

**Department of Agriculture and Resource Economics
2014 Graduate Research Forum
Student Presentation Abstracts**

Linking ecosystem services to climate change adaptation: environmental preferences and choices of residents of the Eastern Shore of Virginia

Ian T Yue, Stephen K Swallow

Department of Agricultural and Resource Economics, University of Connecticut, Storrs, CT

The NSF-funded Long Term Ecological Research (LTER) program has committed itself to examining the linkages between ecosystems and human society, particularly through *ecosystem services*: naturally-occurring processes and provisions that benefit humankind. Natural scientists have pointed to ecosystem services valuation as being a key tool for drawing societal attention to natural capital, and, in turn, encouraging environmental protection. Yet, an oft-neglected question is whether those benefitting from ecosystem services actually value them. The answer to this question could influence the viability of a “natural capital argument” for environmental protection. In partnership with the Virginia Coast Reserve (VCR) LTER site, we investigate this issue through a mail survey of residents of the Eastern Shore of Virginia. In particular, we consider: (1) why Eastern Shore residents care about the environment, (2) what ecosystem services Eastern Shore residents value, and (3) whether such values correlate with preferences for climate change adaptation, namely coastline management. Our survey design was primarily informed by focus groups facilitated on the Eastern Shore over a one year period. Adopting a randomized, six-part, mailing methodology, we sent surveys out to 1000 households in each of the two counties that make up the Eastern Shore. We received approximate 300 usable responses from each county. Our preliminary results suggest that the ecosystem services valued most by residents, particularly if protected or strengthened by a coastline management measure, are preservation of wildlife habitat, saltmarsh accretion to combat coastal flooding, and shoreline protection of property. Respondents overall preferred living shorelines over seawalls for shoreline management. Those ranking ecosystem services highly were more willing to pay for a coastline management plan than take no action; the corollary also held true. Respondents’ willingness-to-pay for coastline management increased as acreage of village land protected increased; this trend did not hold for forest or farm land.

The Influences of Farmers' Technology Choices on the Cost Effectiveness of Credit Stacking Policy

Presenter: Pengfei Liu, Advisor Stephen Swallow

Department of Agriculture and Resource Economics, University of Connecticut, Storrs, CT;

Controversies surround credit stacking policy often goes as the following: credit stacking policy may potentially bring more profit to credit market participants by allowing credit producer to sell all credits stacking on spatially overlapped area; while not allowing credit stacking may enable us to benefit from the “by product” for free due to production complementarity. Previous researches on the credit stacking issue often ignore farmers' behavior responses when the policy change. Build on Woodward's (2011) model, we offer a game theory framework to analyze farmers' technology choices change, especially on choosing the complementarity and specialization level. We show that the relative advantage of credit stacking policy depends on the initial credit production function and the range of flexibility the farmers, or the credit producers have.

**Department of Allied Health Sciences
2234 Graduate Student Research Forum
Oral Presentation Abstracts**

**Impact of Obesity and Low Back Pain on Exercise Self-Efficacy, Physical Activity,
and Health-Related Quality of Life in Nursing Home Employees.**

Winnie Chin, B.S.; Pouran Faghri, MD, MS, FACSM; and Tania Huedo-Medina, PhD.

University of Connecticut

Objective: To examine associations between levels of obesity (BMI) and health-related quality of life (HRQoL) outcomes including exercise self-efficacy, physical activity levels, physical function, and readiness to change, and to determine the extent to which low back pain mediates these relationships.

Design: Cross-sectional analysis.

Setting: Intervention-based data from the 2011 Pound-A-Week weight loss program at four long-term nursing home facilities in the Northeast United States.

Participants: Nursing home employees 18 years and older, who were overweight or obese at the time of recruitment, and agreed to participate. Adults ($N=99$) were classified according to BMI as overweight ($25-29.99 \text{ kg/m}^2$), obese class I ($30-34.99 \text{ kg/m}^2$), obese class II ($35-39.99 \text{ kg/m}^2$), and obese class III ($\geq 40 \text{ kg/m}^2$).

Main Outcome Measures: Main outcome measures were the Physical and Mental Health Summary Scales obtained from the SF-12, the Exercise Self-Efficacy Scale (ESE), and a questionnaire based on the Stages of Change Model. Physical Activity was assessed using self-reports across a typical week, and number of days performing moderate or vigorous physical activity. Pain was assessed according to frequency of low-back pain experienced by participant.

Results: Adults with higher levels of obesity were significantly associated ($p<0.05$) with lower reported general health status, lower reported physical activity, lower number of days performing moderate and vigorous physical activity, and higher physical function limitations, compared to adults who were overweight or of a lower obesity class.

Mediation analysis suggests that pain is a partial mediator of the adverse effect of obesity on physical function and health-related quality of life outcomes in overweight and obese nursing home employees.

Conclusions: Low back pain may be an important mediator of the adverse effect of obesity on health-related quality of life outcomes, and may be an important component of programs that aim to increase physical activity in overweight and obese adults.

Acknowledgements The Pound-A-Week (2011) behavioral modification weight loss program was supported by the Center for Disease Control, Dr. Pouran Faghri (PI).

Stress and emotions as predictors of health behaviors and bodyweight among correctional employees using the Emotion-Behavior-Weight (EBW) model

*C. Mignano*¹, P.D. Faghi¹, T. Huedo-Medina¹, M. Cherniack²

¹Department of Allied Health Sciences, University of Connecticut, Storrs, CT;

²Ergonomics Technology Center, University of Connecticut Health Center, Farmington, CT.

