now National Academy of Medicine) in 2003. Other honors include: the Dannon Institute Mentorship Award from ASN; being named as an Original Member in Agricultural Science by ISI as an Highly Cited Researcher (top 0.05%); and several University of Illinois Excellent and Outstanding Teaching awards. He is a member of the Board of Trustees of ILSI- NA. He received his B.S., M.S., M.Ph., and Ph.D. in Food Science from Rutgers University.

Soy and Breast Cancer (BC) – a Double-Edged Sword
A Summary of 20 Years of Preclinical BC Research

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ABSTRACT: Soybeans and soy foods are the most significant dietary sources of isoflavones. The potential effects of the isoflavone genistein, the aglycone of genistin, have been extensively studied in relation to BC. A series of preclinical studies to evaluate the effects of isoflavones on BC growth and progression from the Helferich laboratory will be presented.

Using athymic mice bearing human breast MCF-7 tumors, we demonstrated that genistein in stimulated the growth of MCF-7 tumors, and subsequent withdrawal of genistein caused rapid tumor regression. Genistein and soy protein isolates containing different concentrations of genistein aglycone equivalents stimulated the growth of MCF-7 tumors in a dose-dependent manner. The mechanisms by which genistein affects breast tumor growth in mice are likely related to its estrogenic properties. Therefore, genistein may interfere with endocrine therapies (aromatase inhibitors or tamoxifen). In a study using an aromatase inhibitor, letrozole, and MCF-7 cells engineered with aromatase, letrozole inhibited tumor growth, while genistein reversed the inhibitory effect of letrozole on tumor growth. Genistein also negated the inhibitory effect of tamoxifen on the MCF-7 tumor growth. Studies with daidzein and its metabolite equol were also conducted and neither daidzein nor equol stimulated estrogen responsive tumor growth in vivo.

Next, we evaluated the effect of low dosages of genistein and observed that tumors grew more slowly, however, tumors had undergone a morphological change and became less responsive to estrogens. We have also evaluated the effect of isoflavones on BC metastasis and demonstrated enhancement of BC metastasis. The profile of components in soy foods is also important in determining how soy foods affect MCF-7 tumor growth in athymic mice. Tumor area was significantly smaller in a group of mice consuming a soy flour-containing diet vs. a group consuming a diet containing a mixture of isoflavone matched for genistein aglycone equivalents, indicating the matrix in which soy isoflavones are consumed can affect tumor growth.

These results suggest intriguing differences in the effects of soy isoflavones on BC in preclinical models, which may be related to the type of consumption (whole food or processed supplement), the timing of exposure and the endpoint being measured. Overall, this research suggests that consumption of a variety of traditional soy foods such as soy flour and tofu should be preferred over purified isoflavone supplements. Consumption of high-doses of purified forms of phytoestrogens is not recommended for women at high risk of BC or BC patients undergoing endocrine therapy.

BIOGRAPHY: Dr. Helferich obtained a B.S. in Nutrition at Ohio State University, M.S. in Dairy Science from University of Maryland and his Ph.D. in Nutrition from University of California at Davis, followed by an NIEHS post-doctoral fellowship in Environmental Toxicology. He was Assistant and Associate Professor at Michigan State University from 1988-1997. In 1997, he came to UIUC and was promoted to Professor in 2002. He was awarded the College ACES sponsored Professorship in Diet, Women's Health and Aging in 2007 for outstanding research achievements, which was renewed in 2012 for an additional five years. He has been funded by NIH for over twenty years and is director of the NIH funded Botanical Research Center at UIUC entitled "Botanical Estrogens: Mechanisms, Dose and Target Tissues".

Abstracts

Graduate Student Poster Session

Validation of general nutrition knowledge questionnaire for adults in Uganda

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Knowledge is a significant component of several behavioral theories used in nutrition, including the health belief and stages of change models. In Uganda, the evaluation of nutrition interventions is limited by the lack of validated tools, especially of nutrition knowledge. The objective in this study was to validate (i.e. construct validity and reliability) a general nutrition knowledge questionnaire (GNKQ) for adults in Uganda. A revised version (i.e. after expert review and face validation) of the GNKQ comprised 47 questions grouped in five domains assessing knowledge on recommendations (4), food groups (17), food choices (10), nutrition and disease relationship (11), and food fortification (5). A purposive sample of head teachers (n=40) from Kampala and students (n=77) from Makerere University was recruited to complete the GNKQ twice, at least within one week apart. Students completed the questionnaire using the Qualtrics online platform; while the head teachers completed the GNKQ by hand. Item difficulty (acceptable range: 0.1-0.9) and discrimination analyses (acceptable above 0.2) were applied to data to remove simple and complex items, and those that failed to predict scores within each of knowledge domains. After removing the items, the questionnaire remained with a total of 28 questions with 89 items. Before deletion of any items, we assessed the internal consistency (Cronbach α), the construct validity (Student t-test) and test-retest reliability for all subjects and each sub-population group. The overall Cronbach alpha (all groups) was 0.93 and 0.94 at the first and second round, respectively. This was 0.84 and 0.85 for the head teachers and 0.94 and 0.95 for the students, at the first and second round, respectively. Overall internal consistencies for the following domains were considered acceptable (i.e. 0.70-0.95), food groups (0.81 and 0.81), nutrition and disease relationship (0.78 and 0.84), and food fortification (0.94 and 0.94) in the first and second rounds, respectively. For nutrition recommendations and food choices the internal consistencies were below 0.7. The overall test-retest reliability using Pearson correlation was 0.89. The Pearson correlation coefficients were 0.93 and 0.63 for students and head teachers, respectively. The overall nutrition knowledge scores of nutrition students (104.8), engineering students (71.8) and head teachers (76.2) were significantly different ($P<0.05$). Trends and differences in knowledge scores remained similar after the second round of the questionnaire, 106.7, 72.0, and 79.7, respectively. Overall findings showed that the GNKQ is valid and reliable to evaluate nutrition knowledge among adults in Uganda. Low internal consistencies for some dimensions require continuous review of specific items. Further studies will address test-retest reliability of the GNKQ using a larger population sample.

Molecular mechanisms of low affinity estrogen action in obese mouse models

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Increased CVD-related deaths associated with obesity is one of the biggest health problems and the number one cause of morbidity among women in the United States. Western diets, characterized by high sugar and fat content, combined with low estrogen levels especially after menopause can also drastically increase the risks of metabolic syndrome and associated CVD. Hormone-replacement therapies (HRT) can alleviate these effects however they increase the risk of breast and endometrial cancers. In our previous studies, we showed that certain low affinity estrogens preferentially activated extra-nuclear initiated ER signaling in non-reproductive tissues and prevented ovariectomy induced weight gain. In the current study, to test the mechanism of low affinity estrogens on metabolism, we treated wild-type and leptin deficient (ob/ob) mice with vehicle, the low affinity estrogen, or estradiol (E2). The treatments were delivered by implanting a mini pump in the mouse, which maintained the constant blood level of the compounds for 6 weeks. During the study, we examined the effects of the low affinity estrogens on food intake and weight gain. EchoMRI allowed us to examine the body lean and fat mass composition throughout the study. We also analyzed the global gene expression changes in the liver by RNAseq, endogenous metabolite change in the serum by metabolomics and preferential signaling pathway activation in various tissues. Our findings will provide the molecular and physiological basis to use these novel low affinity estrogens as HRT alternatives to improve metabolic health of postmenopausal women. Supported by grants from the National Institute of Food and Agriculture, U.S. Department of Agriculture, award ILLU-698-909 (ZME) and Arnold O. Beckman Award-RB15150 (ZME).

