**Oral Presentation Session I, 9:00-10:00, room 277**

Harnessing γ-glutamyl peptides in atherosclerosis prevention through *Akkermansia* modulation

**Sedoten Ogun1,2**, Snigdha Guha1, Amanda Ramer-Tait1,2, Kaustav Majumder1,2

Affiliations: 1University of Nebraska-Lincoln, Lincoln, Nebraska USA; 2Nebraska Food for Health Center, Lincoln, Nebraska USA

Atherosclerosis is a leading cause of cardiovascular diseases marked by plaque buildup in the arteries. Previous studies demonstrated that γ-glutamyl valine (γ-EV), a bioactive peptide abundant in fermented foods, reduces aortic lipid deposition and inflammation in atherosclerosis-prone APOE-/- mice on a high-fat diet. Microbiome analysis via 16S rRNA bacterial gene sequencing and qPCR revealed that γ-EV treatment selectively enriched for *Akkermansia muciniphila,* a beneficial gut bacterium previously shown to limit chronic inflammation and protect against atherosclerosis. However, the mechanism by which γ-EV enhances *A. muciniphila* growth remains unclear. Therefore, we investigated whether γ-EV directly promotes *A. muciniphila* growth *in vitro* and if this effect extends to other dietary γ-glutamyl peptides (γ-GPs). *A. muciniphila* was cultured anaerobically in media with or without 10 mM γ-EV or other γ-GPs (γ-EA, γ-EE, γ-EF, γ-EG, γ-EH, γ-EY, γ-EQ, γ-EM, γ-EI, γ-EL, γ-EC, γ-ECG). *A. muciniphila* growth and pH were monitored over 16 hrs. Polar-charged, nonpolar and polar aromatic amino acid side chain peptides elicited subtle effects on *A. muciniphila* growth. However, nonpolar aliphatic, polar-uncharged and sulfur-containing peptides significantly enhanced *A. muciniphila* growth and induced significant pH reductions across multiple time points versus controls. Altogether, these findings suggest that *A. muciniphila* may utilize γ-GPs to support its growth, potentially explaining the observed *in vivo* increase in abundance of this bacterium following γ-EV treatment. Future research will aim to uncover the precise mechanisms through which γ-GPs promote *A. muciniphila* growth to inform future studies aimed at dietary modulation of the gut microbiota for improved health outcomes.

**Rediscovering ancestral maize: a study to trace the lost functional properties of maize during domestication**

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Breeders have performed selective breeding over the years to turn maize from its wild ancestor, teosinte, into its modern variety (*Zea mays*). Some health-beneficial compounds might be lost in the process. Here, we aim to understand the potential changes in the protein and metabolites in maize due to domestication by conducting a comparative study between 26 modern maize, 25 landraces, and 25 teosinte varieties. We looked at the protein content of all the ground undigested maize lines by the BCA kit assay. The average protein level in teosinte lines was three times higher than that of modern maize and landraces. Analyzing the primary metabolite profile of the undigested maize lines, we found that the relative levels of quinic acid, mucic acid, caffeic acid, and chlorogenic acid were high in teosinte, but sugars were more abundant in modern maize. The samples were processed using simulated gastrointestinal digestion to understand the impact of domestication on the digestibility of maize proteins. Post-digestion, there was no significant difference in the peptide quantity between the teosinte, landrace, and modern maize groups, as measured by the fluorescent peptide assay kit. A high peptide content for modern maize and landraces could be due to their better degree of hydrolysis (digestibility), determined by the OPA technique. While the average digestibility for modern maize and landraces was 72.37% and 42.09%, respectively, it was only 15.13% for teosinte. However, the results from the anti-oxidation activity assay, involving all the maize lines using gastrointestinal cells, show that teosinte lines have higher antioxidative activity, ranging from 9.1 – 31.6 %. The antioxidative properties in digested teosinte samples might be due to bioactive peptides, which shall be confirmed by investigating their peptide profiles. This unique work at deciphering the functional changes in maize can guide us in producing maize hybrids with enhanced protein quality.

**Combining *Gordonibacter urolithinfaciens* and *Lactobacillus taiwanensis* limits body weight gain and decreases fat mass in a mouse model of diet-induced obesity**

**David Gomez Quintero1**, Ashley M. Toney1, Kristin Beede1, Robert Schmaltz1, Jeffrey D. Price1,2, and Amanda E. Ramer-Tait1,2

Affiliations: 1Department of Food Science and Technology, University of Nebraska-Lincoln, Lincoln, Nebraska,

2Nebraska Food for Health Center, University of Nebraska-Lincoln, Lincoln, Nebraska

Multiple preclinical and clinical studies have shown that probiotic treatments can limit the development of obesity and improve glucose metabolism and insulin sensitivity. However, response rates can be variable. We have previously shown that daily supplementation with the putative probiotic *Gordonibacter urolithinfaciens* decreased fat tissue accumulation and lowered glucose and insulin levels in some, but not all, mice fed a high-fat diet. Here, we investigated the contribution of specific gut microbiome features in mediating the variable health effects of *G. urolithinfaciens*. We found that multiple species of *Lactobacillus* increased in abundance following *G. urolithinfaciens* treatment compared to controls, with *L. taiwanensis* abundance significantly negatively correlated with body weight gain and glucose levels. To test for a causal relationship between *G. urolithinfaciens* and *L. taiwanensis* in bringing about metabolic benefits, germ-free mice were colonized with a *Lactobacillus*-deficient microbiome and administered either *L. taiwanensis* only, *G. urolithinfaciens* only, or both species. After eleven weeks of high- fat diet feeding, mice administered *L. taiwanensis* and *G. urolithinfaciens* together gained less weight and were leaner compared to mice treated with *G. urolithinfaciens* alone; however, no mice experienced improvements in glucose or insulin levels. Together, these results demonstrate that *G. urolithinfaciens* can limit the development of obesity when *L. taiwanensis* is present. However, their combination is not sufficient to provide metabolic benefits, suggesting that other species of *Lactobacillus* may be necessary for such effects. These studies highlight the importance of considering the combination of microbe-microbe interactions when developing microbiome-based strategies for preventing and treating obesity-related diseases.