Many factors influence bodyweight, however the literature is dominated by studies focusing on one or a small number of factors. Theory-based, multivariate models of bodyweight predictors are of great interest, particularly in populations with high rates of overweight/obesity such as correctional employees.

The current study proposes and tests one multivariate model, the Emotions, Behavior, Weight (EBW) model, which examines the relationships between emotions, stress, health behaviors, and body mass index (BMI) in correctional employees (n=317).

Height, weight, and body mass index (BMI) were directly measured. Emotional characteristics (overall feelings and depression) and health behaviors (diet and exercise quality) were self-reported on a standardized and validated questionnaire. Structural equation modeling (SEM) with MPlus software was used to create latent variables and test structural models for mediation effects. Four variable combinations were tested.

The hypothesized EBW model was supported with adequate model fit indices and statistically significant indirect effects for all 4 combinations (p=0.0134, 0.005, 0.023, 0.029). Emotions indirectly affected BMI via health behaviors, with those reporting more adverse emotional characteristics (higher depression and poorer feelings) exhibiting poorer health behaviors (less physical activity and poor diet), which in turn resulted in higher BMI. Stress explained variation in BMI above and beyond the basic model, with higher reported stress resulting in higher BMI (p=0.0134, 0.0013, 0.0573, 0.0836).

The theorized EBW was supported, explaining that emotions and stress are contributors to health behaviors and bodyweight. Health professionals should be educated on the links between emotions and health behaviors. Interventions should consider reducing stress and adverse emotions in order to be maximally effective, as focusing on health behavior change alone may set individuals up for failure. It is plausible that the EBW model could be applied to other data sets that utilize different variables to represent emotions and health behaviors.

Impact of a Mediterranean-Style Diet on serum fatty acids and bone turnover markers in postmenopausal women

A. Garrett¹, J. Kerstetter¹, J. Bihuniak¹, T. Huedo-Medina¹, A. Kenny²

Department of Allied Health Sciences, University of Connecticut, Storrs, CT¹; Center on Aging, University of Connecticut Health Center, Farmington, CT².

Osteoporosis is a serious public health concern for the aging population. Preliminary evidence suggests a beneficial role of a Mediterranean-Style Diet (MedSD) in bone health, however the literature is lacking in postmenopausal women.

The objectives of this study were 1) to determine if postmenopausal women following a typical American diet could incorporate and adhere to a MedSD, and 2) to assess the impact of adherence to a MedSD on markers of bone resorption and bone formation.

Sixteen postmenopausal women enrolled in this longitudinal clinical intervention trial. Subjects followed their typical, American diet for 12 weeks, and then were educated on how to follow a MedSD for 12 weeks. During the MedSD phase, each subject was provided with 1.5 ounces walnuts daily, 3 tablespoons extra-virgin olive oil daily, and 3-5 servings salmon and/or tuna weekly. Mediterranean Diet Score (MDS) assessment forms and 3-day food records were collected at 12-week intervals to assess dietary changes, and fasting blood was drawn every 6 weeks to monitor changes in serum fatty acids. N-terminal type 1 procollagen peptide (P1NP) and C-telopeptides of type I collagen (CTX) were used to measure bone formation and resorption, respectively.

MDS significantly increased from baseline to intervention ($p < .001$) periods, suggesting subjects were compliant with the MedSD. Neither P1NP nor CTX changed significantly. Serum palmitic acid (PA) and serum myristic acid (MA) decreased significantly ($p = .001$; $p = .001$), and were positively correlated with P1NP ($r_s = .511$, $p = .0002$; $r_s = .385$, $p = .007$) and CTX ($r_s = .368$, $p = .0002$; $r_s = .329$, $p = .022$). Serum alpha-linolenic acid (ALA) increased significantly ($p = .006$) and was negatively correlated with P1NP ($r = -.381$, $p = .008$) and CTX ($r = -.324$, $p = .024$). Regression analysis revealed that P1NP was significantly predicted by changes in MA ($p = .005$) and ALA ($p = .03$), but not by change in PA. CTX was significantly predicted by change in MA ($p = .0003$) but not by changes in ALA or PA.

Subjects successfully adhered to a MedSD, and the relationships observed between dietary changes, serum fatty acid changes and correlations in bone turnover markers suggest that there may be a beneficial role of MedSD in bone health.

A Measure of Dietary Quality Generated from a Food Liking Survey Links Bitter Phenotype to Adiposity