Influence of family mealtime routines on preschoolers' picky eating behaviors and food consumption

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In the division of responsibility in feeding, parents are responsible for what, when, and where the child is fed, while the child is responsible for how much and whether to eat. Few studies have focused on parent's responsibility for establishing mealtime structure and routine, and how this influences children's eating behaviors, dietary intake, and weight status. The objective of this study was to examine the role of family mealtime routines on children's picky eating behaviors, dietary intake, and body weight. A total of 497 primary caregivers of 2- to 5-year-old children residing in East-Central Illinois were recruited as part of the STRONG Kids observational cohort study. Participants responded to survey questions about their family mealtime routines and children's eating habits. Family mealtime routine was measured using a five-item scale in order to assess the frequency and planning of family mealtimes, and communication during mealtimes. Higher scores on the family routine scale represented a higher sense of positive mealtime climate associated with the family mealtime routine. Child height and weight were measured by trained research personnel and used to calculate body mass index (BMI), BMI percentile, and BMI Z-score. Frequent struggles with the child over food was positively associated with children's food refusals ($r=0.38$, $p<0.01$). Family mealtime routines were associated with fewer food refusals, lower consumption of fatty/sugary foods, and higher consumption of fruits and vegetables (all $p<0.05$). There was no association between BMI percentile and family mealtime routines. Overall, our findings suggest that family mealtime routines may protect against the development of picky eating behaviors and unhealthy dietary patterns in preschoolers. Further

research is needed to define the effects of family mealtime structure and routine on children's long-term weight-gain trajectories. Supported by the National Institute of Food and Agriculture, U.S. Department of Agriculture, under award number 2011-67001-30101.

The sexual dimorphic relationship between dietary fiber intake and visceral adipose tissue

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Accumulation of visceral adipose tissue (VAT) has been mechanistically implicated in compromised metabolic health and increased risk for cardiovascular disease. However, sex is an important determinant of fat tissue compartmentalization or distribution. Substantial differences in VAT between males and females emerge early in life and are sustained throughout adulthood. These differences are thought to contribute to the disproportionate prevalence and incidence rates of cardiovascular diseases between males and females. Thus, it is plausible that relationships between dietary behaviors and VAT are influenced by sex as well. Specifically, meeting dietary guidelines for fiber intake remains a prominent feature of public health policy towards obesity prevention. Although the recommendations for fiber intake are greater among males (38g/d) compared to females (25g/d), the extent to which meeting the sex-specific dietary fiber recommendations protects against VAT remains unclear. This study aimed to elucidate the differential association between dietary fiber intake and VAT among male and female adults. Healthy adults (N=318; 155 females, aged 18-44 y) underwent Dual Energy X-ray Absorptiometry (DXA) to estimate VAT. 3-day food records were used to assess daily fiber intake. The proportion of daily sex-specific fiber recommendation met (%Fiber) was used as the primary dietary variable. Physical activity was recorded among a subsample of participants (n=269) and was assessed as steps/day using an accelerometer (Actigraph GT3X+) worn for at least 4 days (minimum 8 hours/day). As expected, VAT was significantly greater among males ($P<0.01$). Total fiber intake was not different between males and females ($P=0.62$). However, only 6% of participants met their recommended fiber intake. Nevertheless, %Fiber intake was greater among females ($P<0.01$) by 23%, indicating that males consumed significantly less fiber, relative to their daily recommended intake. Among males, VAT was inversely related to %Fiber ($r=-0.18$, $P=0.01$) intake. This relationship persisted even following adjustment of age and physical activity using partial correlations. However, no significant associations between fiber intake and VAT ($r=0.06$, $P=0.23$) were observed among females. In conclusion, these results suggest that fiber was independently and inversely related to visceral fat accumulation in a sexually dimorphic manner. These findings have important public health implications because they suggest that chronically lower fiber intake or failure to meet fiber recommendations may disproportionately compromise metabolic health among adult men. Future research is needed to determine the source of these differential associations and whether interventions targeted at meeting dietary fiber intake recommendations provide adequate protective effects against visceral fat accumulation. Supported by the Office of the Director of National Intelligence (ODNI), Intelligence Advanced Research Projects Activity (IARPA), via Contract 2014-13121700004 to the University of Illinois at Urbana-Champaign.

Accumulation of fat mass during the school year is associated with lower gains in math achievement and cognitive control among preadolescent children

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An emerging body of literature indicates that obesity or excess adiposity has negative implications for both physical health and cognitive function during childhood. However, much of this evidence is based on cross-sectional studies. Thus, the impact of transient changes in adiposity on children's achievement and cognitive function remain unclear. This study aimed to examine the association between changes in children's academic achievement and cognitive control as they related to changes in adiposity over the course of one school year. At baseline, preadolescent children between 8-9-years (N=83), underwent dual energy x-ray absorptiometry (DXA) to assess fat mass-for-age percentile. Academic achievement (Spelling, Reading, and Math) was assessed using the Wide Range Achievement Test 3rd Edition (WRAT-3). Cognitive control was measured using three cognitive control tasks (Go/No-Go, modified flanker, and a color-shape switch tasks). All measures were repeated at follow-up approximately 9 months later. Partial correlations were conducted to study the relationship between change (follow-up - baseline) in fat mass-for-age percentile (ΔFM%tile) and changes in academic achievement and cognitive control measures, following adjustment of time between visits. ΔFM%tile was not significantly related to change in Spelling (r=10.14, P=0.11) and Reading (r=0.13, P=0.13). However, ΔFM%tile inversely related to change in Math achievement (r=-0.22, P=0.03) indicating that greater increase in ΔFM%tile was related to smaller improvement in math achievement scores. ΔFM%tile was correlated with change in reaction time during the Go condition of the Go/NoGo task (r=0.27, P<0.01) indicating that increased ΔFM%tile was related to smaller improvements in reaction time. However, there was no significant relationship between ΔFM%tile and accuracy during the Go/NoGo task (r=-0.04, P=0.36). ΔFM%tile was not significantly related to change in reaction time or accuracy during the flanker task (all P's >0.05). However, ΔFM%tile was related to change in response accuracy interference during the flanker task (r=0.27, P<0.01) indicating that increased ΔFM%tile was related to greater interference with increased demand for cognitive control. Finally, ΔFM%tile was inversely related to change in response accuracy during the heterogeneous trials of Switch task (r=-0.19, P=0.04) indicating that increased ΔFM%tile was related to greater decrements in cognitive flexibility with increased cognitive demands. In conclusion, although preadolescent children progressed in academic achievement and cognitive control during the school year, the degree of improvement was limited by the accumulation of fat mass during this period. Children with the greatest increase in adiposity during the school year exhibited lower gains in math achievement and selective aspects of cognitive control. This work further supports public health concerns related to the detrimental effects of childhood obesity on both physical and mental health among preadolescent children. Supported by NIH (HD055352).