**Integrating Aronia Berries into Fermentation: Boosting Microbial Safety, Nutritional Value, and Consumer Appeal**

Juan Diego Villegas1

Affiliations: 1University of Nebraska-Lincoln, Lincoln, Nebraska USA

Aronia berries, noted for their high levels of polyphenols and anthocyanins, present a promising opportunity to enhance the nutritional profile and microbial safety of fermented products. Recent literature suggests that incorporating these berries into fermentation processes can improve the bioavailability of phytochemicals, promote the development of beneficial metabolites, and potentially mitigate microbial risks. This literature-based study examines current findings on the impact of adding aronia berries on fermentation outcomes, with a focus on aspects such as food safety, phytochemical content, and product quality.

Evidence suggests that the chemical composition of aronia berries, especially their antioxidant capacity, may enhance microbial stability and decrease pathogen presence in fermented foods. The interaction between bioactive compounds derived from aronia and beneficial microbes could lead to a diverse array of fermentation metabolites, improving flavor, color, and overall consumer acceptance. However, some studies highlight the necessity of optimizing aronia berry concentrations, fermentation parameters, and microbial strains to maximize health benefits while preserving taste, texture, and safety.

This oral presentation aims to synthesize existing research, highlighting trends and knowledge gaps. It will place significant emphasis on practical applications for food scientists looking to develop innovative fermented products with enhanced safety and consumer appeal. By demonstrating the potential of aronia-assisted fermentation, this work aims to show the importance of ongoing research into ingredient synergy and fermentation optimization. Ultimately, these findings provide valuable insights for researchers striving to advance the science and technology of fermented food production.

**Poster Presentation Session I, 10:15-11:15, Fourth Floor**

1. **Evaluation of skim mozzarella cheese for pizza**

Jacob Tassemeyer, Maggie Fisher, Ryker Eiler (FDST 132)

**3. Understanding the Influence of Food Matrix and Heat Treatment on Baked Milk and Egg Allergies in Allergic and Tolerant Individuals**

**Temitope Adeyemi1**,Philip Johnson1, Melanie Downs1

Affiliation: 1 Food Allergy Research and Resource Program, Department of Food Science and Technology, University of Nebraska-Lincoln, Lincoln, Nebraska, USA

Food allergies are immune-mediated reactions triggered by specific allergens, with IgE-mediated responses which lead to rapid-onset symptoms that affect multiple organ systems. Among major food allergens, milk and egg allergies are prevalent in children, with cow’s milk and egg allergy affecting about 2 % of young children in the United States. Baked milk and egg products are increasingly incorporated into oral immunotherapy and dietary management strategies due to their potential to induce tolerance while not provoking significant reaction. While milk and egg protein allergens in baked products are likely to be influenced by thermal processing and food matrix composition, these changes and how they relate to reactivity are poorly defined. In this study, we will use a bottom-up proteomics approach to identify milk and egg peptides in baked milk and egg products such as muffins to assess how different food matrices and thermal processing conditions impact milk and egg proteins in baked products. The findings from this study will enhance the understanding of how processing conditions, thermal treatment and food matrix could influence milk and egg allergies in allergenic and tolerant individuals. The knowledge from this study will contribute to improving risk assessment, refining food processing techniques, and optimizing dietary management strategies for individuals with milk and egg allergies.

5. Heavy Metal Tolerance in Pathogenic and Non-pathogenic Bacteria Associated with Meat Processing Environments

L. A. Dinithi S. De Silva1, Byron Chaves1

1Department of Food Science and Technology, University of Nebraska-Lincoln, Lincoln, Nebraska USA

Heavy metals present along the food chain can exert selective pressure on foodborne bacteria. This study estimated heavy metal tolerance of pathogenic and non-pathogenic bacteria commonly found in food processing environments. All strains were grown to 10⁵ CFU/mL and exposed to two-fold dilutions of Zn²⁺, Cu²⁺, and Cd²⁺ solutions ranging from 32 mM to 0.015625 mM, then incubated at 35 °C for 24 h with two replications. The Minimum Inhibitory Concentration (mM) for Zn, Cu, and Cd were as detailed next. *Citrobacter rodentium* ATCC 51459: 2.0, 1.0, 0.5; *Escherichia coli* ATCC 25922: 4.0, 4.0, 1.0; *Klebsiella aerogenes* ATCC 13048: 4.0, 4.0, 1.0; *Pseudomonas aeruginosa*ATCC 27853: 16.0, 8.0, 4.0; *Staphylococcus aureus* ATCC 25923: 0.5, 4.0, 0.5; *Salmonella* spp., including serovars Anatum, Braenderup, Enteritidis, Heidelberg, and Typhimurium: 4.0, 8.0, 0.5; *E. coli* O157:H7: 4.0, 4.0, 0.5; *E. coli* O26: 4.0, 4.0, 1.0; *E. coli* O91: 4.0, 4.0, 2; *E. coli* O121: 4.0, 4.0, 1.0; *Listeria monocytogenes* ATCC 19115: 4.0, 2.0, 0.25; *L. innocua* ATCC 33090: 4.0, 4.0, 0.5; *Lactococcus lactis*: 0.03125 mM for Zn; *Lactobacillus acidophilus*: 0.0625 mM for Zn and 0.03125 mM for Cu; and *Enterococcus faecium*: 8.0 mM for Zn and 4.0 mM for Cu. These results may have implications for microbial adaptation to environmental stresses and cross-tolerance to antibiotics, biocides, and other antimicrobial interventions, potentially affecting food safety and public health. Ongoing experiments are evaluating other phenotypic factors that may influence recovery and molecular detection of foodborne pathogens from environmental samples.

