The University of Texas at Austin
Department of Nutritional Sciences
College of Natural Sciences | School of Human Ecology

2018

Nutritional Sciences Research Retreat

Abstract Booklet

NUTRITIONAL SCIENCES 2018 RESEARCH RETREAT

08:30 am-09:00 am	**Continental Breakfast**
09:00 am-09:15 am	Dr. Paul Goldbart, Dean College of Natural Sciences
09:15 am-09:45 am	**Welcome Session**
	Dr. Molly Bray- Department Chair
09:45 am-10:15 am	**New Faculty Presentations**
09:45	Dr. Marissa Burgermaster
10:00	Dr. Elizabeth Widen
10:15 am-10:30 am	**Break**
10:30 am-11:30 am	**Faculty Presentations- Session 1***
10:30	Dr. Ladia Hernandez
10:35	Dr. Jeanne Freeland-Graves
10:40	Dr. Alessia Lodi
10:45	Dr. Linda deGraffenried
10:50	Drew Hays
10:55	Dr. Natalie Poulos
11:00	Dr. Monica Meadows
11:05	Dr. Sara Sweitzer
11:10	Dr. Christopher Jolly
11:15	Monica Milonovich
11:20	Dr. Jamie Davis
11:25	Dr. Ryan S Gray
11:30 am-11:40 am	**Break**
11:40 am-12:30pm	**Faculty Presentations- Session 2***
11:40	Dr. Charlotte Herzele
11:45	Dr. Laura Lashinger
11:50	Dr. Stefano Tiziani
11:55	Diane Papillion
12:00	Dr. Margaret Briley
12:05	Dr. Alejandra De Angulo
12:10	Dr. Austin Cooney
12:15	Dr. Kumar Kothapalli
12:20	Dr. Steven Abrams
12:25	Dr. Thomas Brenna
12:35 pm-01:30 pm	**Lunch ****

01:30 pm-01:40 pm	**Study Abroad –** Dr. Jeanne Freeland-Graves
01:45 pm-02:15 pm	**Data Blitz Session**
	Mahsa Babaei
	Reem Ghaddar
	Brittany Harlow
	Prageet Kaang
	Erfan Khazaee
	Sangyoung Kim
	Mathew Landry
	Xiyuan Lu
	Ronna Robbins
	Vasavi Shabrish
	Sarvenaz Vandyousefi
02:15 pm-03:00 pm	**Poster Presentation to Judges**
03:00 pm-03:40 pm	**Nutrition Program Presentations***
03:10 pm-03:20 pm	**Online Masters –** Dr. Sara Sweitzer
03:20 pm-03:30 pm	**Susie's Kitchen –** Diane Papillion
03:30 pm-03:35 pm	**HANs Program –** Dr. Ladia Hernandez
03:35 pm-03:40 pm	**Experiential Learning and Community Outreach –** Drew Hays
03:40 pm-04:00 pm	**Award Presentation**
04:00 pm-05:00 pm	**Curriculum Discussion/Teaching****
05:00 pm-06:00 pm	**NTR Happy Hour**

* GEA 105
** GEA 125

List of Student Abstracts

Dr. Margaret Briley
Ronna Robbins (A)

Dr. Jaimie Davis
Reem Ghaddar (B)
Amy Hoover (C)
Erfan Khazaee (D)
Matthew Landry (E)
Sarvenaz Vandyousefi (F)

Dr. Jeanne Freeland-Graves
Mahsa Babaei (G)
Prageet Kaang (H)
Sangyoung Kim (I)
Ashley Neely (J)
Anne Marie Zamora (K)
Jeanette Sands (L)

Dr. Elizabeth Widen
Amy Kweller (M)

Dr. Molly Bray
Diana Gutierrez Lopez (N)
Vasavi Shabrish (O)

Dr. Linda deGraffenried
Margaret Drake-Studstill (P)
Brittany Harlow (Q)

Dr. Stefano Tiziani
Jennifer Chiou (R)
Meghan Collins (S)
Paul Gries (T)
Xiyuan Lu (U)

Undergraduate, HANs and Special Departmental Honors Students
Elizabeth Eichman and Christopher Hsu (UA)
Ali Oberman and Irene Kim (UB)
Peyton Travis (UC)
Emily Equitz (UD)
Laura Winikka (UE)
Caroline McFarland (UF)
Maalini Bommakanti (UG)
Julienne Calamlam (UH)
Lavender Hackman (UI)
Colton Becker (UJ)

Judges

Poster assignments				
Dr. Jaimie Davis	G	J	A	
Dr. Jeanne Freeland-Graves	C	M	B	
Dr. Molly Bray	U	T	S	
Dr. Stefano Tiziani	N	O	P	
Dr. Christopher Jolly	Q	P	O	
Dr. Ladia Hernandez	E	H	D	
Dr. Monica Meadows	H	F	G	
Dr. Steven Abrams	F	G	E	
Drew Hays	D	I	C	
Monica Milonovich	I	E	F	
Diane Papillion	J	D	I	
Dr. Natalie Poulos	K	C	J	
Dr. Sara Sweitzer	M	B	L	
Dr. Tom Brenna	T	U	N	
Dr. Alessia Lodi	O	N	Q	
Dr. Laura Lashinger	UA	UC	UE	
Dr. Ryan Gray	R	S	T	
Dr. Kumar Kothapalli	P	Q	R	
Dr. Briley	B	I	H	
Dr. Marissa Burgermaster	A	K	M	
Dr. Charlotte Herzele	UC	UE	UH	
Dr. Austin Cooney	S	R	U	
Dr. Elizabeth Widen	L	A	K	
Dr. Alejandra De Angulo	UF	UG	UH	UJ
Dr. Fiona Asigbee	UB	UI	UD	
Shannon Sweeney	UD	UJ	UF	
Geoff Solares	UA	UG	UB	UI

ABSTRACT – A

Living on the not so Sunny Side of Life- Examination of Hypovitaminosis D in Elderly Living in Long-Term Care Communities in Central Texas

Robbins R, Briley ME

Background: Prevalence of hypovitaminosis D ranges from 50% to 98% in elderly populations (>65 yo) living in long-term care (LTC) communities. The elderly are at increased risk for hypovitaminosis D because the aging process is associated with decreased appetite, polypharmacy, malabsorption syndromes, renal and liver disease, and limited exposure to sunlight.

Objective/Hypothesis: To compare serum 25-hydroxyvitamin D (25,[OH]D) levels across supplemented and non-supplemented elderly living in LTC communities, and compare the proportion with optimal serum levels (>75nmol/L), across supplemented and non-supplemented elderly living in TLC.

Experimental Approach: Residents (>65 yo) from LTC communities within central Texas will be recruited to participate (n=170). Informed consent and HIPAA release will be obtained from all participating residents or their legal proxies. Using double blind protocols, trained data collectors will review medical records and abstract: demographics, body mass index, years living in LTC, medical diagnoses, prescribed medications and supplements, current diet order, history of fractures, falls and hospitalization, oral nutritional shake supplementation, and complete a mini nutritional assessment. A one-time blood draw will measure serum 25-hydroxyvitamin D (25,[OH]D), complete blood count, basal metabolic panel, c-reactive protein, and interlukin-6 from all participants. Analysis of variance (ANOVA) will be used to compare serum 25-hydroxyvitamin D (25,[OH]D) levels between supplemented and non-supplemented groups while controlling for the amount of vitamin D provided from diet, and physiological, behavioral and demographic covariates. Categorical variable designating whether or not serum level is optimal (<-75 nmol/L vs >75 nmol/L) will then be constructed, and the distribution of this variable will be compared across supplemented and non-supplemented groups, after controlling for covariates.

Future Research: Abstracted data will be used to determine the most effective supplementation regimen out of commonly used supplementation treatments. Followed by the development and validation of a non-invasive clinical screening tool that will identify residents at risk for hypovitaminosis D.