Development of a tool to evaluate the quality of nutrition apps

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Nutrition apps are widely accessible and promoted as tools for nutrition education; however, to our knowledge no systematic approach evaluating quality of nutrition education apps is available. Three domains (nutrition content, usability and technology) were used to develop a tool to evaluate nutrition app quality for educational use and to guide app development. Questions were

modified from a previously validated survey with high internal consistency reliability (Chronbach's alpha=0.92) and inter-rater reliability (Pearson's r=0.88) created to evaluate educational websites, along with two other similar surveys. Additional questions were created based on specific apps' features and nutrition focus. Questions were divided into 3 subcategories: 33 nutrition content (27 from website surveys, 6 newly created), 17 technology (9 from website surveys, 8 new) and 27 user perspective (19 from website surveys, 8 new). Two additional questions asked for app name and supporting devices. Experts in nutrition (n=6) and technology (n=4), and app users (n=10) reviewed the nutrition, technology and user perspective subcategories, respectively. Technology experts suggested including additional items assessing data storage and characterizing the user; nutrition experts suggested including skill building and relating to goals within the survey; and app users suggested reducing repetitive questions. All experts recommended clarification of several survey items. Integration of expert panels' recommendations resulted in a 3-domain evaluation tool that, with further validation in specific audiences, can help educators and developers to evaluate the quality of nutrition apps.

Dietary protein source at breakfast influences subsequent learning and memory performance

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The rapid growth and development of the brains of children and adolescents make them more reliant on regular intake of nutrients and more susceptible to impairments of cognitive performance if the first meal of the day is skipped. Additionally, it is important to understand how breakfast components can be manipulated to maximize benefits from the breakfast meal. Dietary protein provides amino acid precursors to neurotransmitter that may potentially modulate brain function. However, studies looking at the impact of breakfast on subsequent cognitive performance have given limited attention to the protein source of the breakfast meal. The objective of this study was to determine the influence of protein level and protein composition at breakfast on spatial learning and memory performance. Male Sprague-Dawley rats (6 weeks old) were entrained to a meal-feeding schedule consisting of a 30 min meal, equivalent to 20% of average daily intake, one hour into the dark phase then ad libitum access to food the last 5 hours of the dark phase. Rats were divided into one of four treatment groups in which the first meal of the day was manipulated: Egg white (EW) providing 35% energy from protein; Wheat gluten (WG) providing 35% energy from protein, Basal diet providing 20% energy from protein containing equal amounts of EW and WG proteins, or 'no breakfast'. Shortly following the testing meal period, rats were evaluated for spatial learning and memory performance in the Barnes maze. Rats provided 'no breakfast' were less active and displayed compromised short-term recall compared to rats fed Basal diet ($P<0.05$). The higher dietary protein meals (35% energy from protein) resulted in improved learning, with the EW group exhibiting significantly faster learning ($P<0.05$) and improved short-term recall in comparison to rats fed the WG diet ($P<0.05$). Together, these results suggest that EW protein as a part of the breakfast meal may enhance cognitive performance in comparison to WG diet. This highlights the importance of the protein component at breakfast on cognitive performance.

Utilizing machine learning approaches to understand the interrelationship of diet, the human gastrointestinal microbiome, and health

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Background: A growing body of literature supports the ability of specific foods and nutrients to impact the gastrointestinal microbiome. However, there is a dearth of knowledge on the interplay of dietary components (e.g. foods and nutrients), gastrointestinal bacteria, and bacterial metabolites. Current analytical approaches limit investigation of these complex interrelations; therefore, further research utilizing modern machine learning methods is needed. **Objective:** We aimed to fill the gap in knowledge about the interrelationship of diet, the gastrointestinal microbiome, and health by utilizing multivariate approaches that address P>>N, many features but few samples to 1) validate results generated by prototype software with previously published results; and 2) identify novel associations among relevant foods, nutrients, bacteria, and bacterial metabolites. **Methods:** Data generated from a human dietary intervention study that included habitual food and nutrient intake patterns (NHANES food frequency questionnaire), daily dietary intake records, breath gas, and fecal bacteria and metabolite data were analyzed using machine learning approaches. Relevant bacteria, bacterial metabolites, foods, and nutrients were identified using Random Forest and relationships among these relevant features were determined using Maximal Information Coefficient. **Results:** Breath hydrogen and agave inulin supplementation were predictive of Bifidobacterium abundance. Habitual diet factors were highly relevant in predicting participant body mass index (BMI). Among bacteria, Phascolarctobacterium, Collinsella, and Erysipelotrichacea were important features for predicting BMI. Oscillospira was associated with habitual dietary glycemic load. Phascolarctobacterium and Eubacterium were associated with habitual intake of deep yellow vegetables. Dietary polyunstaruated fatty acids were relevant in predicting Bacteroidetes to Firmicutes ratios. Total fiber and butyrate were highly relevant in predicting Faecalibacterium abundance. **Conclusions:** Findings revealed similar associations among diet, bacterial genera, and breath hydrogen measures as previously published results, thereby validating the use of these methods in diet-microbiome studies. BMI, bacterial abundances, dietary fiber intake, glycemic load, and deep yellow vegetable intake were interrelated. As features of a high quality diet were relevant for predicting bacterial abundances and metabolites, additional work is ongoing to calculate healthy eating index scores. These scores will help delineate purported health benefits (or detriments) of dietary components, bacteria, and bacterial metabolites and aid in identifying targets for future diet-microbiome studies.

Dietary comparisons between Mexican and American college-aged adults

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Increasing portion sizes, lack of physical activity, and high consumption of sugar-sweetened beverages are common trends in obesogenic environments such as Mexico and the United States, which currently have two of the highest obesity rates in the world. These factors, along with others, promote weight gain in the citizens of these countries,

and concurrent obesity-related diseases. Two such diseases, hypertriglyceridemia and hyperlipidemia, are on the rise in Mexico, a nation whose obesity rate just surpassed that of the United States. Therefore, this study sought to explore the differences in dietary patterns in two cohorts of college-aged students, one located in central Mexico (UPAMIGOS project, n=223 [females=122, males=101]) and another in central Illinois (NIMIS study, n=68 [females=34, males=34]). Biochemical and anthropometric measurements were assessed in both cohorts. The same food frequency questionnaire (FFQ) was administered to both populations, with some of the Mexican-specific foods omitted for the American cohort. The Mexican cohort (Mex) had significantly higher triglycerides p <0.0001), total cholesterol (p <0.001), and LDL cholesterol (p <0.0001), while consuming significantly more calories (p<0.0001) than the American cohort (US), independent of sex (females: 2,154.3±1,032.7 [Mex] vs. 1,015.1±533.9 [US] and males: 2,433.0±1,250.6 [Mex] vs. 1,309.1±780.2 [US]). The Mexican cohort also consumed more total fat (in grams) than the American cohort. (females: 35.32±7.94 [Mex] vs. 30.57±5.18 [US] and males: 33.33±8.21 [Mex] vs. 31.82±10.27 [US]). These findings, particularly the significantly increased consumption of calories and fat, contribute to the increasing rate of obesity-related diseases and poorer health status in the Mexican population. Future studies should seek to investigate whether metabolic risk factors for obesity-related diseases develop at a younger age in those of Mexican descent and whether dietary changes could effectively manage these values. Supported by the National Institute for Agriculture under the AFRI Childhood Obesity Prevention Challenge Area grant (2015-68001-23248) to the University of Illinois and the Agriculture and Food Research Initiative of the USDA National Institute of Food and Agriculture as part of the AFRI Childhood Obesity Prevention Challenge (2011-67001-30101) to the Division of Nutritional Sciences at the University of Illinois.