7. Risk Ranking of Antibiotic Resistance Genes and Their Impact on Human Health

**Jaber Ghorbani1**, Yanbin Yin1, Xu Li2, Jennifer Clarke1,3, Adina Howe4, Michelle Soupir4, Amy Schmidt5, Shannon Bartelt-Hunt2, Bing Wang1

Affiliations:1Department of Food Science and Technology, University of Nebraska-Lincoln, USA;2Department of Civil and Environmental Engineering, University of Nebraska-Lincoln, USA;3Department of Statistics, University of Nebraska at Lincoln, Lincoln, Nebraska, USA;4Department of Agricultural and Biosystems Engineering, Iowa State University, USA; 5Biological System Engineering, University of Nebraska at Lincoln, Lincoln, Nebraska, USA

The growing threat of antibiotic resistance highlights the need to prioritize antibiotic resistance genes (ARGs) for human health risk assessment, enabling targeted mitigation strategies. This study presents a semi-quantitative risk assessment framework integrating evidence-based methodologies and expert elicitation to generate risk scores for ARGs. Data were extracted from literature and public databases, and combined by logic aligning with principle of probability theory and algebraic operations. As a result, quantitative scores were assigned for each criterion for individual ARGs. Through the expert elicitation process, a multi-criteria decision analysis approach was used to determine the weight of each criterion, leading to a final risk score for each gene (scaled 0–1).A total of 3,027 genes were scored and ranked, spanning 73 gene families across 26 drug classes. Among them, *ant(3'')-IIa* and *aac(3)-VIa*, both conferring aminoglycoside resistance, had the highest risk scores (0.97). To validate this ARG ranking model, metagenomic datasets covering water samples from various sources were retrieved through a systematic search and analyzed based on both ARG abundances and risk scores. Results showed that the model assigned risk scores to at least 90% of ARGs reported in environmental water samples. Notably, 28.05% of genes in hospital wastewater had scores above 0.75, compared to wastewater (18.56%), seawater (5.37%), drinking water (4.97%), river (1.13%), and lake (0%). These findings highlight the model’s reliability, demonstrating a strong association between high-risk ARGs and the environments that likely harbor these genes. This study provides an advanced approach for assessing ARG risk in the absence of dose-response models.

**9. Development of Dietary Fiber Blends for Targeted Gut Microbiome Modulation in Obesity: An Update on Progress**

**Izuchukwu Iwuamadi**1,2, Carmen E. Pérez-Donado1,2, Lisa Whisenhunt2, Devin J. Rose1,2, Edward C. Deehan1,2

1Department of Food Science and Technology, 2Nebraska Food for Health Center

University of Nebraska, Lincoln, NE, USA

Dietary fibers are indigestible carbohydrates that modulate the gut microbiome by selectively enriching beneficial bacteria and promoting key short-chain fatty acids (SCFAs) such as propionate and butyrate. These metabolites regulate metabolism and attenuate inflammation, but their effects are SCFA-dependent. Additionally, SCFA production is fiber-structure-dependent, individualized, and influenced by gut microbiota functions. Combinations of discrete fiber structures may help overcome inter-individual variability, but it remains unclear which fibers consistently promote specific SCFAs and if blends could reduce inter-individual variance. To address this, we obtained fecal microbiota from 20 well-characterized adults with obesity (mean BMI: 34kg/m²). Using a subset of 12 participants, we observed substrate-specific effects on fermentation profiles across 12 discrete fiber structures. The fermentation of galactomannans, arabinoxylans, arabinogalactans, and resistant maltodextrins promoted propionate; while oat β-glucan, chicory inulin, and resistant starches (RS2) favored butyrate. Next, using all 20 participants, we compared the variance in SCFA production between a propiogenic (larch arabinogalactan, partially hydrolyzed guar galactomannan, and tapioca resistant maltodextrin) and butyrogenic (oat β-glucan, chicory inulin, and green banana RS2) blend to the single fibers. We observed no differences in the variability of butyrate outputs between the butyrogenic blend (CV:15.3%) and the three single fibers (CV:13.3-15.6%; *p*>0.1, Levene’s test). For propionate, we detected a difference in propionate variability between the propiogenic blend and larch arabinogalactan (CV: 15.9% vs 13.4%; *p*=0.004). Overall, these findings provide insight into the structure-dependent effect of fiber and individualized responses in SCFA production, which would help inform microbiome-based interventions for meta-inflammation in obesity.

Poster

11. The effect of water activity and fat content on the inactivation and recovery of *Listeria* spp. in dry-cured and dry-fermented ready-to-eat (RTE) meat products after high pressure processing (HPP): A review

**Yhuliana Nino Fuerte**1, Prashant Dahal2, Bing Wang1, Gary A. Sullivan3, and Mary-Grace C. Danao1,2

Affiliations: 1Department of Food Science and Technology, University of Nebraska-Lincoln, USA; 2The Food Processing Center, University of Nebraska-Lincoln, USA; 3Department of Animal Science, University of Nebraska-Lincoln, USA

High pressure processing (HPP) is an intervention approved by the USDA FSIS for controlling *Listeria monocytogenes* (Lm) in post-lethality exposed ready-to-eat (RTE) meat and poultry products. The effectiveness of HPP is affected by intrinsic factors of the food matrix, e.g., fat content and water activity (*aw)*. The PRISMA-ScR reporting guidelines and the Arksey and O’Malley framework were used to conduct a scoping review of the literature. An initial search yielded 986 studies on HPP for Listeria control in RTE meats, with 27 on dry-cured and dry-fermented products reporting *aw* and/or fat content selected for analysis. From these studies, data on microbial inactivation, recovery, and associated HPP and storage conditions were extracted and evaluated. The water activity of dry-cured and dry-fermented meats ranged from 0.784 to 0.983. As *aw* increased, microbial inactivation also increased with rising pressure. Fat levels ranged from 10% to 55.1%. Findings suggested that fat levels > 25% may exert a baroprotective effect, reducing the effectiveness of HPP treatment. Regarding recovery, *aw* > 0.9 was associated with increased microbial growth during storage. Likewise, fat content > 25% in dry-cured products promoted greater microbial recovery and growth post-HPP. Notably, the data indicated that dry-fermented products generally do not support Listeria growth over time, limiting recovery after HPP. This review emphasizes the role of *aw* and fat content in these products, as they greatly influence HPP effectiveness. Additionally, it highlights the importance of accounting for food matrix characteristics when selecting a post-lethality processing technology.