ABSTRACT – B

Socioeconomic Determinants of Fasting Plasma Glucose and Prediabetes in Low-Income Hispanic Children

Reem Ghaddar; Jaimie N Davis, PhD, RD

Background: Hispanic children are more likely to have overweight and obesity, leading to disproportionately higher rates of prediabetes and type 2 diabetes (T2D) among Hispanic adolescents and adults, compared to non-Hispanic Whites (NHW). Hispanic families in the United States also have lower socioeconomic status (SES) than NHW families. To date, no study has examined prediabetes rates in primarily low-income Hispanic children (<12 y) in an elementary school setting.

Methods: Cross-sectional measures collected on 780 3rd-5th grade students (7-11 y) included: height (stadiometer), weight (TANITA scale), age, sex, ethnicity, participation in the National School Lunch Program (NSLP), parent educational attainment, parent employment status (self-administered child and parent questionnaires), and fasting plasma glucose (FPG; optional fasting blood draw). Chi-squared and ANCOVA analyses were run to assess prediabetes rates and mean FPG with NSLP participation and parent educational attainment, controlling for child age, sex, BMI, ethnicity, and parent employment status.

Results: Students were 53.4% female and 65.9% Hispanic with a mean age of 9.3 ±0.9 years; 68.8% participated in the NSLP, and 27.4% had FPG values indicative of prediabetes. Incremental increases in parent educational attainment (≤8th grade, some high school, high school graduate, college graduate) were significantly associated with lower mean FPG and lower prediabetes rates in children ($p<0.001$). Prediabetes rates were significantly higher in children participating in the NSLP compared to those who did not qualify for the NSLP ($p<0.001$).

Conclusions: Strong associations exist between prediabetes rates in children and socioeconomic determinants in the home, indicating a relationship between prediabetes and home environment as well as family SES in children (7-12 y). These findings highlight the importance of early screening for prediabetes and T2D and the need for school- and family-based interventions in low-income Hispanic pediatric populations.

ABSTRACT – C

Austin School Gardens Project

Amy Hoover

August 13, 2018 Abstract

Background: The Austin School Gardens Project, in collaboration with the City of Austin, Office of Sustainability, Austin Independent School District (AISD), and the Sustainable Food Center, is evaluating existing school gardens and gardening programs to assess strengths, barriers, and needed resources to sustain these programs.

Objective: To evaluate barriers and relevant success strategies for school gardening programs in school gardening programs around the Greater Austin area. There are over 220 schools in Austin with existing gardens; however, there is no systematic evaluations of these programs. In order to implement "best practices" and provide strategies, resources and funding to sustain gardening programs, we are surveying all existing school gardens to assess resources, funding, upkeep, usage, and barriers.

Methods: With the help of an expert panel of collaborators, Master Gardeners, and Registered Dieticians, we developed a 70-item teacher/administrative survey and an observation survey of the physical garden. Undergraduate UT nutrition students are working in pairs to go to each school garden to conduct the in-person observation survey, including taking photos of the physical garden, and handing out surveys to teachers and administrators at each of the schools. All data is entered and quality control checked into RedCap.

Results: To date, 57 schools have been evaluated, including 44 physical garden evaluations, 100 teacher surveys, and 56 administrator surveys. Physical garden evaluations showed that 21% are well-maintained, 49% are somewhat-maintained, and 30% are unmaintained. Teachers and students each contribute 25% of garden care, with the rest composed of parents, staff, garden committee and community. Similarly, 60% of garden usage is between teachers and students. Only 49% of schools have garden coordinators, and of those only 22% have a paid garden coordinator position. Volunteer support seems lacking, with 35% of schools reporting any aid, and of those, 88% contributing 0-10 hours. The top four barriers reported to garden success were: 1) lack of harvest; 2) lack of training/organization; 3) no or little administrative support; and 4) lack of organized access/availability to the garden.

Implications: It is important to evaluate and characterize strategies and barriers to school gardening programs so that resources and funding can be established to better help support and sustain existing school garden programs.

ABSTRACT – D

Longitudinal Assessment of Breakfast Consumption Impact on Changes in Adiposity and Metabolic Parameters in Hispanic Children

Khazaee E, Davis JN

Background: Breakfast consumption has been linked to lower adiposity and favorable metabolic outcomes; however, there is a lack of longitudinal studies examining how breakfast intake is linked to changes in adiposity across time using measures beyond weight and BMI, particularly in a Hispanic youth population.

Objective: To assess the relationship between breakfast consumption with adiposity and metabolic parameters across puberty using an exclusively Hispanic youth cohort.

Experimental Approach: Longitudinal data on 146 Hispanic children (8-19y) with overweight/obesity from an average of five annual visits were used. The following measures were collected at each annual visit: height, weight, total body fat via dual-energy X-ray absorptiometry, glucose/insulin dynamics via frequently sampled intravenous glucose tolerance test, lipids via fasting blood draws, dietary intake via two 24-hour recalls, and Tanner via physician examination. Breakfast was defined as foods/beverages constituting ≥15% of total daily energy consumed between 0500 and 1000 hours. Children were categorized as breakfast skippers (n=43), intermittent breakfast eaters (n=63), or always breakfast eaters (n=40). Linear mixed models will assess the effects of breakfast groups on changes in adiposity/metabolic parameters across age, controlling for sex and Tanner.

ABSTRACT – E

Comparison of Diet Quality in Low-Income Hispanic and Non-Hispanic Children

Landry MJ, Asigbee FM, Khazaee E, Vandyoursefi S, Ghaddar R, Davis JN

Background: An approach to measuring diet quality is the Healthy Eating Index (HEI) – 2015, which measures conformity to the 2015 Dietary Guidelines for Americans.

Objective: The purpose of this study was to compare diet quality between low-income Hispanic and non-Hispanic 3rd-5th graders. It was hypothesized that total and component HEI scores would differ between Hispanics and non-Hispanics.

Methods: Cross-sectional data were obtained from 408 low-income 3rd-5th grade students from 12 central Texas schools. Students self-reported age and sex via questionnaire, and their parent provided data on ethnicity and participation in the National School Lunch Program (NSLP). Body mass index (BMI) percentile was calculated from measured height and weight. Two, 24-hour dietary recalls were collected via telephone on each student. HEI-2015 assessed diet quality. General linear models were used to compare HEI scores between Hispanics and non-Hispanics while controlling for sex, age, BMI percentile, and NSLP participation.

Results: Students were 42% male, 58% Hispanic, 64% NSLP participation, and had an average age of nine. Hispanic children, compared to non-Hispanics, had significantly higher HEI-2015 total scores (56.5 ±12.5 vs. 51.4 ±11.0, $p<0.01$) and HEI-2015 component scores for total vegetables (2.9 ±1.6 vs. 2.5 ±1.6, $p=0.03$), total dairy (7.8 ±2.8 vs. 7.0 ±2.9, $p=0.02$), and refined grains (5.2 ±3.6 vs. 4.1 ±3.2, $p=0.03$). Refined grains component scores are reverse scored; therefore, higher scores reflect lower consumption.

Conclusion: Hispanic children had higher overall diet quality compared to non-Hispanics; however, diet quality needs improvement in both groups. Although not casual, these results warrant nutrition interventions focused on increasing diet quality in all low-income children.

ABSTRACT – F

Association of Breastfeeding and Gestational Diabetes Mellitus on the Prevalence of the Prediabetes and Metabolic Syndrome in Offspring of Hispanic Mothers

Authors: Vandyousefi S, Goran MI, Gunderson EP, Khazaee E, Landry MJ, Davis JN

Objective: This study aims to assess the breastfeeding (BF) and Gestational Diabetes Mellitus (GDM) in relation to the prevalence of prediabetes and the Metabolic Syndrome (MetS) in Hispanic children (8-19 years of age). We hypothesized that BF would be protective and associated with decreased prediabetes and MetS risk in offspring of mothers with and without GDM.