Development and validation of a questionnaire to assess irritable bowel syndrome, gastrointestinal symptoms and nutritional habits among endurance athletes

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Background: Gastrointestinal (GI) symptoms are reported in a large proportion of endurance athletes, with many similarities in symptom type and distribution to irritable bowel symptom (IBS) patients. While many studies report athlete GI symptoms, to the best of our knowledge, no studies have examined actual IBS diagnoses or fit to IBS diagnostic criteria among this group. **Objective**: The objective of this study was to develop and validate a questionnaire to assess actual IBS diagnoses by a medical professional or fit to either Manning or Rome III diagnostic criteria for IBS among endurance athletes. **Methods**: A 92 item Endurance Athlete Questionnaire was developed which incorporated portions of an existing athlete GI symptom questionnaire, the Manning criteria and the Rome III Diagnostic Questionnaire for Adult Functional GI Disorders focusing on functional bowel disorders. Other important factors included gastrointestinal symptoms, nutritional habits and symptom mitigation strategies. The questionnaire was targeted at endurance athletes who will have completed at least one of the following events within 2015: marathon, ultra-marathon, half-distance triathlon, or full-distance triathlon. Content validity was established by expert reviewers and face validity was evaluated by endurance athletes who had completed at least one of the qualifying events within the last three years. Test-retest reliability was assessed with a group of target athletes recruited through local running and triathlon clubs as well as social media. **Results**: Six expert reviewers evaluated content validity, of which three were gastroenterologists and three were Registered Dietitians specializing in working with athletes. Reviewers suggested slight modifications in wording, but no major problems were identified. Face validity was evaluated by nine endurance athletes. All

athletes understood the items and a few minor modifications in wording were suggested. Athletes also recommended the addition of a question on tobacco and alcohol use. The questionnaire was administered to target population athletes (n=45) on two occasions, separated by 1-2 weeks. Analysis was performed on the applicable item scores of 42 subjects (3 subjects reported a major GI issue within the last week on only one questionnaire). The Pearson correlation coefficient for the test-retest was significant at 0.810 ($p<0.001$). **Conclusion**: The Endurance Athlete Questionnaire had good content and face validity and proved to be a reliable measure of GI symptoms and IBS diagnostic criteria among endurance athletes. This questionnaire is needed to evaluate diagnosed and undiagnosed IBS in endurance athletes as well as symptomatic athletes who do not fit the diagnostic criteria. This will aid in future research examining nutritional modifications that may help mitigate athlete GI symptoms.

Breastfeeding facilitators and barriers among African-American women in Champaign County: a pilot study

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In the U.S., reducing breastfeeding disparities among ethnicities is a major public health priority due an estimated saving of $13 billion in health care costs and reduced infant mortality if breastfeeding recommendations are met. In order to better understand reasons for this disparity, this study involves in-depth, semi-structured interviews of first-time breastfed African-American mothers (n=15) who participate in the Special Supplemental Nutrition Program for Women, Infants, and Children (WIC) about their breastfeeding experiences using the Theory of Planned Behavior framework. Participants were also asked to complete a "pre-interview questionnaire" that included the Iowa Infant Feeding Attitude Scale, Breastfeeding Self-Efficacy Scale, and questions regarding social support, breastfeeding resources, and returning back to work. Interviews were transcribed, coded, and analyzed using inductive thematic analysis. First-stage coding identified both positive and negative attitudes toward breastfeeding. Positive attitudes were associated with infant bonding and the nutritional benefits of breast milk compared to formula. Negative attitudes were associated with pain and difficulty with breastfeeding, mother wanting to have leisure time with friends, and returning back to work or school. Subjective norm is defined as the mother's perceived social pressure to perform the behavior. The majority of mothers indicated having both positive and negative feedback from family members, friends, and community members about breastfeeding. Perceived behavioral control is defined as the mother's perceived ability to successfully perform the behavior. Mothers were asked about their confidence level and factors that were associated with higher confidence levels. Confidence levels were influenced by the type of social support the other received from her social network, hands-on assistance that she received from a lactation specialist, and ability to latch on and produce adequate amounts of milk. Mothers were asked about interventions that would help other mothers breastfeed. Interventions ranged from providing free breast pumps, having a centralized location and website where reliable, practical information and resources were available, attending a seminar or class about breastfeeding, educating high school students about breastfeeding, and promoting breastfeeding through social media, billboards, and radio to normalize breastfeeding within the African-American community. Supported by Margin of Excellence from the Division of Nutritional Sciences and funding from the USDA NIFA through the Illinois Transdisciplinary Obesity Prevention Program (2011-67001-30101).

Prebiotic short-chain fructooligosaccharides (scFOS) increases abundance of the butyrate producing microbial community differentially when administered with or without probiotic Lactobacillus rhamnosus GG (LGG) in piglets with short-bowel syndrome (SBS)

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Intraluminal butyrate production may enhance absorption in children with SBS. The objective of this study was to define changes in the intestinal microbial community associated with butyrate and lactate production. We hypothesized that scFOS would increase total butyrate producing bacterial species (TBP), LGG would increase total Lactobacillus abundance, and synbiotic combination of the two would result in both changes. Neonatal piglets (48 hours old, n = 87) underwent 80% jejunoileal resection and jugular catheter placement. Piglets received 80% parenteral and 20% enteral nutrition (EN) for 1, 3, and 7 days and received 1 of 4 treatments: (1) control (CON), unsupplemented EN; (2) prebiotic (PRE) 10g scFOS/L EN; (3) probiotic (PRO) $1x10^9$ CFU LGG/L EN; and (4) synbiotic (SYN) scFOS + LGG. Bacterial 16s rRNA genes (V3-V5) were PCR amplified from mucosa (MUC) and digesta (DIG) of the distal ileum (ILE) and proximal colon (COL). DNA Sequencing was performed on Illumina MiSeq. Taxonomy assignment and quality control were determined with Silva 123 and IM-Tornado. Diversity analysis, species level abundance comparisons, network analysis, and linear discriminate analysis were performed with QIIME1.9.1, JMP 12.1, SparCC, and LEfSe respectively. The probiotic, *L. rhamnosus*, was represented by a single OTU which was present in samples assessed from PRO and SYN, but absent in those from CON and PRE. 19 known butyrate producing species and 17 Lactobacillus species were identified for species-level analysis. Main effects of scFOS in ILEDIG day 7 include an increase in Chao1 alpha diversity ($p = 0.029$), a tendency to increase TBP ($p = 0.087$), and enrichment of the Lachnospiraceae family ($p = 0.0031$). Main effects of LGG regardless of day include enrichment of TBP in ILEDIG and ILEMUC (both $p = 0.032$) but a depletion of TBP in COLDIG ($p = 0.047$). Furthermore, LGG enriched total *Lactobacillus spp*. in ILEDIG and ILEMUC ($p = 0.026$ and 0.027) especially *L. reuteri* which was four-times higher in ILEMUC ($p = 0.012$). SYN induced a synergistic increase of butyrate-producing species in ILEDIG. TBP were enriched regardless of day versus all other treatments. Specific species: *Anaerotruncus colihominis, Faecalibacterium prausnitzii,* and *Flavonifractor plautii* were increased by day 7 versus CON. *F. plautii* accounted for a larger proportion of TBP in SYN versus PRE and CON at an average of 20.3%. SparCC correlation network analysis (correlation of all OTUs protected for compositional effects) demonstrated that OTUs related to *A. colihominis, F. prausnitzii,* and *F. plautii* were discrete between treatments, with less total members (more simple relationships) in SYN. These treatments create selective environments that support contrasting butyrate producers and their metabolic partners, which likely result in scFOS fermentation and butyrate production in different intestinal locations (e.g. ILE in SYN and COL in PRE). Optimal location of luminal butyrate delivery requires investigation, and might be responsible for differences in piglet functional intestinal adaptations observed between PRE and SYN groups.