Presentation type: Poster presentation

**13. Protein potential of an emerging legume source: alfalfa seed**

 **Sayantini Paul1**, Kaustav Majumder1, Devin Rose 1, Mukti Singh2, Sean Liu2

Affiliations: 1Department of Food Science and Technology, University of Nebraska-Lincoln, Lincoln, NE, USA; 2Department of Functional Food Research, USDA, Peoria, IL, USA

The rising interest in sustainable protein has led to a demand for diverse protein options. Alfalfa (Medicago sativa L.), with a protein content of 36.5%, has typically been used as animal feed but holds potential as a food protein source. This study optimizes alfalfa protein concentrate (APC) extraction and characterization using alkaline extraction with varying NaCl concentrations and pH levels (2, 10, and 12) across 15 treatments. Alfalfa seeds were defatted using soxhlet extraction, removing 9.25%. Antinutritional factors were evaluated before and after defatting. Defatted flour showed reduced phytic acid levels, but trypsin inhibitors increased, while chymotrypsin inhibitor levels stayed unchanged. Three extraction conditions (0% NaCl at pH 2, 10, and 12) achieved the highest protein recovery (19.39%, 34.91%, and 39.73%) and purity (60.36%, 58.32%, and 57.35%). Defatted flour samples showed greater protein purity (69.76%, 67.84%, and 68.46%) than non-defatted ones. Additionally, APC extracted at 0% NaCl and pH 10 had the highest amino acid content (71 g/100 g) and met FAO essential amino acid requirements, indicating complete protein. Protein solubility, showed promising results for APC (0% NaCl at pH 10 and pH 12), indicating enhanced bio-functional properties. Alfalfa seeds and sprouts contain L-canavanine, a non-protein amino acid linked to autoimmune diseases like lupus. Mass spectrometry results showed < 1% L-canavanine in APC samples. Future studies will involve *in vitro* DIAAS (Digestible Indispensable Amino Acid Score) to evaluate protein digestibility and L-canavanine bioaccessibility. Further research on APC’s bio-functional properties will reinforce its potential as a sustainable protein for food applications.



Graphical overview

15. Title: Identification of abundant gluten target peptides resistant to fermentation for the development of an MS gluten detection method in fermented and hydrolyzed foods

Authors: **Sara Schlange1**, Joseph Baumert1, Melanie Downs1

1Food Allergy Research and Resource Program. Department of Food Science and Technology, University of Nebraska-Lincoln.

Current immunological methods are inadequate for the quantitative detection of gluten in fermented and hydrolyzed foods due to process-induced proteolysis. This creates an analytical deficit that implicates numerous stakeholders, including those with Celiac disease (CD), an immune-mediated enteropathy of the small intestine resulting from the consumption of gluten proteins found in wheat, rye, and barley. The objective was to identify abundant and persistent gluten peptides in a fermentation system for the development of a mass spectrometry (MS)-based detection method. Protein extracts from wheat flour and samples collected throughout production of a commercial fermentation-derived ingredient were digested separately by three proteases (trypsin, chymotrypsin, ProAlanase). Digests and <10 kDa fractions were analyzed by data-dependent acquisition (DDA) (Thermo Scientific™ Orbitrap Exploris™ 240 Mass Spectrometer). *Triticum aestivum* peptides were identified using Proteome Discoverer™ 3.0. Full, semi, and nonspecific cleavages were permitted, according to fraction type to account for fermentation-induced proteolysis.

DDA of the wheat flour calibrant yielded identification of 164 (trypsin), 108 (chymotrypsin), and 117 (ProAlanase) peptides from gluten proteins. The 50 most abundant were selected as candidate peptides for the intact gluten calibrant. For the fermentation-derived ingredient, 240, 100, 127, and 340 gluten peptides were identified in trypsin, chymotrypsin, ProAlanase, and undigested samples, respectively. A qualitative parallel-reaction monitoring (PRM) method was generated to confirm target presence. A product ion and peak area evaluation enabled selection of the best-performing precursors as promising targets. These criteria established 45 high-performing gluten target peptides, originating from gliadins, glutenins, and avenin-like proteins.

17. Comparative Analysis of Protein Structural Alterations in Egg White Powder and Whey Protein Concentrate Subjected to Thermal, Acidic, and Alkaline Treatments

**Zahra Shahbazi1, Curtis L. Weller2**

Affiliations: 1University of Nebraska-Lincoln, Lincoln, Nebraska, USA; 2University of Nebraska-Lincoln, Lincoln, Nebraska, USA

Egg White Powder (EWP) and Whey Protein Concentrate (WPC) are widely used in the food industry for their functional properties such as gelling, foaming, and emulsifying. Understanding the structural changes these proteins undergo under different processing conditions is essential for optimizing food formulations and enhancing product quality. This study examines the structural changes in Egg White Powder (EWP) and Whey Protein Concentrate (WPC) under various processing conditions using tricine and glycine gel electrophoresis. The protein alterations were analyzed after dry heat treatment at 60°C to 120°C and under aqueous acidic and alkaline conditions. For EWP, increasing temperatures led to a gradual reduction in higher molecular weight proteins, with significant degradation by 120°C as bands nearly vanished, indicating severe thermal hydrolysis. Aqueous treatments also caused considerable degradation, affecting allergenicity. WPC exhibited minimal changes at 60°C but showed clear signs of degradation at higher temperatures. By 120°C, there was a substantial breakdown, highlighted by the disappearance of specific protein bands. Acidic and alkaline conditions led to notable degradation, particularly at lower molecular weights, with increased fragmentation. Heating WPC in aqueous environments at 60°C and 75°C also resulted in progressive degradation, more pronounced at the higher temperature. These findings emphasize the impact of processing on protein structural integrity and allergenicity, crucial for developing safer and more stable food products. The insights gained are vital for enhancing the functional properties of food formulations and reducing allergenic risks.

19. *The gut microbiota modulates the severity of experimental autoimmune myocarditis.*

**Xu Shi**1, Paul Velander1, Robert Schmaltz1, Jeff Price1, Jennifer Auchtung1, Jay Reddy1, Amanda Ramer-Tait1

Affiliations: 1 University of Nebraska-Lincoln, Lincoln, Nebraska USA

Myocarditis is an inflammatory disease of the myocardium caused by infection-induced autoimmunity toward heart-specific antigens. Although the gut microbiota has been linked to cardiovascular disease, its role in the pathogenesis of myocarditis is unclear. We therefore investigated whether the gut microbiota modulates disease severity in a mouse model of Experimental Autoimmune Myocarditis (EAM). Germ-free mice were colonized with one of three distinct microbiomes (M31B, W116 or MC608) prior to inducing EAM with adjuvanted myosin. Mice harboring MC608 had significantly higher inflammatory heart scores and myosin-specific autoimmune responses versus mice carrying M31B. Mice with severe signs of EAM also experienced alterations in composition of their microbiota, including a significant decrease in *Lactobacillus*. We further observed negative correlations between EAM severity and both *L. reuteri* and *L. taiwanensis*. To test for protective effects of these species, we inoculated *Lactobacillus*-deficient mice with both *L. reuteri* and *L. taiwanensis* prior to EAM induction. Treatment with both lactobacilli significantly decreased myosin-specific IFN-$γ $and IgG responses compared to controls. Altogether, these results show that the gut microbiota modulates EAM severity and autoreactive responses. Moreover, *L.* *reuteri* and *L. taiwanensis* provide protection against severe EAM, suggesting that live biotherapeutics may be a beneficial adjunct therapy for myocarditis patients.