Methods: Data was obtained from a longitudinal study with 229 overweight or obese Hispanic children (8-13 years of age at baseline) with a family history of type 2 diabetes and an average of four annual visits (AV). Retrospective data on GDM status, BF duration, and birth weight were collected from mothers at the baseline visit via a parent questionnaire. The following measures were collected at each annual visit: Tanner stage via healthcare provider examinations, weight, height, waist circumference, blood pressure, total body fat via DXA, fasting blood glucose, HbA1c and lipids and 2-hour oral glucose tolerance. For this analysis, prediabetes and MetS were defined based on the American Diabetes Association standards and Adult Treatment Panel III criteria modified for children, respectively. Participants with prediabetes or MetS were classified into three groups: Never (negative for prediabetes or MetS at ≥3 AVs); Intermittent (positive for prediabetes or MetS at 1 or 2 AVs); and Persistent (positive for prediabetes or MetS at ≥3 AVs). Multinomial logistic regression was used to evaluate the effects of BF, GDM, and BF-GDM interaction on the prevalence of prediabetes and MetS at the child's final AV with sex, Tanner stage, total body percent fat, and birth weight as covariates.

Results: GDM compared to non-GDM offspring had six times higher risk of persistent prediabetes ($p<0.0001$) and MetS ($p=0.0011$). There was a significant BF-GDM interaction on the prevalence of prediabetes and MetS ($p=0.045$ and $p=0.034$). Compared to GDM offspring who were not BF (referent), GDM offspring who were BF had lower odds of persistent prediabetes (OR=0.18, 95%CI: 0.04-0.82, $p=0.02$) and persistent MetS (OR=0.10, 95%CI: 0.02-0.55, $p=0.008$). Compared to referent group, non-GDM offspring who were BF, and non-GDM offspring not BF had a lower prevalence of persistent prediabetes (OR=0.10, 95%CI: 0.03-0.37, $p=0.0008$ & OR=0.05, 95%CI: 0.01-0.18, $p<0.0001$) and persistent MetS (OR=0.14, 95%CI: 0.04-0.59, $p=0.01$ & OR=0.05, 95%CI: 0.02-0.13, $p<0.0001$).

Conclusions: These findings suggest that GDM offspring have significantly higher risk of persistent prediabetes and MetS. BF is protective against the prevalence of prediabetes and MetS in offspring regardless of GDM. These finding suggest that the beneficial effects of BF may help decrease the deleterious effects of GDM on health outcomes in the offspring in this population.

Keywords: Gestational diabetes mellitus, breastfeeding, prediabetes, metabolic syndrome

ABSTRACT – G

Influence of Diet on Prevalence and Severity of Periodontal Disease

In Low Income Women

Mahsa Babaei, M.S. and Jean Freeland-Graves, Ph.D.

Background
Periodontal disease is a chronic inflammatory disease that affects the gingival tissue and alveolar bone supporting the teeth. In the United States (U.S) almost one out of every two adults, aged 30 and over, exhibit periodontal disease. This condition is more frequent, and more severe, in individuals of low socioeconomic status. It is well established that diets high in added sugars, saturated fatty acids and low in fruits and vegetables and dairy are linked to periodontal disease. The goal of this research is to examine the relationship between diet and prevalence of periodontal disease in low-income women.
Objective/Hypothesis
Low income women who consume foods high in added sugars, saturated fatty acids and low in fruits and vegetables and dairy will demonstrate higher prevalence and severity of periodontal disease.
Experimental Approach
This is a cross-sectional study that will examine 220 women during one visit to dental clinics in central Texas. Inclusion criteria in the study will be: low-income, women, ages 18-50 years, and a nonsmokers. A Food Frequency Questionnaire FFQ will be administered and Probing Pocket Depth (PPD) and Clinical Attachment Loss (CAL) will be determined in order to access the prevalence and severity of periodontal disease.
Results and conclusions:
It is anticipated that diets high in added sugars, saturated fatty acids and low in fruits and vegetables and dairy will be associated with higher prevalence/severity of periodontal disease.

ABSTRACT – H

Title: Development and Validation of Dental Nutrition Knowledge Competency Scale
Authors: Prageet K. Sachdev, Jeanne H. Freeland-Graves
Background: Dental caries is a chronic disease characterized by decalcification of the teeth by the acids released by the bacteria in the oral cavity. Approximately 91% of the adults, 20-64 years, in the U.S. have caries in their permanent teeth. There is a higher prevalence of dental caries in economically disadvantaged populations. Inadequate nutrition knowledge contributes significantly to the existing disparities. The U.S. Dietary Guidelines of 2015-2020 recommends consumption of less than 10% of calories from added sugar. In 2016, FDA mandated inclusion of added sugars on the nutrition label. To date there is a lack of a validated and reliable instrument to assess knowledge concerning recent added sugar dietary guidelines, identification of sugars on food labels, and cariogenicity of foods.
Objective: To develop and validate a Dental Nutrition Knowledge Competency Scale to assess dental nutrition knowledge in low-income women.
Experimental Approach: 150 low-income women (<250% of Federal Poverty Level), 18-50 years were recruited. A literature search of all dietary factors related to dental caries was conducted. A panel of ten nutrition professionals evaluated the questionnaire for its content. A focus group of six people evaluated it for readability. A subsample of 40 women completed the instrument at two different points, two weeks apart. Internal consistency reliability was assessed using Cronbach's α. Construct validity was established via item discrimination and exploratory factor analysis.

Results: Exploratory factor analysis, with varimax rotation resulted in 3 constructs. The internal consistency of each section ranged from 0.7 ± 0.97 and test-retest reliability ranged from 0.8 ± 0.87. The final version of the questionnaire has 24 items.

Conclusions: Dental Nutrition Knowledge Competency Scale is a validated and reliable instrument to measure dental nutrition knowledge in low-income women.

ABSTRACT – I

Quantifying Examination of Fermented Food Consumption and Nutrient Intake from the South Korean National Health and Nutrition Examination Survey (KNHANES)

Sangyoung Kim and Jeanne H. Freeland-Graves

Assessment of the diet and its quality of a population are important for monitoring health. Fermented foods such as kimchi, fermented soybeans, and soy sauce are traditional foods in South Korea. These fermented foods generally are considered to be healthy, as they may be protective against cancer and cardiovascular disease. The goal of this research is to examine the consumption of fermented foods by South Koreans using data from the Korean National Health and Nutrition Examination Survey (KNHANES). The target population of the study is South Korean adults, aged 19 to 64 years. Assessment of nutrient intake and foods will be via a 24-hour dietary recall and the total diet will be assessed for diet quality via the Korean Healthy Eating Index (KHEI), 2015. The proposed research will provide information on the current status of fermented foods of South Koreans based on the 2009 and 2016 KNHANES data and how it has changed in recent years.

ABSTRACT – J

Development and validation of a food frequency questionnaire to evaluate dietary patterns among adults in South African Xhosa townships

Ashley Neely, Jeanne Freeland-Graves, Ph.D., R.D.

Background: As South Africa continues to become more industrialized, the county is experiencing a triad of transitions in demographics, epidemiology, and nutrition. By tracking the progression of the nutrition transition, which is characterized by a shift from traditional to refined foods, health professionals can not only better advise their patients, but also evaluate nutrition intervention programs. South Africa has one of the highest Gini Indexes in the world, which is a measure of a country's income inequality ranging from 0 (perfect equality) to 100 (perfect inequality). Because of the high level of income inequality, adults who reside in impoverished townships of South Africa will be most greatly affected by the nutrition transition.

Objective/Hypothesis: To create and validate a food frequency questionnaire (FFQ) to analyze the dietary patterns present in South African Xhosa townships. Due to the current nutrition transition taking place in South Africa, a 'Western diet' will be more prevalent than traditional diets.

Experimental Approach: Content validity will be established by panel of nutrition experts and construct validity by comparison with repeated 3-day diet records. Pearson correlation coefficients will be computed to examine relationships in diet between the proposed FFQ and diet records. Test-retest reliability will be assessed by intraclass correlations.

Expected Results: Younger respondents will follow a more 'Western diet,' high in saturated fats and processed foods as compared to older generations who follow more 'traditional diets.' In both groups, the diet will be high in starches and meat and low in fresh produce.

Conclusions: Development of such an FFQ will allow for more insight into the dietary patterns found in township-dwelling, low income South Africans. Repeated measurements could serve as a method of evaluation of nutrition interventions.