Observed differences in child picky eating behaviors between the child's home and center- or home-based childcare

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Picky eating (PE), which typically defined as having low dietary variety and rejecting new and familiar foods, is a commonly reported problematic eating behavior that emerges

during early childhood. PE causes parental concern and has been linked to lack of dietary variety and increased risk of depression, underweight, and developing an eating disorder in the child. Traditionally, parents have been primarily responsible for determining their child's dietary intake. However, the number of children placed in non-parental, i.e., center-based childcare (CBC) or home-based childcare (HBC), has risen substantially, increasing care providers' influence on the development of children's eating behaviors. Currently little is known about PE behaviors manifested by the child across the home and childcare settings. Furthermore, most research in the area of early childcare focuses on CBC, although 15% of children in non-parental childcare are cared for in HBC. Therefore, the objective of this research was to investigate observed child PE behaviors across settings, while controlling for the food provided to the child in each setting. Children, ages 3-5 years, were recruited from a CBC (n=26) or HBC (n=24) childcare locations in the Champaign-Urbana area. Children were videotaped consuming two different lunchtime meals in both their home and childcare for a total of 200 observed mealtimes. Physical and verbal food refusals and avoidances were coded from the videos as PE behaviors. Inter-rater reliability of Cohen's Kappa >0.90 was achieved for all coders. The McNemar test results revealed that children in CBC expressed all PE behaviors more often at home than at childcare ($P<0.0001$). Children in HBC expressed more physical refusals and verbal avoidances at home compared to their childcare location ($P<0.0001$). However, there was no significant difference in the number of verbal refusals between home and HBC and significantly more physical avoidances at HBC than home ($P<0.001$). Thus, children were observed to respond differently to the same foods based on the mealtime location, and, overall, expressed more PE behaviors at home than in either childcare setting. The findings from this study add to the knowledge base of child eating behaviors and can be used to create specialized, location-specific intervention and education programs with the goal of raising healthy, independent eaters.

Pectin feeding for 16 weeks improves learning and memory in young C57Bl/6J mice: a relationship to the gut microbiota?

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Pectin is a soluble, fermentable dietary fiber that can improve intestinal homeostasis in mammals. Beyond the gut, recent evidence suggests a positive relationship between fiber intake and learning and memory in humans. The potential mechanisms by which fermentable, dietary fibers can modulate behavior have not been fully explored. We hypothesized that mice fed pectin (5%) for 16 weeks would have enhanced learning and memory compared to mice fed only cellulose and that these differences would be related to the gut microbiota. Two cohorts of C57Bl/6J mice were randomized to a pectin (n=20) or cellulose diet (n=20) and fed for 16 weeks. Thereafter, learning and memory tests were conducted and distal colon contents were analyzed by 16S rRNA sequencing to measure compositional changes in the microbiota. Mice fed pectin displayed shorter distance traveled during acquisition and shorter average distance from the platform during the 24 hour probe trial of the Morris water maze when compared to the mice fed cellulose. Unweighted UniFrac revealed a significant shift in the community structure of the microbiota as a result of pectin feeding. Further analysis found that two microbial genera, *Oscillospira spp.* and *Bilophila spp.*, were positively associated with distance from the platform during the 24-hour probe test and latency to find the platform at day 5 of the acquisition phase. These genera, which were significantly reduced by pectin feeding, are strongly associated with gut

paracellular permeability and systemic inflammation in mice and humans. Together, these data suggest that dietary pectin improves learning and memory, likely through alteration of the gut microbiota. Further study is needed to elucidate the mechanisms involved, including microbial-host interactions and gut-brain communication.

Nutritional status dictates the rate and mode of intestinal epithelial stem cell proliferation

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The intestinal epithelium plays an integral role in digestion and immune function. Maintenance of the epithelium is driven by continuous proliferation of stem cells localized near the base of the crypts, differentiation of the newly produced cells and replacement of cells normally lost by apoptosis at the villus tip. The amount and type of diet is known to influence these processes and changes the size and cellular make-up of the tissue. More specifically, an increase in food intake across species results in a greater number of epithelial cells, villi height and crypt depth. In Drosophila, this nutrient-driven expansion of the tissue is the result of an increase in the rate and change in the mode of division of the intestinal epithelial stem cells. Specifically, high nutrient availability induces greater symmetric division, which results in two stem cells. Low nutrient availability results in greater asymmetric division, where a stem cell divides to produce one new stem cell and one daughter cell. We hypothesized that this same nutrient-driven change in stem cell proliferation also occurs in mammals and that there is a difference in stem cell proliferation along the proximal to distal axis of the intestinal epithelium. To test this hypothesis we utilized 3-D intestinal epithelial organoids to study the effect of glucose on the mode of stem cell division. Epithelial organoids were treated with differing amounts of glucose and immunohistochemically processed to visualize tubulin. Mitotic spindle orientation was determined by measuring the angle between the apical border and the spindle poles of dividing cells. We also studied nutrient driven expansion in vivo using 24 male C57/B6 mice. Mice were fed varying amounts of chow diet and were separated into 4 equal groups; 1) ab libitum fed 2) fifty-percent of their average consumption 3) fasted or 4) fasted-refed. Four hours prior to sacrifice BRDU injections were given in order to track stem cell proliferation. Spindle orientation was measured as described above. In vitro, high glucose conditions greatly increased the chance of symmetric division when compared to organoids kept in low glucose conditions. Our in vitro results showed similar trends when analyzed as a whole organ with adlib fed animals showing higher amounts of symmetrically dividing cells when compared to the 50% fed animals. However, fasted animals showed very little cell division in the duodenum and jejunum but hyper proliferation in the ileum, with equal amounts of asymmetric and symmetric division. Furthermore, duodenal sections showed high symmetric division regardless of diet and jejunal segments, when compared across diets, showed similar trends to that of our whole organ analysis. These data suggest that high nutrient availability increases symmetric division of intestinal epithelial stem cells with differential changes across the distal to proximal axis. These differences may reflect environmental conditions influencing stem cell proliferation at each axis, and/or independent cell proliferation mechanisms.

Mismatched maternal and post-weaning diet alters genome-wide DNA methylation and impairs hepatic lipid metabolism pathways

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Early life diet programs offspring such that discrepancy between intrauterine and postnatal nutrition will have negative consequences later in life. Specifically, exposure to high-fat diet (HF) at critical developmental stages is potentially associated with metabolic syndromes. We hypothesize that due to differences in DNA methylation, a mismatched perinatal diet and post-weaning diet is more metabolically detrimental than a lifelong HF diet. In the present experiment, male Sprague-Dawley rats were exposed to HF diet during gestation and lactation. At weaning, half the animals were kept on the HF diet (HF/HF) and half were switched to a control AIN-93G diet (HF/C). Complementary methylated DNA immunoprecipitation sequencing (MeDIP-seq) and methylation-sensitive restriction enzyme sequencing (MRE-seq) methods were used to quantify DNA methylation in the liver. We identified 3,966 differentially methylated regions (DMRs) between HF/C and HF/HF groups. Of these DMRs, 37% were mapped to gene bodies while 6% fell within promoter or downstream regions. Differentially methylated genes were clustered in the type II diabetes mellitus and the adipocytokine signaling pathways, two metabolically relevant systems that are known to respond to HF intake, alter fat metabolism, and lead to insulin resistance. Quantitative PCR showed altered expression of many genes in these pathways, including carnitine palmitoyltransferase 1A (Cpt1a), adiponectin receptor 1 (Adipor1), peroxisome proliferator-activated receptor alpha (Ppara), retinoid X receptor (Rxra and Rxrb), and acetyl-CoA carboxylase (Acacb). Our results indicate that compared to a lifelong HF diet, exposure to mismatched early- and late- life diets induces DNA methylation that downregulates fat oxidation and upregulates triacylglycerol synthesis.