Mastaneh Sharafi¹, Shristi Rawal¹, Valerie B Duffy¹

¹ University of Connecticut/Allied Health Sciences, Storrs, CT, United States

Excessive adiposity results from over consuming energy dense foods and under consuming nutrient-rich/lower energy foods. Most taste-diet-adiposity research has examined single food groups (eg, fats, vegetables), not overall dietary quality. The USDA forms a dietary quality index from food records or frequency surveys based on the Dietary Guidelines (DG). We have shown that food liking surveys rapidly assess dietary intake to explain variability in health measures. Here, we formed a dietary quality index from our liking survey to test relationships between bitter phenotype and adiposity in 46 adults (mean age=27, range 18-62 y). Liking survey scores on food groups (sweet, fruit/vegetable, fat, salty, protein) and variety were weighted following DG and previous latent variable analysis, and averaged into a Healthy Eating Preference Index (HEPI). Phenotype was measured with the NHANES protocol (anterior tongue quinine bitterness) and propylthiouracil (PROP) bitterness. From measured weight/height, 17 adults were overweight/obese. Using statistical modeling and added variables (age, gender, eating behaviors, ear infections), separate Structural Equation Models showed that those tasting less bitterness from quinine or PROP had lower HEPI scores (ie, lower dietary quality), and lower HEPI, in turn, associated with higher BMI. Since quinine bitterness also had direct association with BMI, a mediation analysis was conducted for the quinine model. The HEPI fully mediated the effect of quinine bitterness on BMI. In summary, these results suggest that dietary quality may explain associations between taste phenotype and adiposity and that quinine is a good bitter phenotype for nutrition and health studies. Additionally, a simple food liking survey continues to show relevance for connecting taste with health.

Probiotic supernatants decrease cholera toxin production, motility and adhesion of *Vibrio cholerae* *in vitro* and down regulate the expression of virulent genes.

Varun Bhattaram, and Kumar Venkitanarayanan
Department of Animal Science, University of Connecticut, Storrs, CT, 06269

Background:

Vibrio cholerae (VC) is a significant pathogen responsible for causing a toxin-mediated profuse diarrhea in humans. The pathogenesis of VC is initiated by its adhesion to the intestinal epithelial cells, followed by the production of cholera toxin (CT). Additionally motility produced by the bacterium are critical in facilitating the infection in hosts. Therefore, attenuating these factors could potentially control cholera in humans.

Objectives:

This study investigated the efficacy of sub-inhibitory concentrations (SICs, concentrations not inhibiting bacterial growth) of probiotic supernatants of *Bifidobacterium bifidum*, *Lactobacillus plantarum*, *Lactobacillus reuteri* and *Lactococcus lactis* in reducing VC adhesion to intestinal epithelial cells, CT production and motility. Further, the effect of these supernatants on VC virulence gene expression was studied. The experiment was replicated with duplicate samples of treatment and control.

Methodology:

The supernatant of VC cultures (ATCC 11623, BAA-25870, BAA-2163) grown in the presence or absence of SICs (12.5 %) of probiotic supernatants at 37°C was collected at 0 and 24 h, and CT was quantified. Additionally, effect of probiotic supernatants on VC motility was determined. The effect of probiotic supernatants on VC adhesion to Caco2 intestinal epithelial cells was also studied. Further, the effect of probiotic supernatants on VC virulence genes [*ctxB* (toxin production), *fliA* (motility) and *tcpA* (adhesion)] was determined by real-time qPCR.

Conclusion:

The probiotic supernatants significantly reduced VC adhesion to intestinal epithelial cells, toxin production and motility in all 3 VC strains ($P < 0.05$). The reduction in VC adhesion to intestinal cells was ~ 3 log CFU/ml, whereas Cholera toxin production and motility were reduced by ~ 90% in treated VC, compared to untreated control. Probiotic supernatants also down-regulated VC virulence genes, *ctxB*, *fliA* and *tcpA* compared to controls ($P < 0.05$). Results justify follow up *in vivo* studies to confirm the inhibitory effect of aforementioned probiotic supernatants on VC virulence.

Efficacy of Octenidine Hydrochloride in Reducing Hyper-virulent *Clostridium difficile* Spores on Stainless Steel Surface

Genevieve Flock, Shankumar Mooyottu and Kumar Venkitanarayanan
Department of Animal Science, University of Connecticut, Storrs, CT, 06269

Clostridium difficile (CD) is a spore forming nosocomial pathogen which causes a serious toxin-mediated enteric infection in humans. The spores of CD can survive on surfaces for several months, and act as a source of new and recurrent infections by feco-oral route. High concentrations of chlorine are sporicidal against CD; however, these concentrations can be corrosive to most surfaces and handlers. Octenidine hydrochloride (OH) is a positively charged bispyridinamine that exhibits antimicrobial activity against a variety of bacteria. This study investigated the sporicidal efficacy of OH against CD spores on stainless steel surface.

Two hypervirulent, CD isolates (ATCC BAA 1870 and BAA1805) were used for the study. The CD isolates were separately grown in brain heart infusion agar for 10 days at 37°C in an anaerobic chamber in the presence of 80% N₂, 10% CO₂ and 10% H₂. Spores were harvested and purified using standard protocols. Suspensions containing 10⁶ spores per 100 µl were inoculated on stainless steel coupons (16 mm diameter). The coupons were air-dried for 1 h, and were treated with 0, 1, 3 and 5% of OH in 62% ethanol for 10 min. Untreated control (0% OH) and ethanol control were also included. Following incubation, the coupons were transferred into tubes containing 5 ml PBS and glass beads, vortexed and sonicated for 2 min each to remove viable, attached spores from the coupon surface. Serial-dilutions were made and one ml of the dilutions was pour-plated in duplicates on BHI agar with 0.1% sodium taurocholate (BHIS). Additionally, the coupons were transferred onto BHIS plates to determine the residual viable spores surviving on the coupons. The plates were incubated under anaerobic conditions for 48 h, and germinated colonies were counted.