ABSTRACT – K

Systematic Review on International Trace Mineral Requirements

Annemarie Zamora Binderberger, Jeanne H. Freeland-Graves

Background: Government and other agencies establish dietary standards around the world to promote optimal health for their population. Developing countries often use the dietary standards established by World Health Organization to prevent diseases. In contrast, Europe, the United States and other developed countries have committees that routinely make recommendations to promote better quality of life, in addition to prevention of chronic diseases. The RDA's for Zn, Cu and Se established by the Indian Council of Medical Research in India are significantly lower than the US standards. Most developing countries are mainly concerned about zinc compared to copper and selenium since their main public health concern is malnutrition.

Objective/Hypothesis: To conduct a systematic review to summarize trace element requirements and dietary standards in adults all across the globe. Dietary standards for Zn, Cu and Se in adults in developing countries will be significantly lower compared to more developed countries.

Experimental Approach: Sample of 100 countries throughout the world that publish dietary standards for trace minerals for adults only. Standards will have to be published or updated after 2009. Recommendations for zinc, copper, and selenium in adults will be collected and compared to dietary intake.

Expected Outcomes: Developing countries will have to increase their requirements to promote better dietary intake and well-being of the population. The soil quality of the country will also impact the level of trace mineral requirements.

Conclusions: This research will provide a summary of updated standards to improve understanding of the suggested diets for Zn, Cu, and Se status. It will also serve to provide more scientific evidence to show the physiological importance of dietary intake. Developing countries will establish nutrition campaigns to enforce dietary intake and supplementation as needed on every stage of life cycle.

ABSTRACT – L

Associations between nutrition knowledge, environmental, social, and individual factors and grocery purchase conformance to the Thrifty Food Plan in women receiving Supplemental Nutrition Assistance Program benefits

Jeanette Sands and Jeanne Freeland-Graves

As the largest food assistance program in the United States the Supplemental Nutrition Assistance Program (SNAP) plays a pivotal role in attenuating hunger and poverty in low income populations. Recent evidence indicates that SNAP meets these goals only modestly. At present, resource allocation of SNAP benefits is based on the Thrifty Food Plan (TFP) developed by the United States Department of Agriculture. This plan acts as a guide for low income participants to purchase nutritious foods on a limited budget. It is a useful metric of the success of the program, alongside other common measures such as diet quality, food security, and health outcomes. Many factors potentially influence food choices, including SNAP program design and benefit distribution, participant education, and food incentivization or restriction. Nutrition knowledge is low in the SNAP population, resulting in less healthy food choices and subsequent negative health outcomes. Environmental, social, and individual factors, as detailed in the Social Ecological Model, also may significantly impact food choices. In order to explore how nutrition knowledge and environmental, social, and individual factors are related to food choices, women receiving SNAP benefits, 18-50 years of age, were recruited from sites in Central Texas from January 2015 to Summer 2017. Demographic, nutrition knowledge, and health behavior information was gathered by survey and grocery purchases were obtained by grocery receipts. Data analysis is currently in progress to examine relationships between nutrition knowledge, environmental, social, and individual factors, and grocery purchasing conformity to TFP recommendations.

ABSTRACT – M

Weight Trajectory Effects in High-Risk Pregnancies: Maternal Obesity and Twin Gestations

Amy Kweller, Elizabeth Widen

Background: Evidenced-based pregnancy weight gain recommendations do not exist for women with twin gestations and are limited for women with obesity—both high-risk pregnancies that result in a disproportionate rate of complications. A majority of women enter pregnancy affected by overweight or obesity, and most gain weight above 2009 Institute of Medicine (IOM) guidelines. These recommendations do not provide appropriate guidelines delineated by severity of obesity. Those with twins are advised to gain even greater weight, but the IOM recommendations during twin pregnancy remain provisional due to lack of adequate evidence. It is unclear the pattern, timing, and total amount of weight change that would benefit high-risk pregnancies, or if recommendations should differ by severity of obesity.

Objective: Among twin pregnancies and women with obesity in singleton pregnancies, we aim to determine optimal gestational weight gain and trajectory patterns that minimize adverse outcomes.

Hypothesis: Increasing pregravid BMI and distinct pregnancy weight gain trajectory patterns typified by 1) high gain across pregnancy in singletons or 2) low or high gain across pregnancy with twins are associated with greater likelihood of poor outcomes.

Experimental Approach: We will leverage data from three large, multi-cultural cohorts, the

1) National Vital Statistics System (NVSS), a cross-sectional, national collection of mother-infant dyads and triads;
2) Kaiser Permanente Northern California (KPNC) 2008-2013 Pregnancy Cohort, a retrospective cohort of mothers with obesity (n=32,574); and
3) Austin Maternal Fetal Medicine (AMFM) 2012-2018 Twin Pregnancy Cohort, a retrospective cohort of mother-twin triads (n=600).

Primary outcome measures include size for gestational age, gestational age at delivery, mode of delivery, and maternal and infant complications. For modeling weight trajectories across pregnancy, semi-parametric methods will characterize optimal trajectories into distinct weight gain trajectory classes. Multivariable linear and logistic regression models will ascertain how outcomes are affected by prepregnancy BMI, gestational weight gain, and weight gain trajectory class membership in cohorts 2 and 3.

Implications: These results will inform evidence-based gestational weight gain guidelines and interventions, and help identify women and infants who need early, enhanced intervention.

ABSTRACT – N

Title: Effects of time-of-day dependent macronutrient intake on gut microbiota diurnal oscillations.

Diana E. Gutierrez, Laura M. Lashinger, and Molly S. Bray
Department of Nutritional Sciences, The University of Texas at Austin, Austin TX

Introduction: The gut microbiome (GM) is a key factor in the control of energy homeostasis. Time-restricted feeding (TFR) has been associated with fluctuations in GM bacterial families that may influence host metabolism. The purpose of this study was to examine the effects of time-restricted macronutrient intake on the circadian oscillations of the gut microbiota.

Methods: Four feeding groups (n=6/group) with Male and female FVB/N mice were used. High-fat (HF; 45% kcals fat) and low fat (LF; 10% kcals fat) chow, matched for protein content, was used. Two control groups received access to either HF or LF chow throughout the active (dark) phase of the light/dark cycle (zt12- zt24), while two timed-feeding groups received two simulated "meals" given during the first four (zt12- zt16) and last four (zt20-zt24) hours of the dark cycle, with a 4-h period of no food access. The Early High Fat (EHF) group had access to HF food from zt12-zt16 and LF food from zt20-zt24, the Early Low Fat (ELF) group received the opposite meal pattern. After 13 weeks of diet, fecal samples were collected at 4h intervals, and 16s sequencing was used to quantify bacterial taxa. Cosinor analysis was used to examine rhythmicity of the microbiota.

Results: Significant ($p < 0.05$) rhythmicity was detected in the phyla *Bacteroidetes,* and *Firmicutes* only in the early high fat feeding condition, with peak abundance of each phylum phase-shifted by approximately 12 h, consistent with the presentation of high fat or high carbohydrate to the colon. Within the *Bacteroidetes* phylum, the *Rikenellaceae* family presented rhythmic oscillations. In contrast in the *Firmicutes* phylum, the genera *Clostridiales* presented rhythmicity, and at the level of family *Streptococcaceae*, *Mogibacteriaceae,*and *Erysipelotrichaceae* presented diurnal oscillations.

Conclusion: Timed macronutrient intake under early high fat feeding paradigm is associated with diurnal oscillations of the gut microbiota with potential consequences for the metabolic capacity of the gut microbiota community in response to nutrient entrainment.

ABSTRACT – O

Acute effects of rotating shift work paradigm on activity and metabolism

Vasavi Shabrish, Dr. Laura M. Lashinger and Molly S. Bray

Background. Many of our body's biological processes follow approximately 24-hour rhythms that regulate physiological functions in mammals. The cellular circadian clock system synchronizes internal clock timing with external cues or zeitgebers. Shift work is characterized by out-of-phase feeding, activity, and sleeping patterns, inducing a multitude of changes in the physiological state of an individual. Coordination of circadian rhythm entrainment between central and peripheral clocks is compromised in a rotating shift work paradigm due to the repeated shifts in exposure to light/dark, food, and physical activity every three to four days.