I would like to present in poster session.

**21. Method Development and Optimization for Aflatoxin B1, B2, G1, and G2 Quantification and Microbiological Quality Assessment in Buckwheat**

1**La Fontaine Bahatsi**, 1,2Jaqueline Garda Buffon, 1Jayne Stratton, 1Andreia Bianchini

1Department of Food Science and Technology, University of Nebraska, Lincoln, Nebraska, USA

2Laboratory of Mycotoxin and Food Science, Chemistry and Food School, Federal University of Rio Grande, Rio Grande, Rio Grande do Sul, Brazil

Abstract

Aflatoxins and microbial contamination in grains are significant global health concerns. Rapid and cost-efficient high-performance liquid chromatography (HPLC) methods are under investigation for quantifying aflatoxins (Afs) B1, B2, G1, and G2 in buckwheat flour. Samples were extracted using a solution of 80% methanol and cleaned by immunoaffinity columns. Eluates were air-dried and reconstituted in a trifluoroacetic acid (TFA) solution consisting of water, acetonitrile, and TFA (20:72:8, v:v:v). Aflatoxin separation was performed using a C18 column (3.9 x 150 mm) with a mobile phase of water, acetonitrile, and methanol (60:25:15, v/v/v) at a flow rate of 0.5 mL/min. The fluorescence detector was set at an excitation wavelength of 360 nm and an emission wavelength of 440 nm. Calibration curves for all toxins, ranging from 0.5 to 10 ng/mL, were linear with correlation coefficients of 0.999. For all toxins, the limit of detection ranged from 1.8 to 3.54 ppb, the limit of quantification ranged from 6.06 to 11.82 ppb, and the matrix effect ranged from 8.7 to 17.0%. Microbial analysis was conducted using culture-based methods and 3M Petrifilm™. For buckwheat flour, microbial counts of 6.7 logs and 5.1 logs were observed for APC and *Enterobacteriaceae*, respectively, while 7.6 logs and 5.3 logs were observed in groats, with no *E. coli* detected in either flour or groats. This study demonstrates that the developed HPLC method provides a reliable and accurate approach for quantifying aflatoxins in buckwheat flour. Additionally, it shows that microbial contamination can occur during both grain harvesting and milling, emphasizing the necessity for enhanced handling and processing practices to prevent chemical and microbiological contamination of buckwheat products.

**23. Microbial Responses to Chlorine Disinfection in Drinking Water Systems**

**Zhisong Cui¹**, Xinpeng Zhang¹, Xuehuan Feng¹, Ian Struewing², Jingrang Lu², Yanbin Yin¹

**Affiliations**: ¹Nebraska Food for Health Center, Department of Food Science and Technology, University of Nebraska-Lincoln, Lincoln, NE, USA; ²Office of Research and Development, United States Environmental Protection Agency, Cincinnati, OH, USA

**Abstract**:
Engineered water systems (EWSs) treated with chloramination are widely used to maintain drinking water quality. However, nitrification in EWSs can deplete disinfectants and promote the proliferation of opportunistic pathogens (OPs), raising public health concerns. Chlorine burns, a temporary replacement of chloramines with free chlorine, are often employed to mitigate nitrification. Yet, the long-term effects of chlorine burns on microbial community structure, particularly on OPs, are not well understood. In this study, we applied metagenomic profiling to monitor microbial community dynamics across pre-burn, burn, and post-burn phases in a full-scale EWS. Our findings revealed that the top 15 most abundant metagenome-assembled genomes (MAGs) post-burn included several potential OPs—such as *Mycobacterium phocaicum*, *Acinetobacter johnsonii*, and *Afipia* spp.—that significantly increased in relative abundance after the burn. These organisms are recognized for their resistance to disinfection and links to healthcare-associated infections. Their regrowth following chlorine dissipation suggests that chlorine burns may have limited long-term efficacy in controlling OPs. This study highlights the need to reassess current disinfection strategies and emphasizes the value of metagenomics in understanding microbial responses to operational interventions in drinking water systems.

25. Effect of temperature and Aw in *Salmonella*’s growth in raw chicken: a static model

**Mora-Lee, Diana1,2**, Chaves-Elizondo, Byron2

Affiliations: 1University of Costa Rica, San José, Costa Rica; 2University of Nebraska-Lincoln, Lincoln, Nebraska USA.

Among foodborne pathogens, *Salmonella* is one of the leading causes of illness worldwide. Chicken meat serves as a favorable reservoir for *Salmonella* growth, highlighting the critical role of maintaining the cold chain during transportation and storage. This study aimed to evaluate the growth of *Salmonella* under different temperature and salt conditions. Two batches of ground chicken were prepared with 0.5% and 1.5% (w/w) NaCl, respectively. Each batch was inoculated with a cocktail of five *Salmonella* strains previously isolated from chicken and incubated at 4 °C, 8 °C, and 12 °C. *Salmonella* populations were monitored over 20 days, and growth curves were constructed.

At 4 °C, *Salmonella* showed no noticeable growth, with cell counts remaining relatively stable throughout the storage period. In contrast, at 12 °C, the bacteria entered the exponential growth phase within 48 hours and reached the stationary phase by day 5. At 8 °C, an increase of 1–3 log CFU/g was observed, although a clear exponential phase was not evident during the experiment. Across all temperatures, samples with 1.5% NaCl tended to yield slightly lower *Salmonella* counts than those with 0.5% NaCl, suggesting a minor inhibitory effect of higher salt concentration. Overall, the findings confirm that refrigeration temperatures slow but do not eliminate *Salmonella*, and even modest temperature abuse can result in significant bacterial growth—regardless of salt content up to 1.5%. This study provides insight into the behavior of *Salmonella* in chicken meat under storage conditions commonly encountered in the food supply chain.