Octenidine hydrochloride was significantly effective in killing CD spores on steel coupons ($P < 0.05$). In both CD strains, 1% OH reduced spores by 1 log CFU/ml, where as 3 and 5% OH decreased the spores by ~ 3 log CFU/ml compared to controls. Moreover, no residual spores were found on OH-treated coupons after washing, whereas a substantial amount of residual spores were present on control coupons. The results suggest that OH could be used as a sanitizer to reduce CD spores on stainless steel surfaces, and potentially control nosocomial infections of the pathogen.

Plant-derived compounds, *trans*-cinnamaldehyde and eugenol, reduce adhesion and invasion of *Staphylococcus aureus* in bovine mammary epithelial cells *in vitro*.

Devi Jaganathan *, Anup Kollanoor-Johny *, Kumar Venkitanarayanan *, Gary W. Kazmer *,
Yu-Bo Wang#, Lynn Kuo#, and Kristen E. Govoni *

*Department of Animal Science #Department of Statistics.

Staphylococcus aureus is one of the major bacterial pathogens involved in ruminant mastitis globally. We hypothesized that two plant-derived antimicrobials, *trans*-cinnamaldehyde (TC) and eugenol (EG), would reduce *S.aureus* adhesion to and invasion of primary bovine MEC *in vitro*. Confluent MEC monolayers were inoculated with four *S.aureus* strains (Strain DST 35, Thorn 17, 15, and M9175) at mid log phase separately (multiplicity of infection – 100:1) either in the presence or absence (control) of sub-inhibitory concentrations (SICs: greatest concentration that did not inhibit bacterial growth) of TC (0.006%) and EG (0.03%), and incubated for 2 h for bacterial adhesion. Infected cells were treated with gentamicin (100 µg/mL) for 1 h at 37°C for enumerating invaded bacteria. All experiments included duplicate samples and were repeated three times. Data were analyzed using PROC ANOVA and significance determined at $P < 0.05$. For strain Thorn 17, pre-exposure of *S.aureus* (5 h) and MEC (12 h) to EG reduced *S.aureus* adhesion to and invasion of MEC by $\sim 1.6 \pm 0.01 \log_{10}$ CFU/mL (control = $6.67 \pm 0.01 \log_{10}$ CFU/mL; $P < 0.0001$) and $2.8 \pm 0.11 \log_{10}$ CFU/mL (control = $3.9 \pm 0.02 \log_{10}$ CFU/mL; $P < 0.0001$), respectively. Pre-exposure of *S.aureus* and MEC to TC also had significant effect in reducing *S.aureus* adhesion to and invasion of MEC *in vitro*. Similar results were observed with strains DST 35, M9175 and Thorn 15. In conclusion, SICs of TC and EG reduced *S.aureus* adhesion to and invasion of MEC. *In vivo* studies using a mammalian model to validate these results are warranted.

Effect of sub-inhibitory concentrations of selenium on enterohemorrhagic *Escherichia coli* O157: H7 verotoxin production, cytotoxicity and Gb3 receptor expression

Meera Surendran Nair and Kumar Venkitanarayanan*

Department of Animal Science, University of Connecticut, Storrs, CT

*Corresponding author

Escherichia coli O157:H7 (EHEC) is a major foodborne pathogen that causes hemorrhagic diarrhea and kidney failure in humans. The pathophysiology of EHEC infection in humans is primarily mediated by verotoxins which bind to globotriaosylceramide (Gb3) receptor in host cells. Antibiotics are contraindicated for treating EHEC infection since it leads to bacterial lysis and toxin release. Thus, there is a need for alternate strategies for controlling EHEC infections in humans.

This study investigated the efficacy of sub-inhibitory concentrations (SICs, concentrations not inhibiting bacterial growth) of selenium, a dietary essential mineral, in reducing EHEC verotoxin production, cytotoxicity and toxin gene expression. Additionally, the effect of selenium on Gb3 receptor expression and Gb3 synthesis genes was investigated.

Three strains of EHEC (ATCC 43895, E163, and E137) were separately cultured with or without the SICs of selenium (29 mM and 41 mM) at 37°C for 24 h. The total verotoxin concentration in the culture medium was determined by ELISA. The efficacy of selenium in reducing EHEC-induced Vero cell (African green monkey kidney cells) toxicity was investigated using standard cell culture assay. The effect of selenium on Gb3 receptor production and Gb3 synthesis gene expression was analyzed on human lymphoma cells by flow cytometry and real-time quantitative PCR analysis (RT-qPCR), respectively.

Selenium reduced verotoxin production by 40–60% in all the three EHEC strains compared to untreated control ($P < 0.05$). Selenium also inhibited toxin-mediated Vero cell cytotoxicity, and down-regulated the expression of verotoxin and Gb3 synthesis genes by at least two folds ($P < 0.05$). In addition, specific mean fluorescence data from flow cytometric analysis revealed that the SICs of Se reduced the expression of Gb3 receptor significantly ($P < 0.05$) in lymphoma cells compared to the control. Results justify follow up *in vivo* studies for validating the efficacy of Se in controlling EHEC.