Objective. The purpose of this study is to investigate the acute effects of rotating shift work on molecular circadian rhythms, metabolism, and body composition.

Experimental approach. Eleven-week-old FVB/N background mice were individually housed. Mice were randomly assigned to a control group or a rotating shift work group. Control group were exposed to regular 12:12 light/dark cycle while shift work group were exposed to altered 12:12 dark/light cycle, closely simulating rotating human shift work, for 2 weeks of the study. All mice received ad libitum access to wireless running wheels, chow, and water. Glucose tolerance tests and body composition were measured at baseline and end of study.

Results. Acute exposure to rotating shift work resulted in the shift work group being significantly more active between zt0-zt12 ($p<0.001$) and during lights on ($p<0.05$) compared to the control group. Activity in the shift work group was distributed throughout the 24-hour period more than the control group. Acute exposure demonstrated significant differences between groups for fasting glucose ($p<0.05$) indicating dysregulation in carbohydrate metabolism. No significant differences were observed in body weight and body composition between groups.

Conclusion. Acute exposure to a rotating shift work paradigm disrupts normal activity patterns and dysregulates carbohydrate metabolism.

ABSTRACT – P

Investigating the Role of Tumor Associated Macrophages in Obesity-Induced Prostate Cancer Progression

Margaret Drake-Studstill and Linda deGraffenried

Over-treatment of prostate cancer is a major medical issue; aggressive and unnecessary treatment leads to a decreased quality of life and increased healthcare costs. Reliable biomarkers help physicians determine when to treat and when to place patients under surveillance. Obesity significantly increases the risk of developing aggressive prostate cancer, and rodent studies have found associations between obesity and tumor-associated macrophages (TAMs). Immunohistochemistry will be used to evaluate TAMs as possible biomarkers. Samples from normal weight and overweight prostate cancer patients with similar Gleason scores will be analyzed to determine 1) if TAM concentration predicts disease recurrence and 2) if TAM concentration is higher in obese patients.

In addition to their potential as biomarkers, the pro-angiogenic, pro-tumorigenic TAMs may be prime targets to reduce proliferation, metastasis, and immune system suppression. Previous studies have identified markers associated with TAMs – IL-10, an anti-inflammatory cytokine; VEGF, a factor involved in angiogenesis and metastasis; MMP-9, a metalloproteinase involved in extracellular matrix degradation and metastasis; arginase-1 and TGF-beta, anti-inflammatory molecules involved in immunosuppression. Preliminary RT-qPCR data indicates that the use of rapamycin, an mTOR inhibitor, targets TAMs to reduce the expression of these markers. It is hypothesized that rapamycin reduces expression of these markers in part by blocking the mTOR-regulated nuclear localization of the transcription factor NFκB. This hypothesis will be tested by probing for nuclear localization of NFκB and by immunofluorescence.

Rapamycin may be a useful drug to reduce TAMs, either by blocking polarization of classically-activated, pro-inflammatory M1 macrophages towards the TAM phenotype, by re-polarizing TAMs back to the M1 phenotype, or by promoting apoptosis preferentially in TAMs. Apoptosis will be tested by annexin-V stained flow cytometry. If rapamycin is shown to eliminate TAMs, it could be a useful treatment to block disease progression in obese prostate cancer patients placed under surveillance.

ABSTRACT – Q

Obesity Induces a Proinflammatory Phenotype in Stromal Fibroblasts

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Background: Approximately 40% of American women suffer from obesity, and about 1 in 8 women will be diagnosed with breast cancer during her lifetime. The concurrence of these trends has the potential to be particularly detrimental, as obesity confers a worse prognosis for both pre- and postmenopausal breast cancer patients. While the precise mechanisms by which obesity impacts breast cancer prognosis remain to be discovered, evidence suggests that obesity upregulates components of cancer-associated fibroblast (CAF) and senescent cell secretomes, both causally associated with carcinogenesis. Specifically, obesity has been shown to induce expression of the senescent secretory products as well as CAF products, such as reactive oxygen species. However, studies have yet to determine whether obesity imparts a senescent- or CAF-like phenotype from any individual cell type in the breast tumor microenvironment. Because fibroblasts constitute 80% of the tumor stromal mass, it is of the utmost importance to study obesity-stimulated changes in this cellular compartment and their effects on cancer cell aggressiveness.
Hypothesis: We hypothesize that obesity induces a proinflammatory senescent- or CAF-like phenotype that supports breast cancer growth and progression.
Experimental Approach: *In vitro* obesity models were used to assess the direct and paracrine-mediated effects of obesity. To evaluate direct effects of obesity on fibroblast phenotype, fibroblasts were exposed to 2% v/v sera derived from lean or obese women and assessed for changes in expression of proinflammatory genes, including IL-1α, IL-6, and IL-8, as well as IKBα protein expression and nuclear localization of p65, a subunit of NFkB, which transcribes about 75% of genes involved in the senescent secretome. The fibroblasts were assessed in kind following exposure to CM from breast cancer cells exposed to the lean or obese sera to assess the influence of obesity as mediated by other components of the breast tumor microenvironment.
Results and Conclusions: Obese conditions induced a proinflammatory phenotype in fibroblasts in both direct and paracrine-mediated manners, as evidenced by loss of IKBα; p65 nuclear localization; and increased IL-1α, IL-6, and IL-8 gene expression. These data contribute to the identification of a mechanistic link between obesity and proinflammatory, senescent phenotypes and will ultimately allow for elucidation of the means by which obese conditions confer a worse prognosis for breast cancer patients.

ABSTRACT – R

Pediatric Glioblastoma: Identifying Potential Therapeutic Targets by High Throughput Screening

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Background: Pediatric glioblastoma (p-GBM) is a rare but aggressive brain cancer. Current treatment options include tumor resection, radiation, and chemotherapy, which is the standard of care for adult glioblastoma. Adult and pediatric glioblastomas, however, are distinct diseases and require unique treatments. Tumor resection is not always possible due to location in both adult and p-GBM, and furthermore, radiation therapy is too harsh for patients younger than 3 years. Therefore, life expectancy of p-GBM is less than 2 years from diagnosis. Research is lacking in the area of p-GBM due to its rarity, but development of a standard treatment is still warranted.
Objective/Hypothesis: Screen a library of current chemotherapeutic agents to identify individual drugs or drug classes that are potentially effective p-GBM treatments.
Experimental Approach: Two p-GBM cell lines were screened with a library of 290 anti-cancer drugs at 100nM to assess their ability to decrease cell viability 24 hours after treatment. Cell viability was measured by luminescence assay. Drugs that were able to decrease cell viability in both models by 25% when compared to their respective controls were considered for further analysis in combination treatments. Furthermore, metabolic pathways and targets of the selected drugs will be considered as areas of future exploration.
Results: From the library of 290 cancer drugs, thirteen drugs were selected for their ability to decrease cell viability of the two p-GBM cell lines by at least 25% when normalized to control viability. Ten of the 13 drugs targets either an HDAC, proteasome, mTOR pathway, or heat shock protein.
Conclusions: Targeting HDACs, proteasomes, mTOR, and heat shock proteins show promise as p-GBM therapies. Further studies need to be conducted to assess the safety of the drugs with normal human astrocytes. Combination treatments of multiple drug targets should also be assessed at varying concentrations to show if lower doses of multiple drugs is more effective than single drug therapies.

ABSTRACT – S

Isolation of synergistic natural products to target metabolic dysfunction of B-cell lymphoblastic leukemia by high throughput screening

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ABSTRACT

Background: Acute lymphoblastic leukemia is the most common pediatric cancer. Though approximately 90 percent of patients can be cured, the long term side effects of chemotherapy take a tremendous toll on patients. In comparison to healthy children, leukemia survivors report an increase in psychosocial disorders such as social phobias, negative body images, increased social challenges at school, and deterioration of family relationships. Less toxic alternatives and adjuvant therapies that can decrease chemotherapeutic doses or duration is an unmet need. Evaluating a diverse drug library of natural products at low concentrations permits the isolation of treatments that specifically decrease the viability of leukemic cells, but exhibit negligible effects on non-malignant cells.