27. Chemical and microbial stability of Archaeological canned food Recovered from a Steamboat Wreckage from 1865

**Yueyan Dai1**, Ram Kumar Shrestha**1**, Jayne Stratton**1**, and Andreia Bianchini**1**

Affiliations: **1**University of Nebraska-Lincoln, Lincoln, Nebraska USA

In 1865, the Steamboat *Bertrand* sank in the Missouri River near Omaha, Nebraska. The shipwreck was excavated between 1968 and 1970, and its cargo was preserved as a historical collection. As part of a preservation project by the Nebraska State Historical Society, four cans of oysters in sauce were brought to the UNL Food Innovation Campus for assistance with opening and preserving them. The objective was to assess the physical condition of the cans, microbial viability, and chemical changes of the contents after so many years of storage. Cans were externally examined for seal integrity and deformation, then opened aseptically. Microbial analysis showed no viable aerobic or anaerobic microorganisms were detected in any of the tested samples. Proximate analysis revealed protein levels between 6.5–8.8 g/100 g, which is slightly below but still close to the modern range of 8–12 g/100 g for this product. Lipid content ranged from 0.40 to 1.01 g/100 g, which aligns with expectations for low-fat seafood. The relatively low but preserved fat levels suggest that lipid degradation caused by oxidation was minimal, likely due to effective hermetic sealing and the anaerobic environment within the cans. Sodium content ranged from 170–186 mg/100 g, well within the modern commercial range of 150–400 mg/100 g for canned oysters. These findings support that the food maintained a significant degree of chemical integrity, even after more than a century in ambient storage, demonstrating the effectiveness of 19th-century canning techniques and offering valuable insights into historical food preservation.

**29. Impact of Hands-on One-day Camps on Knowledge and Interest in Food Science Careers**

**Author: Karen Nieto-Flores1,** Jayne Stratton1, Andreia Bianchini1

**Affiliations: 1**University of Nebraska-Lincoln, Lincoln, Nebraska USA

Food science engages students in exploring the science behind the food they consume. This study examined the impact of three one-day food science camps designed for middle and high school students: “Pizza: The Rise of the Dough,” “The Science of Ice Cream,” and “The Science of Cookies.” These camps used experiential learning activities with familiar foods to illustrate scientific principles. The study assessed how these interventions influenced students' food science knowledge, awareness of food science careers, and interest in Science, Technology, Engineering, and Mathematics (STEM), particularly food science, as a career. A mixed-method approach integrated quantitative and qualitative data collection. Pre- and post-tests evaluated food science knowledge and career awareness, while surveys measured STEM interest. An adapted “Draw a Scientist Test” was used, in which participants drew a food scientist at work before and after the interventions. Data analysis included statistical tests and content analysis of drawings. Results showed a significant increase in food science knowledge (p<0.05), but no significant change in career knowledge. Qualitative findings indicated more complex conceptions of food scientists, with five career roles emerging: food safety experts, product developers, food chemists, food processors, and the misconception of food scientists as chefs. Campers reported feeling comfortable engaging with STEM professionals and enjoyed STEM activities. While career interest remained moderate, findings highlight the value of hands-on, food-based education in fostering scientific knowledge and broadening students’ understanding of food science. Expanding such initiatives could inspire the next generation of food scientists and strengthen the STEM workforce through meaningful experiences.

**31. Elucidating a novel hypertension treatment approach through egg white hydrolysate and gut microbiome synergism *in-vitro***

Emerson Nolasco1, Devin Rose1, Kaustav Majumder1

1University of Nebraska-Lincoln, Lincoln, Nebraska USA

* 1. Introduction
	2. Hypertension, a major cardiovascular risk, involves vascular inflammation, the renin-angiotensin system, and the gut microbiome. Egg white hydrolysates (EWH) exhibit antihypertensive potential, yielding a digestion-resistant fraction post-gastrointestinal digestion. This study investigated the bioactivity of EWH fractions. Egg white hydrolysate (EWH) was prepared by sequential hydrolysis combining two different endopeptidases under alkaline and acidic conditions. EWH was further subjected to *in vitro* gastrointestinal digestion (EWH-GI) and fractionation. The <3000 Da fraction (EWH-GI-D) was evaluated for its bioactivity using endothelial cells along with *in-vitro* ACE inhibition. The >3000 Da fraction (EWH-GI-U) was subjected to *in-vitro* microbial fermentation. Fermentation metabolites such as ammonia, short (SCFA), and branched-chain fatty acids (BCFA) were analyzed. EWH-GI-D anti-inflammatory activity by reducing inflammation markers VCAM-1 and ICAM-1 in HUVEC cells at 100 and 500 µg/mL. The ACE inhibition IC50 was significantly lower for EWH-GI-D at 734 µg/mL compared to EW-GI-D at 3340 µg/mL. Gut microbiome detrimental metabolites such as ammonia and SCFA/BCFA were significantly lower in EWH-GI-U compared to peptone (control) except for propionate, which has shown anti-inflammatory activity. The genus *Phascolarctobacterium* and *Lachnospiraceae* composed 50% of the microbiome and have been associated with SCFA production. The results are promising as EWH could reduce hypertension progression by simultaneously modulating its mechanisms directly, and systematically via modulation of gut microbiome metabolites.

# **33. CAZyme3D: A Database of 3D Structures for Carbohydrate-active Enzymes**

**N.R. Siva Shanmugam1**, Yanbin Yin1, \*

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**Abstract**

CAZymes (Carbohydrate Active EnZymes) degrade, synthesize, and modify all complex carbohydrates on Earth. CAZymes are extremely important to research in human health, nutrition, gut microbiome, bioenergy, plant disease, and global carbon recycling. Current CAZyme annotation tools are all based on sequence similarity. A more powerful approach is to detect protein structural similarity between query proteins and known CAZymes indicative of distant homology. Here, we developed CAZyme3D (<https://pro.unl.edu/CAZyme3D/>) to fill the research gap that no dedicated 3D structure databases are currently available for CAZymes. CAZyme3D contains a total of 870,740 AlphaFold predicted 3D structures (named Whole dataset). A subset of CAZymes 3D structures from 188,574 nonredundant sequences (named ID50 dataset) were subject to structural similarity-based clustering analyses. Such clustering allowed us to organize all CAZyme structures using a hierarchical classification, which includes existing levels defined by the CAZy database (class, clan, family, subfamily) and newly defined levels (subclasses, structural cluster [SC] groups, and SCs). The inter-family structural clustering successfully grouped CAZy families and clans with the same structural folds in the same subclasses. The intra-family structural clustering classified structurally similar CAZymes into SCs, which were further classified into SC groups. SCs and SC groups differed from sequence similarity-based CAZy subfamilies. With CAZyme structures as the search database, we created job submission pages, where users can submit query protein sequences or PDB structures for a structural similarity search. CAZyme3D will be a useful new tool to assist the discovery of novel CAZymes by providing a comprehensive database of CAZyme 3D structures.