Effects of poor maternal nutrition on mesenchymal stem cell (MSC) activity and development of bone and adipose tissue and in offspring

S.M. Pillai¹, M.L. Hoffman¹, K.N. Peck¹, E.V. Valley¹, T.D. Crenshaw², S.A. Zinn¹, and K.E. Govoni¹

¹Department of Animal Science, University of Connecticut, Storrs, CT

²Department of Animal Science, University of Wisconsin, Madison, WI

Poor maternal nutrition may alter bone and adipose development in offspring by affecting MSC function. To determine if poor maternal nutrition during gestation affects bone and adipose development and function of MSC, offspring of ewes fed 100%(CON), 60%(RES) or 140%(OVER) of requirements (NRC, 1985) beginning at d 31 ± 1.3 of gestation were euthanized within 24 h of birth (d 1; n = 18) or at 3 mo of age (n = 15). At necropsy, bones were collected for MSC culture and mineral analysis, and backfat thickness and BW were measured. Proliferation of MSC was determined by bromodeoxyuridine assay. Gene expression was quantified using real-time RT-PCR. Data were analyzed using PROC MIXED in SAS. As previously reported, BW were 13% greater in OVER than CON at 1 d and 3 mo ($P \leq 0.05$). No effects of maternal diet ($P > 0.2$) were detected for bone parameters at d 1 or at 3 mo. Backfat thickness was reduced 50% in RES compared with CON at 3 mo ($P = 0.01$) but no difference in OVER. Compared with CON, MSC proliferation was reduced 51% and 58% in RES ($P = 0.07$) and OVER ($P = 0.03$), respectively in the presence of serum and reduced 27% and 44% in RES ($P = 0.11$) and OVER ($P = 0.05$), respectively without serum. *P2Y purinoceptor 14* was reduced 1.7 ± 0.1 fold in OVER ($P = 0.09$) and *P2Y purinoceptor 1* was reduced 1.7 ± 0.1 fold in OVER ($P = 0.09$) vs. CON, whereas *C/EBP β* , *Msh homeobox 1*, *Protein delta homolog 1*, *P2Y purinoceptor 2* were not affected by maternal diet ($P > 0.3$). In conclusion, poor maternal nutrition reduces the proliferation of MSC in offspring which may contribute to altered bone and adipose tissue development.

Effect of carvacrol and trans-cinnamaldehyde on *Aspergillus flavus* and *Aspergillus parasiticus* growth and aflatoxin production in poultry feed

Hsinbai Yin, Michael J. Darre, and Kumar Venkitanarayanan*

Department of Animal Science, 3636 Horsebarn Hill Rd Ext., Unit 4040, University of Connecticut, Storrs, Connecticut, CT 06269, USA

* Author to whom correspondence should be addressed.

Aflatoxins are toxic and hepato-carcinogenic metabolites primarily produced by molds, *Aspergillus flavus* and *Aspergillus parasiticus*. Contamination of poultry feed with aflatoxins is a major concern to the poultry industry due to significant economic losses originating from poor performance, reduced egg production and impaired egg hatchability. Aflatoxins concentrations in poultry feed are strictly regulated by the U.S. Food and Drug Administration due to their potential accumulation as residues in meat and egg. This study investigated the efficacy of two generally regarded as safe, plant-derived compounds, namely carvacrol (CR) and trans-cinnamaldehyde (TC), in reducing *A. flavus* and *A. parasiticus* growth, and aflatoxin production in chicken feed. Two hundred gram portions of chicken feed supplemented with CR or TC (0%, 0.4%, 0.8%, and 1.0%) were inoculated with *A. flavus* (NRRL 3357) or *A. parasiticus* (NRRL 2999 or NRRL 4123) and stored at 25°C for 3 months. The mold population and aflatoxins concentrations in the feed were determined at 0, 1, 2, 3, 4, 8, and 12 weeks of storage. Moreover, the effect of subinhibitory concentrations (compound concentrations not inhibiting the growth of mold) of CR (0.02%) and TC (0.005%) on the expression of *A. flavus* and *A. parasiticus* genes critical for aflatoxin production (*aflC*, *nor1*, *norA*, and *ver1*) was determined using real-time quantitative PCR. All experiments had duplicated samples and were replicated three times. Carvacrol and TC (0.8 and 1.0%) inhibited *A. flavus* and *A. parasiticus* growth ($P < 0.05$), and reduced aflatoxin concentrations in feed by at least 50% in comparison to control ($P < 0.05$). Moreover, CR and TC down-regulated the expression of all aflatoxin synthesis genes in *A. flavus* and *A. parasiticus* ($P < 0.05$). The results suggest that CR and TC could potentially be used as natural feed additives to control mold growth and aflatoxin contaminations in poultry feed.

Key words: Feed additives, poultry feed, aflatoxin, carvacrol and trans-cinnamaldehyde

**Department of Nutritional Sciences
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Degradation of chromatin modifiers, histone deacetylases, by *Spirulina platensis* extracts

Tho X. Pham, Jiyoung Lee

Department of Nutritional Sciences, University of Connecticut, Storrs, CT 06269

The effects of dietary components to modulate chromatin modifiers, such as histone deacetylases (HDACs), to control gene transcription remains relatively unexplored. We previously demonstrated that the organic extract of *Spirulina platensis* (SPE) potently inhibited inflammatory gene expression and cytokine secretion. Here we show that SPE facilitates the degradation of HDACs in RAW 264.7 macrophages. The degradation of HDACs by SPE differentially affects HDAC isoforms and occurs in a time and dose-dependent manner. More specifically, HDAC4 was both more labile and sensitive to SPE when compared to HDAC2. The enhanced degradation of HDACs by SPE was not unique to RAW 264.7 macrophages, but also occurred in bone marrow-derived macrophages, 3T3-L1 preadipocytes, Caco-2 enterocytes, HepG2 hepatocytes, and LX-2 hepatic stellate cells. Inhibition of the proteasome, autophagy, or calpain proteases with MG132 (10 μ M), chloroquine (50 μ M), or calpeptin (10 μ g/mL), respectively, revealed that SPE enhances the degradation of HDAC4 through these pathways. In contrast, the degradation of HDAC2 was not inhibited by inhibition of the protein degradation pathways, suggesting an alternative degradative pathway. These results demonstrate that SPE can regulate the protein levels of HDACs and therefore might potentially possess an epigenetic mode of action.