Methods: Two rounds of high-throughput screening were used to treat 13 different human cell lines to isolate a synergistic treatment pair stemming from a library consisting of 136 structurally diverse natural products. The final concentration of treatment was 10μM and ranged from 10nM to 10μM in the first and second rounds of screening, respectively. Cell viability was assessed by ATP quantification at 24 hours. To determine synergism the BLISS model was utilized.

Results/Future Experiments: Of the 136 treatments examined, nine had an inhibition average of at least 20% in the B-ALL cell lines. Parthenolide had the most negligible effect on the non-malignant cell lines, the highest efficacy across the all B-ALL cell lines, and was therefore selected as the top candidate. The remaining treatments were grouped as toxic or selective depending on if the average inhibition of the non-malignant cell lines was greater than 20%. Data acquisition is ongoing in the second round of screening where parthenolide is being be tested in combination with the other top eight candidates. The results from this screen will warrant further investigation by metabolomics analysis utilizing direct infusion and liquid chromatography mass spectrometry.

ABSTRACT – T

Title: Automated Detection of Fatty Acids in Glioblastoma Pediatric-Glioblastoma after Chemotherapeutic Intervention

Authors: Paul Gries, Jennifer Chiou, Stefano Tiziani

Background: Fatty acids perform numerous critical roles inside cells. Fatty acids in their free and complex forms comprise important structural components of cells, sources of chemical energy and recent studies indicate a role as cell-to-cell signaling molecules. Glioblastoma, an aggressive cancer of the brain and spinal cord commonly exhibits altered lipid metabolism than normal neurological tissue. Many currently used chemotherapeutics have been shown to act as inhibitors of fatty acid metabolism, both at the peroxisomal and mitochondrial levels.

Objective/Hypothesis: Treating glioblastoma cells with inhibitors of fatty acid oxidation will cause shifts in the levels of free fatty acids. Inhibition of mitochondrial fatty acid β-oxidation will lead to an increase in the levels of medium and short chain fatty acids, while inhibition of peroxisomal β-oxidation would result in an accumulation of very long chain fatty acids.

Experimental Approach: Cultured pediatric and adult Glioblastoma cells were treated with etomoxir, thioridazine and temozolomide alone and in combination. Fatty acids were isolated from treated cells through a modified Folch extraction. Samples were chemically modified by MTBE and TMSH derivatization before they were injected into a gas chromatography-mass spectrometer for analysis. Area under a chromatographic peak was used to determine relative concentration of each fatty acid.

Results: Targeted fatty acid data was obtained from at least 3 replicates of each treatment group. The majority of the free fatty acid levels were not significantly different across the different treatment groups.

Conclusions: No significant accumulation of free fatty acids were observed under any specific treatment or combination. Recent experimental studies have indicated that glioblastomas' altered fatty acid metabolism may center on medium chain omega-6 metabolism and should be reconducted with an emphasis on essential fatty acids.

ABSTRACT – U

Targeting ASCT2-mediated glutamine uptake blocks prostate cancer growth and tumor development

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Background: The vast molecular diversity offered by natural compound libraries represents an invaluable resource for identification of synergistic combinatorial treatments. Metabolomics, an emerging field of biomedical and nutrigenomics research entails the measurement of a comprehensive pool of small molecules, called the metabolome, in biological samples. Besides being nutrients essential for cell growth, in the context of cancer, metabolites represent sensitive markers of major alterations in cancer cell metabolism and contribute to oncogenic signaling.
Objective/Hypothesis: Specific natural compound combinations will result in synergistic effects on prostate cancer. The wealth of information obtained from the multivariate metabolic readout will offer an unprecedented opportunity to investigate the metabolic consequences of the administration of natural compound combinations and thereby identify synergies in their chemopreventive activity.
Experimental Approach: High-throughput screening of a natural compound library was performed to identify the most efficacious combinatorial treatment on prostate cancer. Selected compound combinations were tested in vivo in a mouse allograft model of prostate cancer. A subsequent untargeted metabolomics and metabolic flux analysis using isotopically labeled glutamine were applied for investigating the synergistic mechanism in metabolic level.
Results: From the top hits of the high-throughput screening, ursolic acid, curcumin and resveratrol were selected for further analyses and administered in vivo via the diet, either alone or in combination. All possible combinations of these natural compounds produced synergistic effects on tumor size and weight, as predicted in the screens. The result from metabolomics analysis revealed that the compound combinations modulated glutamine metabolism. In addition, ASCT2 levels and STAT3, mTORC1 and AMPK activity were modulated to a greater extent by the combinations compared to the individual compounds.
Conclusions: This approach can be useful for identifying synergistic combinations of natural compounds for chemopreventive and therapeutic interventions.

ABSTRACT – UA

Obesity-Induced Enrichment of Stem-like Cells in the Breast Tumor Microenvironment
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Background: Several studies have shown that obesity plays a role in inducing a "stem-like" phenotype. Preliminary data from the deGraffenried lab suggest a "reprogramming" occurs, although the exact mechanism through which this occurs is unclear. This reprogramming coincides with transformation of well differentiated cells to a dedifferentiated stem-like phenotype in a process termed epithelial mesenchymal transition (EMT). In addition, earlier studies have shown that exposure to obese sera in both MCF-7 and T47D cells increases expression of TWIST and SNAIL, both known EMT transcription factors with a potential role in stem-cell reprogramming.
Hypothesis: We hypothesize that several factors associated with obesity induce disease progression in breast epithelial cells through epigenetic reprogramming, including interleukin-6 (IL-6), insulin-like growth factor-1 (IGF-1), and leptin.
Experimental approach: The factors in obese sera that induce a stem-cell reprogramming will be investigated using well-differentiated luminal A cells. Quantitative polymerase chain reaction (qPCR) will be used to measure expression levels of factors known to be associated with stem-cell and EMT programming, while flow cytometry will be used to investigate cell surface markers associated with stem-like cells.
Results and Conclusions: Flow cytometry was optimized using MDA-MB-231 cells treated with 50ng/uL IL-6 for 10 days, yielding a positive stem-like control. As revealed by gene expression analyses, obese conditions increased expression of Snail and Twist in MCF-7 cells by two-fold and five-fold, respectively, compared to lean sera. The effect was at least partially reversed by neutralization of IL-6 in the obese sera, which reduced Snail and Twist expression by about 50%. Additionally, addition of recombinant IL-6 to lean sera increased Snail and Twist expression by approximately 30% and 200%, respectively. These preliminary findings indicate that obese conditions may induce a stem-like phenotype in well-differentiated luminal A breast cancer cells. This study will ultimately help identify therapeutic targets to improve survival in the obese patient population.

ABSTRACT – UB

Modulation of FASN under Obese Conditions in the Breast Tumor Microenvironment

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Introduction: Obesity promotes a worse breast cancer prognosis in pre- and postmenopausal women, in part through alteration of metabolism in cells of the breast tumor microenvironment. At the same time, cancer cells often demonstrate changes in fatty acid utilization, including changes in expression and activity of fatty acid synthase (FASN). This enzyme may impact tumor growth and behavior through modulation of beta-oxidation and plasma membrane signaling, among other processes. Previous studies in our laboratory have demonstrated that exposure to obese conditions induces significant changes in breast cancer cell proliferation and that obesity modulates activity of other breast tumor cells, including preadipocytes. *We hypothesize that obesity induces breast cancer proliferation through modulation of FASN.* Our studies will help determine whether FASN represents a viable target to limit obesity-induced breast cancer progression.
Methods: FASN has been shown to promote cancer cell proliferation through generation of fatty acid precursors required for cell proliferation, membrane fluidity, and oncogenic signaling pathways. To determine if modulation of FASN is an important mechanism by which obesity promotes disease progression, MCF-7 and T47D breast cancer cells and human adipose stromal cells (ASC) were exposed to 2% sera from obese postmenopausal women or 2% sera from non-obese (control) women and the FASN inhibitor TVB-3166. Changes in gene expression patterns, viability, and survival were determined using qPCR, MTT, and colony formation assays, respectively.
Results: Exposure to the obese sera resulted in increased expression of FASN in MCF-7 and T47D breast cancer cell lines. Preliminary results also demonstrate that the FASN inhibitor hindered obesity-induced breast cancer cell viability and survival.
Conclusions: Our findings indicate that obesity promotes upregulation of FASN in MCF-7 and T47D breast cancer cells and that using a FASN inhibitor limits cancer cell proliferation. The results of these studies will provide a better understanding of the mechanism by which obesity promotes a more aggressive breast cancer. These data also suggest that FASN inhibitors may serve as novel therapeutics for treatment of breast cancer in the obese patient population.