Effects of choline deficiency on composition of sow's milk

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Choline is an essential micronutrient required for many biological functions including synthesis of phospholipids, proper neurodevelopment and DNA methylation. Moreover, choline is known to be expressed at high concentrations in early postpartum milk and decreasing in concentration throughout lactation. To date much of the choline research has focused on the impact of perinatal choline deficiency in the developing neonate, with little emphasis placed on the maternal milk composition from deficient mothers. As such, the objective of this study was to use the choline deficient sow model to assess the compositional changes of expressed milk throughout lactation and its impact on piglet growth. Up to 250 ml of milk was collected from 14 sows (n = 7 choline deficient lactation diet, n = 7 choline sufficient lactation diet) at each of three time points from farrowing to weaning: d 0 (colostrum), d 7-9 (mature milk), and d 17-19 (weaning). Colostrum was collected within 6 h of farrowing and three day intervals were used for mature and weaning milk to ensure adequate and representative milk collection. To promote milk letdown at collection time intramuscular injections of oxytocin were administered. Piglet growth was measured on d of age 1, 8, and 18 and no differences ($P > 0.05$) due to maternal dietary choline status were observed in piglet bodyweight measures. Proximate analysis of milk resulted in a main effect of day ($P < 0.05$) for each of the following measures: dry matter, ash, crude protein, organic matter, gross energy, acid-hydrolyzed fat, lactose, phosphorus, and calcium. Total free choline exhibited a main effect of day ($P < 0.05$) with choline concentrations decreasing from colostrum to mature and finally weaning milk, no interactive effect (i.e. diet x day) or main effect of diet was observed. Analysis of free amino acids indicated diet by day interactions (i.e., diet x day) for phospho-ethanolamine ($P = 0.02$), threonine ($P = 0.01$), asparagine ($P = 0.04$), cystathionine/allocystathionine ($P = 0.01$), whereas a main effect of diet was observed for alpha-amino-n-butyric acid ($P = 0.04$). Fatty acid methyl ester analysis also revealed interactive effects (i.e., diet x day) for the following milk fatty acids: 14:0 ($P < 0.01$), 16:0 ($P < 0.01$), 16:1

C9 (P < 0.01), 18:0 (P = 0.02), and 18:1 C9 (P = 0.04), and a main effect of choline status (P < 0.01) was observed for 18:3 C6,9,12. Taken together, these data indicate maternal choline status appears to impact saturated fatty acid and free amino acid composition of sow's milk.

Peer-education about weight steadiness (PAWS Club): Pilot test of family menu planning lesson for parents and their young adolescents

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School-aged children exceed intake recommendations for foods containing solid fats and added sugars. This dietary pattern contributes to excess energy intake and inadequate intake of fiber and nutrients of concern. Peer interaction has been shown to influence childhood behaviors. Programs have successfully utilized peer leaders to influence participant behaviors when focused on discouraging tobacco and alcohol abuse. However, peer education is a novel approach for obesity prevention/weight maintenance in young adolescents. The objective of this study was to evaluate the effects of a workshop focused on family menu planning in families with young adolescents, and compare the efficacy of an adult-led to a teen-led mode of education. Families with 11-14 year old adolescents were recruited from the Champaign-Urbana, IL area, using convenience sampling techniques, and 15 families consented (15 parents, 17 adolescents) to participate. Participants were randomly assigned to an adult-led workshop (ALW) group or a teen-led workshop (TLW) group. Both adult and teen leaders received identical training on lesson curriculum for approximately three hours before leading workshops. Families in both groups attended one 75-minute session with other families. Parents and adolescents were assessed pre- and post-lesson with explorative, investigator-designed surveys; results of surveys measuring menu-planning related self-efficacy (score=0-5) and knowledge (score=0-5) are presented here. Score differences over time were assessed using Wilcoxon Signed-Rank and Student's t-tests, and interactions of group and time were explored using ANOVA. Analyses were conducted using SAS software (version 9.4, 2011, SAS Institute Inc). Participating families were primarily non-Hispanic (93.3%) and Caucasian (80%); parents were an average of 45.4 (±4.2 [SD]) years old and teens were an average age of 12.2 (±1.0) years old. Teens in the TLW (n=11) increased self-efficacy [0.5±0.5 (mean±SD), P<0.05], while teens in the ALW (n=5) did not (0.6±0.6, P>0.05). Parents in the ALW increased self-efficacy more than those in the TLW (1.0±0.5 vs. 0.4±0.3, P<0.05). Neither teens nor parents had knowledge changes after attending the TLW or ALW (P>0.05). However, when family knowledge scores were averaged, family knowledge scores decreased after the TLW (-0.5±0.6, P<0.05). Positive change in self-efficacy for some of the participants is promising as an indicator of potential behavior change. The self-efficacy results, where only teens in the TLW had significant increases and the adults in the ALW had significantly more increases than adults in the TLW, indicate that the respective peer-led model impacted participants. Decreases in overall family knowledge was an unforeseen circumstance of the TLW and may be an indication that an audience including parents and teens or the family menu planning construct may be a difficult concept for teen educators to appropriately convey. Further pilot testing of factors that influence the efficacy of peer-led education, such as training quality or construct difficulty, are necessary. Supported by the National Institute of Food and Agriculture, U.S. Department of Agriculture, under award number 2012-68001-22032.

Perceived onset of obesity in sleeve gastrectomy candidates

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Sleeve gastrectomy (SG) procedures are becoming increasingly common in response to the rising prevalence of morbid obesity. Post-operatively, SG patients experience positive outcomes beyond weight loss, including metabolic disease resolution and improved quality of life, which may be impacted by previous life experiences, such as onset and duration of obesity. The degree of influence of these factors is unknown. Therefore, the aim of this research is to describe the characteristics of a cohort of SG candidates and to highlight differences between individuals who reported earlier onset of weight gain and obesity with those who experienced weight gain later in life. Candidates for SG (n=28, 29% male, 46.8 ± 9.0 yrs) completed surveys in which they identified their perceived age of obesity onset and their child body size using a set of child images that represented varying body mass index (BMI) percentiles. Three-day food logs, physical activity records and body composition via bioelectrical impedance were collected prior to the preoperative diet, on the morning of surgery and one month post-operatively. At baseline, mean BMI was 48.4 ± 7.4 kg/m2 and body fat percentage was 50.9 ± 5.0%. The most common reported cause of weight gain was poor eating habits (82%), followed by physical inactivity (75%), genetics (46%), stress (36%) and depression (29%). The most common comorbidities were hypertension (54%), hypercholesterolemia (43%), anxiety (36%), type 2 diabetes (32%) and depression (32%). Nine women and two men identified with the child's image that was greater than the 90th percentile (OW). These participants were compared to those who perceived themselves to be normal weight children. Women who reported that they were OW as children had higher BMIs at initial visit (p=0.002). Participants who reported OW as children reported less minutes walking (p=0.05) and no differences in diagnosed comorbidities. Men lost 5.8 ± 1.7 kg and 1.9 ± 0.6 BMI units and women lost 5.5 ± 1.8 kg and 2.0 ± 0.8 BMI units following the two week pre-operative diet. Men lost significantly more body fat (1.75 ± 2.0 %) than women (0.05 ± 1.3%). Weight loss during pre-operative diet was not significantly different based on perceived onset of obesity or child body size perception. Although data collection in this cohort is ongoing, our findings suggest that perceived child size and onset of weight gain is associated with adult BMI, however, it does not predict the ability of an individual to lose weight pre-operatively. Supported by the Agriculture and Food Research Initiative of the USDA National Institute of Food and Agriculture as part of the AFRI Childhood Obesity Prevention Challenge (2011-67001-30101) to the Division of Nutritional Sciences at the University of Illinois.