Level of Cytoplasmic Thioredoxin Reductase 1 in Prostate Tissue is Associated with Prostate Cancer Gleason Score, Total Antioxidant Capacity and Erythrocyte Glutathione Peroxidase Activity

Terrence M. Vance¹, Gissou Azabdaftari², Elena A. Pop², Sang Gil Lee¹, L. Joseph Su,³
Elizabeth T. H. Fonham⁴, Jeannette T. Bensen⁵, James L. Mohler², Ming-Hui Chen¹, Sung I.
Koo¹, Ock K. Chun¹

¹ University of Connecticut, Storrs, CT; ² Roswell Park Cancer Institute, Buffalo, NY; ³ National Cancer Institute, Bethesda, MD; ⁴ Louisiana State University, New Orleans, LA; ⁵ University of North Carolina, Chapel Hill, NC

Thioredoxin reductase 1 (TrxR1) is a member of the thioredoxin system, and a ubiquitous protein disulfide reductase involved in various intracellular inflammatory and oxidative processes. This study was conducted to determine the association between prostate tissue expression of TrxR1 levels and prostate cancer (PCa) Gleason score, dietary total antioxidant capacity (TAC), and erythrocyte glutathione peroxidase (GPx) activity using data from PCaP, a study of incident PCa among African and Caucasian Americans. Cytoplasmic and nuclear TrxR1 levels were measured using immunohistochemical staining of PCa on diagnostic biopsy sections from 55 men and visually scored in a blinded fashion by a pathologist (slides scored 0 to 3, with larger numbers indicating greater intensity of staining). Associations between PCa Gleason score and cytoplasmic TrxR1 levels of benign and malignant cells, and the difference in TrxR1 level between benign and malignant cells (Δ TrxR1), were determined using Fisher's Exact test, $\alpha=0.05$. TrxR1 was associated with dietary TAC ($p<0.05$) in benign cells and GPx ($p<0.05$) in malignant cells; Δ TrxR1 was found positively associated with Gleason score ($p<0.05$). These results warrant additional research on oxidative stress and prostate carcinogenesis.

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Exploring the influence of paternal feeding practices and style on child eating behavior

*R.L. Vollmer*¹, K. Adamsons², J.S Smith¹, A.R. Mobley¹

¹Department of Nutritional Sciences, ²Department of Human Development and Family Studies, University of Connecticut, Storrs, CT

The association of parental feeding practices and styles with childhood obesity have gained more attention in the literature recently; however, fathers are rarely included within these studies. The aims of this research were to identify the relationship of paternal feeding practices and feeding style to their preschool children's eating style, diet quality, and weight status. This study included a one-time, one-on-one interview with biological fathers of preschoolers (n=150) to assess feeding practices (Child Feeding Questionnaire), feeding style (Caregiver Feeding Style Questionnaire), child eating behaviors (Child Eating Behavior Questionnaire), and diet quality (24 hour recall, Healthy Eating Index). Height and weight for each father and child were also measured and Body Mass Index (BMI) or BMI z-score calculated. Linear regression was used to test the relationship between paternal feeding practices, style and child diet quality and/or body weight.

Overall, the findings revealed that a father's feeding practices and style does not directly predict a child's diet quality or weight status. However, child eating behaviors are associated with child BMI z-score and these relationships are moderated by paternal feeding practices. For example, child satiety responsiveness is inversely ($\beta = -.421$, $p = 0.031$) associated with child BMI z-score, only if paternal restriction scores are high. This relationship is not significant when paternal restriction scores are low ($\beta = -.200$, $p = 0.448$). These results suggest that some child appetitive traits may predict child weight status when exposed to certain paternal feeding practices. Future studies should consider the inclusion of fathers as their feeding practices and/or style may influence a child's eating behavior.

**Department of Plant Science and Landscape Architecture
2014 Graduate Student Research Forum
Oral Presentation Abstracts**

A Novel gene RED1 plays a vital role in maturation of Arabidopsis seeds

Qian Du

Department of Plant Science and Landscape Architecture
University of Connecticut, Storrs

In higher plants, the seeds development is comprised of two stages: embryogenesis and maturation. The term embryogenesis is the process of transformation from a single cell to a multicellular entity which is a functionally specialized organization. During the maturation stage, the embryo and seed lose water and begin to accumulate oil, carbohydrates, proteins and other storage compounds. In *Arabidopsis thaliana*, there are many well-studied important transcription factors control the process of seed development, especially in seed maturation. According to previous studies, four major transcription factors (ABSCISIC ACID INSENSITIVE3[ABI3], FUSCA3[FUS3], LEAFY COTYLEDON1[LEC1] and LEC2 play key roles in accumulation of storage compounds, cotyledon identity, acquisition of desiccation tolerance and dormancy. These four regulators form a local and redundant network to regulate their sustained expression levels in embryo. Here we report the characterization of a novel gene named RED1, which encodes a plant specific protein and is localized in nucleus. The mutation of this gene causes retarded embryo development (RED) and seed abortion, which can block the embryogenesis in late heart stage or bent-cotyledon stage. Overexpression of RED1 gene in *Arabidopsis* wild type results in increased expression levels of the four master regulators and elevated oil content in mature seeds. These results suggest that RED1 gene may function upstream of the four regulators and play a vital role in late stage of embryogenesis and seed maturation.