ABSTRACT – UC

Obesity Induced T-cell Dysfunction Promotes Prostate Cancer Progression

Peyton Travis, Alejandra De Angulo, Gloria C. Galván, Linda A. deGraffenried

Background: Obese men are at a higher risk for aggressive forms of prostate cancer. Obesity has been associated with low-grade chronic inflammation and metabolic dysregulation. Immune cells from obese subjects may have a role in prostate cancer aggressiveness by secreting disease promoting factors, such as the pro-inflammatory cytokine interleukin-6 (IL-6).

Objective/Hypothesis: We propose to test the hypothesis that obesity-modified CD4+ T-cells promote a more aggressive phenotype in prostate cancer cells.

Experimental Approach: Mimicking the prostate tumor environment, an in vitro model consisting of prostate cancer epithelial cells, macrophages, and sera from obese and non-obese men was used to assess the impact of obesity-induced paracrine signaling on T-cell dysregulation and understand the mechanism by which this occurs in the prostate cancer microenvironment. Splenic T-cells were isolated from mice and stimulated with anti CD3 and CD28. qPCR was used to measure IFNγ, IL-6, IL-2, and IL-10 expression in T-cells exposed to obese or non-obese macrophage conditioned media (CM). To determine if obese conditions modify the impact of T-cell dysfunction on prostate cancer cell signal transduction pathways, western blot analysis was used to evaluate the modulation of STAT3 and qPCR was used to measure STAT3 target genes related to prostate cancer progression in prostate cancer cells exposed to obese or non-obese T-cell CM. Invasion chambers were used to determine if obesity-modified T-cell CM impacts the invasive capacity of prostate cancer cells.

Results: Obese conditions suppressed the expression of IFNγ and IL-2 in T-cells, but up-regulated the expression of IL-6 and IL-10. Prostate cancer cells exposed to obese T-cell conditions induced more phosphorylation of STAT3, decreased expression of E-cadherin, increased expression of Snail1, MMP-9, Twist, FN-1, and Vimentin, and showed a higher invasive capacity.

Conclusions: These data suggest that obese conditions may induce T-cell dysregulation, contributing to tumor growth and metastasis associated with prostate cancer in obese patients. A better understanding of the link between obesity, T-cell dysregulation, and prostate cancer progression will provide new avenues for treating prostate cancer in the obese population.

ABSTRACT – UD

Obesity Increases COX-2-Induced PGE2 Production in an AMPK-dependent Manner

Emily Equitz

Background: Obesity is associated with a worse prognosis of breast cancer due to increased endocrine activity of adipose tissue. This is in part due to increased cyclooxygenase-2 (COX-2)-induced proinflammatory eicosanoid prostaglandin E2 (PGE2). Obesity decreases AMP-activated protein kinase (AMPK) phosphorylation, possibly due to increased circulating levels of leptin that decrease AMPK activity. Metformin is a drug used to treat Type 2 Diabetes but has also showed anticancer effects. The mechanism of action is unknown, but it is suggested to activate liver kinase B1 (LKB1) or decrease AMP levels which in turn activates AMPK.

Objective/Hypothesis: This project seeks to examine the role of obesity-related factors such as leptin in upregulating PGE2 production and promoting growth of estrogen receptor-positive (ER+) breast cancer. I hypothesize that obese conditions will increase PGE2 production through decreased activation of AMPK, which would otherwise suppress the COX-2 enzyme. Metformin in addition to hormone therapy is hypothesized to decrease COX-2-mediated PGE2 production in obese conditions.

Experimental Approach: I aim to determine if obese conditions modulate COX-2 in an AMPK-dependent manner. Preliminary data were collected to demonstrate the decreased phosphorylation of AMPK in ER+ breast cancer cells treated with 2% obese sera (BMI>30kg/m^2) relative to cells treated with 2% lean sera (BMI<25kg/m^2) through Western Blot analysis. I aim to silence AMPK using siRNA in obese-conditioned media to examine the impact on COX-2 expression. COX-2-mediated PGE2 production in macrophages after treatment with metformin will be measured by enzyme-linked immunosorbent assays.

Expected Results: Western blot analyses demonstrate decreased phosphorylation of AMPK in obese conditions compared to lean. The obese condition is expected to show increased COX-2 expression relative to lean conditions when AMPK is silenced. Metformin is expected to decrease COX-2-induced PGE2 production by activating AMPK.

Conclusions: Results from this study will confirm the prognostic value of COX-2 and have the potential to unveil new therapeutic targets in the process of breast tumorigenesis.

ABSTRACT – UE

The Effect of the Ratio of Omega-6 to Omega-3 Fatty Acids on Breast Cancer Phenotype in the Obese Environment

Laura Winikka, Duan Quach, Lucy Lengfelder, Brittany Harlow, Gloria Galvan, Alejandra deAngulo, Christopher Jolly, Andrew Brenner, and Linda deGraffenried

Background: Studies have shown that obesity is associated with a worse breast cancer prognosis. Recent data from published *in vitro* and retrospective studies suggests that this phenomenon may occur because the obese state promotes a more aggressive cancer phenotype through the cyclooxygenase (COX-2) pathway and its production of prostaglandin E2 (PGE2). The metabolization of omega-3 fatty acids decreases the production of PGE2, which has been shown to have potential benefit to cancer patients by reducing aromatase activity and therefore estradiol production.
Objective/Hypothesis: A previous clinical trial showed mixed results in the effect of omega-3 PUFA (polyunsaturated fatty acid) supplements on PGE2 production in post-menopausal obese women. This led to the hypothesis that *the ratio of omega-3 to omega-6 PUFAs have differential effects on cell types within the tumor microenvironment, impacting cancer cell phenotype.*
Experimental Approach: In vitro experiments will be performed to investigate the mechanism of the effect of omega-6 and omega-3 fatty acids and PGE2 on the breast cancer tumor microenvironment. Conditioned media from macrophages will be generated by treating for 24 hours with omega-6 *(arachidonic acid (AA)*) to omega-3 (*eicosapentaenoic acid (EPA*) and *docosahexaenoic acid (DHA)*) fatty acid ratios of either 46:1 or 10:1, and obese or lean sera from post-menopausal females. The cells will be serum-starved for 24 hours, and this media will be collected and used as treatment for prea-dipocytes. Aromatase expression in these pre-adipocytes will be quantified using qPCR.
Results/Conclusions: The increased macrophage PGE2 production resulting from treatment with higher ratios of omega-6 and omega-3 PUFAs may increase aromatase activity in pre-adipocytes, potentially leading to a more aggressive tumor. By investigating this mechanism, it may be possible to define an ideal ratio of omega-6 to omega-3 PUFAs that could limit the effects of chronic inflammation in the obese state on the aggressiveness of breast cancer.

ABSTRACT – UF

Association of Physical Activity with the Prevalence of Prediabetes in Low-Income 3rd-5th Graders

McFarland CB, Vandyousefi S, Asigbee FM, Davis JN

Background: Prediabetes is defined as having higher than normal levels of fasting plasma glucose (FPG), OGTT 2-hour blood glucose, hemoglobin A1c, or a combination of these. Early onset of prediabetes during childhood increases risk of type 2 diabetes mellitus (T2D) and cardiovascular disease later in life. Once considered "adult-onset diabetes", T2D is becoming prevalent in children and adolescents, especially in the United States. Over 30% of Hispanic adolescents with overweight/obesity have been shown to have prediabetes. Evidence suggests that physical fitness and physical activity may influence childhood metabolic risk. However, few studies have examined the association of physical activity with prediabetes rates in younger children.