35. Survival and recovery of *Aliarcobacter butzleri* in ground chicken at refrigerated temperatures

**April Jiménez-Artavia1**, Byron Chaves-Elizondo2.

Affiliations:

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*Aliarcobacter butzleri* is an emerging foodborne pathogen of increasing concern due to its potential health risks and relevance in food safety. Poultry meat is a major source of *A. butzleri* contamination, often linked to inadequate hygiene during slaughter. Despite its high occurrence in poultry, limited information is available on its survival and recovery under refrigeration. This study aims to evaluate the survival dynamics and potential recovery of *A. butzleri* in ground chicken stored at 4, 8, and 12°C.

Ground chicken samples were prepared with two salt concentrations (0.5 w/w and 1.5% w/w) and inoculated with *A. butzleri* at an initial level of 4 log CFU/g. Following a 30 min incubation at 4°C to allow bacterial attachment, samples were assessed every 48 h over 20-day period. Enumeration was performed via serial dilution and plating on Blood Free Campylobacter Selective Agar supplemented with Cefoperazone, Amphotericin B, and Teicoplanin (CAT), followed by incubation at 37°C for 48 h under microaerophilic conditions. Additionally, total aerobic psychrophilic counts were conducted at 4°C over 8 days. Physicochemical parameters —including pH, water activity, and fat content—were measured prior to inoculation. All treatments were conducted in duplicated, and statistical analysis performed to assess significance.

Although data collection is ongoing, the resulting growth curves for *A. butzleri* at 4, 8, and 12°C will help characterize its behavior under typical refrigeration conditions. This study will provide valuable insights into the persistence of *A. butzleri* in poultry meat and support the development of improved food safety strategies for refrigerated products.

Presentation type: Poster Presentation.

**Flash Talks Session I, 11:15-12:00, room 277**

Title: “Characterization of gut bacterial genes for degradation of dietary condensed tannins”

**Lucas Townsend1,2**, Qinnan Yang2, Bo Peng2, Kristin Beede2, Andrew Benson2, Amanda Ramer-Tait1,2

*1Complex Biosystems, University of Nebraska-Lincoln; 2Department of Food Science and Technology, University of Nebraska-Lincoln*

Inflammatory bowel disease (IBD) is a chronic relapsing inflammatory disease affecting the colon, with U.S. prevalence exceeding 2 million and rising. Although the disease etiology remains unclear, it is recognized that select members of the gut microbiota, particularly *Faecalibacterium*, play a crucial role in IBD pathogenesis. *Faecalibacterium* produce butyrate, a short chain fatty acid (SCFA) that is positively correlated with gut health. Restoring *Faecalibacterium* to the microbiota of IBD patients via prebiotic substrates may be a promising approach to reducing intestinal inflammation. Condensed tannins (CT) enhance *Faecalibacterium* growth *in vitro*, suggesting a prebiotic effect, yet the mechanism for CT utilization remains unknown. We previously isolated novel intestinal *E. coli* strains capable of degrading CT *in vitro*, suggesting that such an ability may not be limited to *Faecalibacterium.* This project therefore aims to identify the gene(s) responsible for CT degradation by gut microbes through a comparative genomics approach. Using an overlay assay, where tannin degradation is determined by growth on CT-containing agar, we found that 58 out of 72 strains from the intestinal *E. coli* reference collection (ECOR) could degrade CT. Next steps include additional screening of ECOR isolates for CT degradation using a vanillin assay and then comparing the genomes of CT-degrading strains with non-degrading strains to identify candidate genes responsible for CT degradation. Eventually, we will delete or insert these genes into bacterial genomes to evaluate their role in tannin degradation. Our results will ultimately aid in understanding the mechanisms underlying the prebiotic effect of CT on *Faecalibacterium*.

**Salt and pH Influence the Accuracy of Aerobic Plate Counts in Low-Water-Activity Foods**

**Waraporn Mahlman**, Jayne Stratton, Reka Howard, Andreia Bianchini

University of Nebraska-Lincoln, Lincoln, Nebraska, USA.

Abstract

The Aerobic Plate Count (APC) method is widely used to quantify aerobic microorganisms in food products. This study evaluated the impact of varying salt (NaCl) concentrations ranging from 33 to 234 mg/g and pH levels from 2.88 to 5.96 on three APC enumeration methods—Petrifilm™ AC, pour plate, and spread plate—using pancreatin powder as a model of low-water-activity food samples with high and low microbial loads. Results indicate that salt concentration and pH significantly influenced bacterial enumeration across all methods (p = 0.0019 and p = 0.0001, respectively). However, no significant differences were observed among the three methods at high microbial loads (p = 0.2691). In contrast, at low microbial loads, the methods produced significantly different results (p = 0.0121), indicating that salt concentration and pH continued to affect bacterial recovery (p = 0.014 and p = 0.0001, respectively). A significant interaction between salt and pH was observed in low microbial load samples (p = 0.0192). Statistical contour plot analysis suggests that the pour plate and spread plate methods achieve better bacterial recovery than Petrifilm™ AC at lower pH and higher salt concentrations. These findings highlight the influence of salt and pH on APC results and suggest that the pour plate and spread plate methods are more robust under varying conditions. This study provides valuable insights for selecting the most suitable enumeration method for assessing the microbiological quality of low-water-activity foods with various salt and pH levels.