Landscape Level Patterns of Genetic diversity in Coastal and Roadside Switchgrass (*Panicum virgatum*)

G. Ecker and C. Auer

Department of Plant Science and Landscape Architecture
University of Connecticut, Storrs

Switchgrass (*Panicum virgatum* L.) is a native perennial grass with potential as a bioenergy crop. It is an adaptable species that can be found in diverse habitat types in the Eastern US including coastal zones, disturbed sites and roadsides. In recent years, breeding programs and genetic engineering (GE) have created switchgrass with novel traits and these genotypes should be evaluated through ecological risk assessment. Potential hazards include changes in plant communities, ecosystem services and non-target organisms. Potential exposure pathways include pollen mediated gene flow, seeds and rhizomes. Our research focuses on characterizing switchgrass distribution, genetics, and gene flow in the Northeastern US. Microsatellite (SSR) markers were used to infer the genetic relationships between switchgrass cultivars and wild plants collected in coastal and inland ecoregions in the Northeastern US. Habitats included major highways, secondary roads, disturbed sites and natural coastal zones. Molecular analysis revealed three main genetic assignments for the plants: two putatively native lowland tetraploid genotypes and an introduced upland octoploid genotype derived from the Ohio River Valley and the Central Appalachian Mountains. Plants collected from inland roadsides were identified as 5% native, 86 % cultivar, and 8% mixed. Plants from the coastal ecoregion (natural and disturbed areas) were 69% native, 14% cultivar and 7% mixed. Our findings suggest that native and feral populations of switchgrass exist in both inland and coastal habitats in Southern New England. These populations could serve to facilitate transgene escape should GE cultivars be release either as field trials or commercial plantings in this region. This project was supported by the Biotechnology Risk Assessment Program Competitive Grants no. 2008- 39211-19566 and no. 2011-02189 from the USDA National Institute of Food and Agriculture to Carol Auer and Thomas Meyer. Funding was also provided by the Storrs Agricultural Experiment Station and the University of Connecticut.

Effect of pruning heights on growth and visual appeal of under-utilized native shrubs

Pragati Shrestha and Jessica D. Lubell
Department of Plant Science and Landscape Architecture
University of Connecticut, Storrs

The utilization of native plants for landscaping is increasing due to restrictions on invasive ornamentals and interest in sustainable landscaping. Nursery growers must expand their native product offerings to meet increasing demand from the consumers. A good nursery system doesn't just require best growing conditions but also a correct pruning. Pruning reduces apical dominance and promotes side branches growth resulting on a fuller and more appealing plant. Therefore, the objective of this study was to evaluate the growth and visual appearance of three different native species in response to different pruning heights. For this, *Cornus rugosa* plants were subjected to three different pruning heights: 25 cm, 50 cm (from the base of the plant) and control with no pruning. They were evaluated for their growth habit and visual appeal. Control had significantly taller plants in comparison to both pruning heights at $\alpha=0.05$. 50 cm pruned plants were significantly denser and wider with more number of shoots in comparison to control at $\alpha=0.05$. Similar study was conducted with *Viburnum acerifolium* and *Viburnum cassinoides* with two pruning heights: 14 cm (from the base of the plant) and control with no pruning. With *V. acerifolium*, control plants were significantly taller at $\alpha=0.05$. With all the three native shrubs, pruned plants were visually more appealing as compared to control at $\alpha=0.05$.

Evaluation of short-growth mutants of perennial ryegrass for their shade tolerance

Wei Li, Chandra Thammina, Junmei Chen, Hao Yu, Huseyin Yer, Kaishuang Cao, John Inguagiato, Yi Li.

Department of Plant Science and Landscape Architecture
University of Connecticut, Storrs

Shade tolerance is an important trait for perennial ryegrass (PRG; *Lolium perenne* L.). Under shade environment, typical symptoms of PRG include thin, narrow and elongated leaf blades, reduced leaf appearance and tiller number, poor wearing ability, and weak root system. We have used mutagenesis techniques to breed short-growth (dwarf) mutant PRG varieties. A number of M2 generation plant lines were selected based on height, tiller number and leaf width. One line, named EMS18, displayed lower leaf extension rate (shorter leaf blade), better leaf appearance (greener color) and longer root when compared to the wild-type controls under greenhouse conditions. FN4, another line, also showed reduced elongation in leaf blade and internodes length when grown in the field.

We have further evaluated their responses to shade under field conditions. EMS18 and FN4 were planted in woods and mowed at a height of 3 inches regularly. After 1.5 months of totally shaded (no direct sunlight) environments, these two mutant lines were green in color and healthy in general, while the wild-type controls became yellow and some leaves were dying. The root systems, particularly the root lengths of both EMS18 and FN4, were similar to that of the wild-type controls. After two months, the wild-type controls totally died but EMS18 survived and appeared to be healthy.