Objective/Hypothesis: This study aims to assess physical activity in relation to the prevalence of prediabetes in low-income, primarily Hispanic, children. We hypothesized that higher physical activity will be associated with decreased prediabetes risk in children.

Experimental Approach: Baseline data will be analyzed from waves 1, 2, and 3 of TX Sprouts, a school-based gardening, cooking, and nutrition cluster randomized controlled trial with around 2,600 3rd-5th grade, primarily Hispanic, students. Of the 2,600 students, approximately 40% (n=1,040) of children participated in the blood draws. The following measures were collected at each wave: weight, height, waist circumference, FPG, and physical activity via child questionnaire. For this analysis, the American Diabetes Association standard definition of prediabetes will be used. ANCOVA and logistic regression will be used to evaluate the association of physical activity with prediabetes rates with child age, sex, BMI, ethnicity, and parent education as covariates. Data will be analyzed using SPSS (version 24).

Future Implications: Understanding the impact of physical activity on prediabetes rates in Hispanic children will provide valuable information to aid in clinical screening practices for children and in developing future interventions targeting prediabetes.

ABSTRACT – UG

The Association between Screen Time and Prediabetes Rates in Primarily Low-income Hispanic Children

Maalini Bommakanti, Reem Ghaddar, Fiona Asigbee, Dr. Jaimie N Davis

Background: Prediabetes is a condition in which blood glucose levels are elevated, leading to an increased risk of type 2 diabetes (T2D). Prediabetes can be indicated by a glycated hemoglobin (HbA1c) level of 5.7% to 6.4% or a fasting plasma glucose (FPG) level of 100-125 mg/dL. In a study of 2606 adolescents (12-19 y), 17.7% had prediabetes, with higher prevalence in Hispanic participants compared to non-Hispanic Whites. Increased screen time is associated with T2D risk in adults. Television viewing is the most common form of sedentary behavior in industrialized countries and is associated with unhealthy eating in both adults and children. Limited research examines screen time of Hispanic children and prediabetes/diabetes.

Objectives: The purpose of this study is to examine the association between screen time and prediabetes rates in primarily Hispanic youth (7-11 y). It is hypothesized that there is a positive association between the two.

Methods: Baseline data from TX Sprouts waves 1, 2 and 3 will be analyzed. Sixteen elementary schools (≥ 50% Hispanic, ≥ participating in the National School Lunch Program) were randomly assigned to a school year-long nutrition, gardening, and cooking intervention or to a control group (delayed intervention). Eighteen weekly gardening and nutrition lessons were taught to 3rd – 5th graders during school hours. Data collected at baseline included age, sex, grade, and hours of screen time (via survey), height, weight, BMI percentile, waist circumference, and blood pressure (measured by trained staff), and FPG and HbA1c (optional fasting blood draw). Data will be analyzed using SPSS (version 24). Linear regression analysis will be used to examine associations between screen time and FPG as well as HbA1c in waves 2 and 3. A priori covariates include: age, sex, and BMI percentile.

Implications:
These findings will inform public health messages targeting reductions in screen time for children.

ABSTRACT – UH

Relationship Between National School Breakfast Program Participation and Breakfast Consumption

Julienne Calamlam

August 6th, 2018

Background: The National School Breakfast Program (SBP) is a federal meal assistance program provided in public or non-profit private schools that provides breakfast at a reduced or no cost. The SBP gives children from low-income families access to breakfast at least five days of the week; however, few studies have examined the connection between SBP participation and breakfast consumption.

Objectives: The purpose of this study is to assess the impact of participation in the SBP on the frequency of breakfast consumption in elementary school children. It is hypothesized that there will be a positive correlation between SBP participation and breakfast consumption.

Methods: Data from baseline TX Sprouts waves 1, 2, and 3 will be used for this analysis. TX Sprouts is a large school-based nutrition, gardening, and cooking randomized controlled trial including approximately 2,500 low-income, primarily Hispanic, 3rd-5th grade students from 16 schools in central Texas. All ethnicities/races will be included in analyses. Breakfast consumption will be determined using data from the TX Sprouts Child Questionnaire, and SBP participation will be evaluated based on student information. Data will be analyzed using SPSS (version 24), $p< 0.05$. Chi-square analyses will be performed to assess differences in weekly breakfast consumption frequency across SBP participation status.

Implications: Understanding the influence of SBP on the frequency of breakfast consumption in young children will provide valuable information to support the continuation of federal school-based nutrition programs.

ABSTRACT – UI

Identification of Synergistic Combinatorial Treatment with Cyst(e)inase and Cancer Library in AML

Lavender Hackman, Meghan Collins, Stefano Tiziani

Background: Acute myeloid leukemia (AML) is a cancer of the blood and bone marrow. AML causes the bone marrow to produce irregular white blood cells that impair immune function and interferes with the bone marrow's ability to produce normal red blood cells and platelets. Chemotherapy is the current standard of care for AML, however, the effects cause widespread and untargeted cell death. For this reason, less toxic treatment alternatives that can decrease the quantity of chemotherapy required to treat AML are needed.

L-cysteine is an amino acid that the body uses for cell proliferation and protein synthesis and is a precursor for the synthesis of glutathione, an important antioxidant. Cyst(e)inase is an enzyme that depletes serum cystine and effectively prevents tumor growth in various cancers by starving the cells of L-cysteine and preventing antioxidant synthesis which leads to an accumulation of ROS and subsequent cell death.

Objective/Hypothesis: The objective of this project was to identify and isolate drugs from the Selleck Cambridge Cancer Compound Library that act synergistically with cyst(e)inase to selectively target AML cells.

Experimental Approach: High-throughput screening techniques were employed to assess and compare the viability of stromal and AML human cell lines after treatment with cyst(e)inase in combination with a library of 290 drugs from the Selleck Cambridge Cancer Compound Library. The treatments from the library were examined for synergistic effects with cyst(e)inase in their ability to inhibit the cell growth of AML while having negligible effects on normal cells.

Results/Conclusions: Nine drugs were identified using the Bliss independence model for their ability to inhibit cancer cell growth in combination with cyst(e)inase while minimally impacting normal cell growth. The metabolic response induced by these drugs will be further evaluated between the cell lines via untargeted metabolomic analyses such as nuclear magnetic resonance and mass spectrometry.

ABSTRACT – UJ

The Impact of Gene-Exercise Interaction in Predicting Mood

Colton R. Becker, Laura M. Lashinger, Molly S. Bray

Background. Exercise has been shown to have both physical and mental health benefits. Physical health benefits can include improved weight management and quality of life, cardiovascular and metabolic disease risk reduction, increased bone and muscle strength, and greater life expectancy.[1] Mental health benefits include reduced risk of depression and anxiety, improved sleep quality, and sharper cognitive skills.[2] However, exercise has also been associated with adverse affective outcomes.[3] What is not known is whether variation in mood response to physical activity (PA) is related to exercise parameters, genetic variation, or both. It is also not known how mood predicts exercise adherence.

Objective/Hypothesis: The purpose of my study will be to better understand the gene-exercise interaction in predicting mood. To do this, I will focus on two aims: 1) to determine how and why mood changes with exercise, and 2) to identify the genetic variation underlying the relationship between physical activity and mental affect.

Experimental Approach: Analyses will be performed using plasma samples and data gathered during the Training Interventions Genetics of Exercise Response (TIGER) study. Young adults (18-35 y) participated in 15 weeks of aerobic fitness training, within a prescribed duration and intensity, three days per week, using computerized heart rate monitors. Subjects completed a series of visual analog scales (VAS) to assess mood prior to and immediately following one exercise session per week, anchored in the following manner: Tired-Energetic, Tense-Calm, Happy-Depressed, Hungry-Full. Single nucleotide polymorphisms (SNPs) in genes within the serotonin, dopamine, and circadian clock pathways were genotyped. Analysis of variance will be used to examine the relationships between mood states, exercise parameters, genetic variation, and exercise adherence.

Conclusions: A better understanding of the mechanisms that drive exercise adherence may precede the development of more effective behavioral interventions targeting overweight and obese subjects.

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