Early detection of nonalcoholic fatty liver disease utilizing a novel QUS method

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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. While conventional ultrasound and other imaging techniques can diagnose advanced stages of fatty liver and hepatic cirrhosis, existing techniques are imprecise and not able to

detect early stage NAFLD which may lead to a delayed diagnosis of complications. The goal of this study was to utilize the novel non-invasive quantitative ultrasound (QUS) method to detect and quantify hepatic fat content at stages of steatosis. In a pilot study, 8-week-old male C57BL/67 mice were divided into one of three different dietary groups (n=15/group): control (Con) or one of two different atherogenic diets (Ath or Ath-Casein). The control diet was a casein-based purified diet (17.2% fat kcal). The Ath diet was a standard chow diet supplemental cocoa butter, cholesterol and sodium cholate (32.4% fat kcal). The Ath-casein diet was a modification of the control diet supplemented with cocoa butter, sodium cholate and cholesterol (32.3% fat kcal). The livers of each animal received weekly ultrasound scans starting prior to being placed onto one of the three diets until euthanasia. Each week, five animals were euthanized. At euthanasia, serum was collected and the liver was harvested. Half of the liver's lateral left lobe was stained with H&E (3- m section). Animals on the Ath-Casein diet had significantly higher steatosis grading than animals on the Ath diet ($P<0.05$) and control diet ($P<0.001$). Lobular inflammation experienced a similar trend with inflammation being significantly increased in the Ath-Casein ($P<0.001$) and Ath ($P<0.01$) diets compared to the control. Portal inflammation was statistically significant in both of the atherogenic diets compared to the control ($P<.001$). Interestingly, a significant effect of liver cell injury was only visible in the Ath-Casein group ($P<0.01$ against Ath, and $P<0.0001$ against control). Overall, histology revealed that animals on either of the atherogenic diets were in a worse metabolic condition. In vivo and ex vivo ultrasound of the liver display increased attenuation and backscatter in both of the atherogenic diets compared to the control. Total hepatic lipids were evaluated by the Folch method and will be further compared to ultrasound for trends corresponding to steatosis and inflammation in the liver. Total serum and hepatic cholesterol will be measured. Additionally, serum alanine aminotransferase (ALT) and tumor necrosis factor α (TNFα) will be analyzed to determine liver damage and systemic inflammation. The development of a QUS method to identify early stages of NAFLD and NASH would provide the capability to noninvasively quantify and monitor liver condition and test methods for intervention. Supported by NIH R37EB002641.

Impact of almond consumption on the composition of the gastrointestinal microbiota of healthy adult men and women

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Background: Dietary fiber has been shown to diversify and support growth of beneficial bacteria in the human gastrointestinal tract. Almonds contain fiber as well as phytonutrients that may impact the microbiome. Diets rich in nuts, including almonds, have beneficial effects on cardiovascular disease risk factors including blood lipids and inflammation. Much of this research has been conducted using whole almonds. Emerging data also suggests the gastrointestinal microbiome may play a role in mediating cardiovascular disease risk factors. The interrelationship of almond consumption, the gastrointestinal microbiome, and cardiometabolic health of humans remains to be investigated. An important first step is characterizing the impact of dietary consumption of almonds and almond processing on the human gastrointestinal microbiota. **Objective:** We aimed to assess the interrelationship of almond consumption and processing on the gastrointestinal microbiota in healthy adult men and women. **Methods:** A controlled-feeding, randomized, crossover design study

consisting of five 3-week treatment periods with washouts between treatment periods was conducted in healthy adult men and women (n=18). The 5 treatments were: 1) 0 servings/day of almonds, 2) 1.5 servings (42 g)/day of whole almonds, 3) 1.5 servings/day of whole roasted almonds, 4) 1.5 servings/day of diced almonds, and 5) 1.5 servings/day of almond butter. Urine, fecal, and blood samples were collected at the beginning and end of each period for metabolic, immunologic, and microbial analyses. 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. Sequence data were analyzed using QIIME 1.8.0 and SAS 9.4. **Results:** Principal coordinates analysis (PCoA) of UniFrac distances between samples based on their 97% OTU composition and abundances indicated that bacterial communities were impacted (p=0.05) by treatment. Furthermore, the composition of the microbiota of participants consuming whole almonds (whole raw and whole roasted) was different (p=0.01) than when participants did not consume whole almonds (almond pieces, almond butter, and control). At the phyla level, almond consumption decreased the relative abundance of Actinobacteria compared to control, 3.9% vs. 5.5%, respectively (p=0.03). Shifts in bacterial genera following almond consumption included a decrease in the relative abundances of *Bifidobacterium* (p=0.03), *Parabacteroides* (p=0.02), and *Clostridium* (p=0.04), and increases in the relative abundances of *Lachnospira* (p=0.01) and *Roseburia* (p=0.03). Comparisons between control and each of the four almond treatments revealed that chopped almonds increased the relative abundances of *Oscillospira* (p=0.02), *Roseburia* (p=0.02), and *Lachnospira* (p=0.04). **Conclusions:** Our data reveal that almond consumption induced changes in the microbial community composition of the human gastrointestinal microbiota. Furthermore, the degree of almond processing differentially impacted bacterial genera with chopped almonds having the largest effect compared to control. Additional study is ongoing to determine if connections exist between the changes in microbial taxa and metabolic improvements. Supported by USDA and Almond Board of California.

Effect of frequent broccoli intake on rat gut microbiota metabolism and composition

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The aim of this study is to investigate whether frequent cooked broccoli intake can modify the composition and metabolism of gut microbiota, specifically if broccoli feeding improves the ability of gut microbiota to hydrolyze glucoraphanin (termed myrosinase activity) and release bioactive sulforaphane. Myrosinase activity of cecal microbiota from adult male F344 rats fed with either 10% freeze-dried cooked broccoli diet or control diet (AIN93G) was measured as the evaluation parameter. Results showed that feeding rats the broccoli diet for 4 days significantly increased myrosinase activity *ex vivo* compared with control diet ($p<0.001$). The stimulated myrosinase activity maintained those elevated levels when rats were fed the broccoli diet for longer periods (7 and 14 days). Remarkably, high-throughput DNA sequencing data revealed a corresponding change in the gut microbiota composition based on microbial community analysis (MCA). The community composition of cecal microbiota from rats fed with the broccoli diet for 4, 7 and 14 days was clearly different from those fed for 0 and 1 day. To further identify which components in the broccoli diet that caused the change, a glucoraphanin-free broccoli diet was made by hydrolyzing all the glucoraphanin to sulforaphane with exogenous myrosinase and was then fed to rats. Results showed cecal microbiota of rats fed with the whole broccoli diet exerted 4-fold higher myrosinase activity than those rats fed the glucoraphanin-free broccoli diets, indicating

that it was the glucoraphanin in the broccoli, rather than sulforaphane, fiber or other components, that played the causative role of stimulation in the gut microbiota. Interestingly, the increased myrosinase activity was lost when the 4-day broccoli diet was switched back to control diet for 3 days prior to harvest. Similar changes in glucoraphanin metabolic activity were observed using feces in place of cecal microbiota, indicating the potential for fecal metabolism to act as a biomarker of exposure. This study suggests that frequent ingestion of cooked broccoli may enhance the capability of gut microbiota to release the anti-cancer bioactive sulforaphane from cooked broccoli. Supported by USDA/NIFA 2016-67017-24430.