**Department of Pathobiology and Veterinary Science
2014 Graduate Student Research Forum
Research Presentations Abstracts**

Development of replication-repressible vaccinia virus vectors for vaccines and therapeutics

Allison Titong and Paulo H. Verardi

Department of Pathobiology and Veterinary Science, College of Agriculture and Natural Resources, University of Connecticut, Storrs, CT 06269, USA

Vaccinia virus (VACV) was used to successfully eradicate smallpox and has now been developed into powerful vaccine, immunotherapeutic, and oncolytic vectors. Like any viral vector, VACV can cause adverse reactions that result from uncontrolled viral replication. To increase the clinical potential of VACV vectors, we designed a tetracycline-based safety mechanism. In this system, elements from the *tetracycline (tet)* operon and a reverse TetR mutant (revTetR) control the expression of a gene that is essential for virus replication (A6L or D6R). In contrast to the natural TetR, mutant revTetR bind operators with high affinity only in the presence of tetracyclines. To test if a revTetR-based system would function in VACV, we developed a tetracycline-repressible gene expression system in VACV by placing the promoter of a reporter gene (EGFP) under the control of a *tet* operator sequence and constitutively expressing six different reverse mutant *tetR (revtetR)* genes. In the presence of doxycycline, EGFP expression was effectively repressed in cells infected with the recombinant VACVs, albeit at various levels depending on the *revtetR* gene and doxycycline concentration. EGFP expression was repressed even when doxycycline was added at several time points post-infection. We next generated replication-repressible VACVs using multiple *revtetR* genes to control the expression of essential genes A6L or D6R. In the absence of tetracyclines, these VACVs formed plaques in cell culture that were indistinguishable from wild-type VACV plaques. As expected, in the presence of doxycycline, only abortively-infected cells were detected. These replication-repressible VACVs should replicate at wild-type levels after administration and be effective vaccine and therapeutic vectors. More importantly, treatment of complications would be as simple as antibiotic therapy, since it would prevent A6L or D6R gene expression and stop further viral replication.

**The Immunotoxic Effects of Brominated Flame Retardants in Beluga Whales
(*Delphinapterus leucas*) Upon *in Vitro* Exposure**

Erika Gebhard, Milton Levin, Sylvain De Guise

Department of Pathobiology and Veterinary Sciences, University of Connecticut, 61 North Eagleville Road, U-89, Storrs, Connecticut 06269

Brominated flame retardant (BFR) compounds are used in common household applications and have found their way in different ecosystems, resulting in marine mammal exposure. There is increasing concern that these chemicals may exert chronic, sub-lethal effects, such as immunotoxicity. This is especially important, as the immune system is an important interface between an individual's health and the pathogens present in its environment. Concentration-response experiments were performed to quantify changes in innate (phagocytosis) and adaptive (mitogen-induced lymphocyte proliferation) immune functions upon *in vitro* exposure of beluga whale (*Delphinapterus leucas*) peripheral blood leukocytes to two BFR compounds, tetrabromobisphenol A (TBBPA) and hexabromocyclododecane (HBCD). TBBPA significantly decreased neutrophil phagocytosis compared to unexposed control at 25 μM , but did not modulate monocyte phagocytosis. TBBPA did not modulate T or B-induced lymphocyte proliferation. HBCD significantly decreased neutrophil phagocytosis compared to unexposed control between 15 and 25 μM as well as monocyte phagocytosis at 20 and 25 μM . HBCD significantly increased suboptimal ConA-induced T lymphocyte proliferation as well as optimal LPS-induced B lymphocyte proliferation between 0.5 and 20 μM and between 1 and 10 μM , respectively. This is the first report demonstrating the toxic effects of two BFRs on beluga whale immune functions. Modulation of immune functions, whether stimulatory or suppressive, may increase an individual's risk to bacterial, virus, or parasite infection, which may result in increased morbidity or mortality. This research will help establish a relationship between chemicals present in beluga whales (including real-life exposure as determined by others) and early indicators of disease to signal or predict changes in health outcomes.

The Effect of Cyclophilin A on Vaccinia Virus Replication *in vitro*

Kathryn Korhonen, Edan Tulman, Paulo Verardi, David Wunschel, Xiaofen Liao, Debra Rood, Katie Pflaum, Kara Rogers, and Steven Geary

Previous research done in the Geary laboratory, in collaboration with Pacific Northwest National Laboratory, identified a host protein, cyclophilin A, which remains highly associated with vaccinia virus virions even after successive rounds of purification. To further characterize this association, *in vitro* and *in vivo* techniques are now being used to investigate the role of cyclophilin A in vaccinia virus replication and pathogenesis. We are currently breeding for cyclophilin A knockout (KO) mice to study the affect of cyclophilin A on vaccinia virus pathogenesis. Pathogenesis is being assessed *in vivo* by weight loss over the period of infection and by histological comparison of the tissue lesions between KO and control mice. The purpose of this project is to further investigate how cyclophilin A interacts with vaccinia virus *in vitro* using primary tissues that will be harvested from KO mice to determine the difference in viral growth kinetics. Altogether, this research addresses the necessity of cyclophilin A in vaccinia virus replication and adds to the significance of cyclophilin A in viral infections since previous research has shown that this protein is necessary for viral replication in other viruses, including *human immunodeficiency virus* and hepatitis C virus.