Nutrient-induced metabolism dictates intestinal epithelial crypt proliferation

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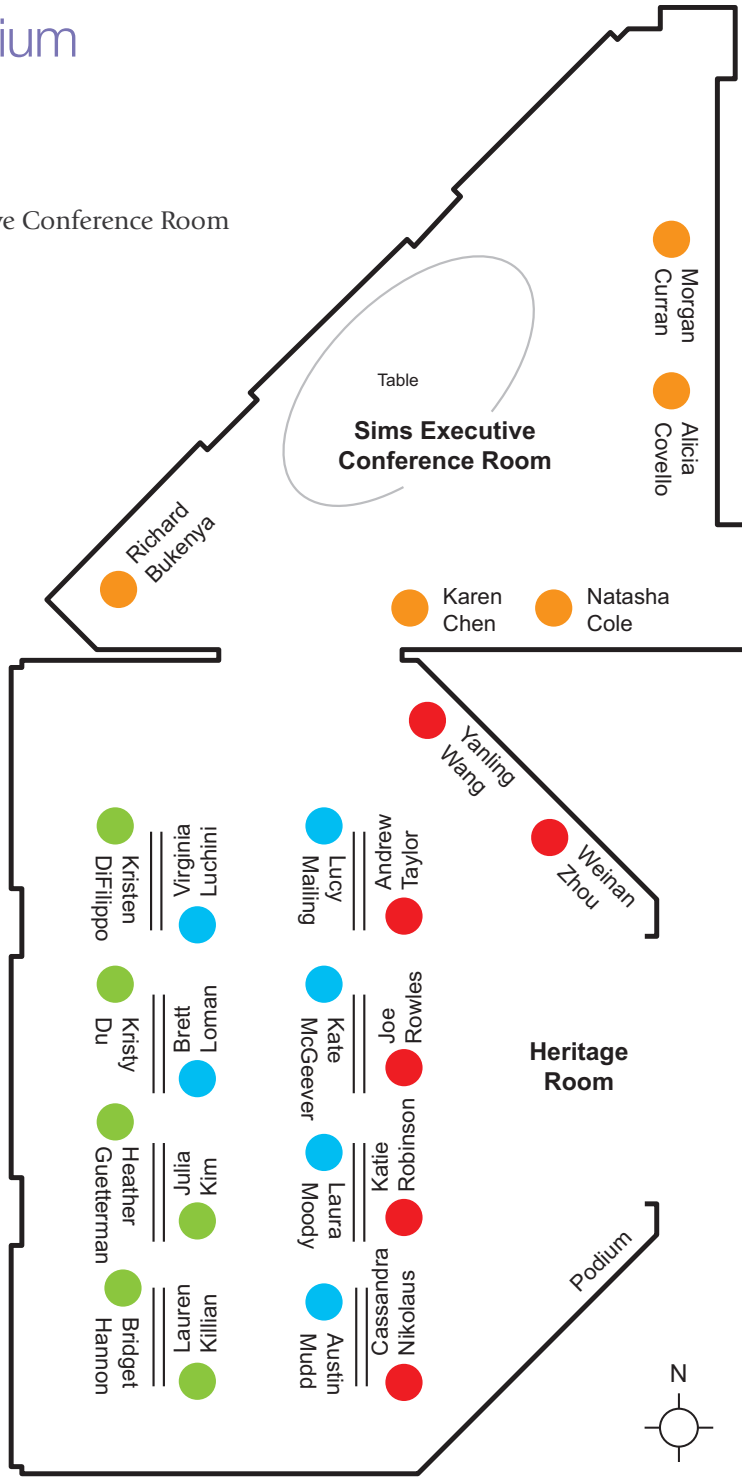
The intestinal epithelium plays an essential role in nutrient absorption, hormone release and barrier function. Maintenance of the epithelium is driven by continuous cell renewal by stem cells located in the intestinal crypts. The amount and type of diet influence this process and result in changes in the size and cellular make-up of the tissue. We have found that glucose induces an increase in the rate of proliferation in intestinal epithelial crypts in a concentration dependent manner. The mechanism underlying this nutrient-driven change in crypt proliferation is not known, but may involve a shift in intracellular metabolism that allows for more nutrients to be used to manufacture new cells. We hypothesized that nutrient availability drives changes in cellular energy metabolism of small intestinal epithelial crypts that could contribute to the increase in crypt proliferation. To test this hypothesis, we utilized primary small intestinal epithelial crypts from C57BL/6J mice to study the effect of glucose on crypt metabolism using a Seahorse XFe96 Extracellular Flux Analyzer for real-time metabolic measurements. Glycolysis was determined by measuring the extracellular acidification rate (ECAR) in response to glucose and the glycolytic pathway inhibitor 2-Deoxy-D-glucose (2-DG). Glucose oxidation was determined by measuring oxygen consumption rate (OCR) in response to glucose and the glucose oxidation pathway inhibitor UK-5099. Glucose-induced mitochondrial respiration was determined by measuring OCR in response to glucose and modulators of mitochondrial respiration (i.e. ATP synthase inhibitor oligomycin, uncoupler FCCP, complex I inhibitor rotenone, complex III inhibitor antimycin A). The maximum respiration capacity (i.e. the capacity to oxidize any substrates present to meet metabolic challenges) was determined by measuring FCCP-stimulated OCR. We found that glucose increased ECAR in a concentration dependent manner, and the glycolytic pathway inhibitor 2-DG reduced glucose-induced ECAR, indicating that glucose stimulates glycolysis of crypts. However, neither glucose nor the glucose oxidation pathway inhibitor UK-5099 affected OCR, indicating that glucose oxidation is not active in crypts. Furthermore, glucose increased FCCP-stimulated OCR, indicating that the presence of glucose is necessary for crypts to utilize substrates for oxidation. These data suggest that high nutrient availability drives metabolism towards utilization of glucose for glycolysis in crypts, and glucose might indirectly induce an increase in the oxidation of other nutrients (e.g. fatty acids, amino acids) in crypts. These metabolic changes may contribute to the nutrient-induced crypt proliferation.

Nutrition Symposium Poster Session

ACES Library, 1st Floor
Heritage Room and Sims Executive Conference Room
Wednesday, March 30, 2016
5:15 p.m. – 6:40 p.m.



Poster Judges

Orange Team
Dr. Hans Stein (captain)
Dr. Naiman Khan
Dr. Marcus Lawson

Green Team
Dr. Juan Andrade (captain)
Dr. Aditi Das
Dr. Rita Strakovsky

Blue Team
Dr. Manabu Nakamura (captain)
Dr. Juan Loor
Dr. Brandt Pence

Red Team
Dr. Ryan Dilger (captain)
Dr. Maria Cattai de Godoy
Dr. Jon Mun

Presenting Author Index

Winners of the 2015 University of Illinois Nutrition Symposium poster and oral competitions with keynote speaker, Dr. Michael Grandner.

Notes

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