My presentation type is Flash Talk

**Evaluating effects of microbial community composition on kombucha fermentation**

Baishakhi Biswas1, Edward C. Deehan1, Jennifer M. Auchtung1

 1Department of Food Science and Technology, Nebraska Food for Health Center, University of Nebraska, Lincoln, NE, USA

**Abstract**

Kombucha is a fermented tea beverage known for its slightly sweet and acidic flavor. The potential health benefits of kombucha, including improved immune function, enhanced digestion, and improved metabolic regulation, have contributed to increased demand for kombucha among consumers. Traditionally, kombucha is produced using black tea and sucrose with a symbiotic community of bacteria and yeast (SCOBY) dominated by acetic acid bacteria and yeast. We are interested in determining whether SCOBY communities can be altered to increase the levels of microbes with potential health benefits, including bifidobacteria and lactic acid bacteria, while preserving production of beneficial fermentation end products and sensory properties. A recent study reported that co-cultivation of milk kefir grains with SCOBY increased the concentration of lactic acid bacteria and enhanced the antibacterial and antioxidant capacities of the kombucha. As a follow-up to these studies, we have been studying the effects of microbial community composition on kombucha fermentation by comparing properties of kombucha made with a traditional SCOBY along with water kefir or dairy kefir grains, to each community alone. In addition, to improve kombucha's overall functionality, we are concerned with producing fiber-rich and different substrate-based (sorghum) kombucha.

In a pilot study, we measured microbial community composition and pH over three rounds of 14-day fermentations with sucrose. We observed that Bifidobacteria were not identified on day 0 of the first fermentation cycle in WK (<1 organism per sample volume), but by day 14, they had increased to 7.33 log CFU/mL (2.12 × 10⁷ CFU/mL). Co-fermentation of traditional SCOBY with water kefir also led to an 8-fold increase in levels of acetic acid bacteria and an>8-fold increase in levels of lactobacilli relative to SCOBY alone in the second round of fermentation. Future studies will measure differences in metabolite profiles and sensory properties of the kombucha products.

**Exploring Sequence-Structure-Function Relationships in Anti-Prokaryotic Immune System (APIS) Proteins**

Md Numan Islam1, and Yanbin Yin (yyin@unl.edu) 1

*1Nebraska Food for Health Center, Department of Food Science and Technology, University of Nebraska - Lincoln, Lincoln, NE 68588, USA.*

**Abstract**

Prokaryotes (bacteria and archaea) have evolved a diverse arsenal of defense mechanisms, which are collectively known as prokaryotic immune systems (PIS), to protect against phage infections. In response, phages have developed a range of counter-defense strategies. Among these, phage-encoded anti-prokaryotic immune system (APIS) proteins play a crucial role in neutralizing host defenses. However, the diversity and evolutionary history of APIS proteins, excluding anti-CRISPRs, remain poorly understood. This project aims to uncover the structural diversity and evolutionary trajectories of APIS proteins through a structure-guided discovery approach. Our primary objective is to identify putative APIS structural homologs within the INPHARED, IMG/VR, MGV, and GPD databases. Using an advanced computational pipeline, we will predict and refine high-confidence 3D structures of candidate APIS proteins with AlphaFold2. These structural models will support detailed analyses to explore functional and architectural similarities between APIS proteins and known immune system components. We will also perform phylogenetic analyses to investigate the evolutionary divergence between newly identified APIS proteins and established prokaryotic immune systems. The outcomes of this project will enhance our ability to identify APIS proteins through structural analysis and contribute to the development of novel therapeutic tools targeting bacterial infections. Ultimately, this work will deepen our understanding of APIS functionality and highlight their essential role in phage-host coevolution.

Flash talk

**Microbiological Food Safety and Regulatory Measures in Nepal**

Ram Kumar Shrestha1, Janak Dhakal2, Andreia Bianchini1, and Byron D. Chaves1[[1]](#footnote-1)

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Foodborne diseases (FBDs) are a major public health concern worldwide. Developing nations encounter higher occurrences of FBDs owing to substandard food handling practices and inadequate regulatory measures. We reviewed the prevalence of the most common foodborne pathogens and the illnesses they cause in high-risk commodities such as poultry, meat, eggs, dairy, fresh produce, and street foods in Nepal. *Escherichia coli, Staphylococcus aureus,* and *Salmonella* were the predominant organisms consistently reported in all studies. Despite the inherent variations in the prevalence among the reports, the occurrence of these pathogens was markedly high in meat, dairy, and street foods under examination. The reported prevalence of *E. coli* ranged from 31.6- 100% of meat samples. Similarly, the prevalence of *S. aureus* ranged from 7.9% to 80% on examined commodities. In addition, an alarming number of isolated pathogens were resistant to one or more clinically significant antibiotics. Considering heightened pathogenic contamination and antibiotic resistance, we highlight the need for a multiprong approach to ensure food safety, including consumer awareness, legislative amendments to enact and enforce proper and updated food safety regulations, technical strengthening, workforce training, and educating the producers and processors. Additional measures encompass addressing water safety, improving the infrastructure and resources, and promoting the prudent use of antibiotics. Moreover, implementing the Slaughterhouse & Meat Inspection Act 1999 and the mandatory adoption of Good Manufacturing Practices (GMP) and Hazard Analysis and Critical Control Points (HACCP) for high-risk commodity producers and processors would significantly enhance consumer food safety in the country.

*Evaluation and training assistance visits to help small Ready-to-Eat (RTE) food manufacturers comply with current Good Manufacturing Practices (cGMPs*)
**Soojung Kwon1**

Affiliations: **1**University of Nebraska-Lincoln, Lincoln, Nebraska USA.

This project, "Evaluation and Training Assistance Visits to Help Small Ready-to-Eat (RTE) Food Manufacturers Comply with Current Good Manufacturing Practices (cGMPs)," aims to enhance food safety compliance among small RTE food producers in Nebraska. Utilizing a comprehensive GMP Facility Checklist derived from FDA FSMA, FDA Food Code, SQF, BRCGS, and FSSC 22000 standards, the initiative conducts initial assessments of 3-4 manufacturers, evaluating 10 sub-sections (e.g., Qualified Individual, Personnel) across 67 questions. Each question is rated as Satisfactory, Minor, Major, or Critical, with a scoring system requiring a 70% or higher rating for compliance. Facilities scoring below this threshold receive targeted training and, after 2-3 months, follow-up visits focusing on their 2-3 most deficient areas using expanded, scheme-specific checklists. The project concludes with a final report assessing compliance improvements and a processor survey evaluating the effectiveness of training and visits. By addressing critical GMP areas like sanitation, allergen control, and defect management, the project not only improves food safety but also builds capacity among small manufacturers to meet regulatory requirements. Preliminary results suggest enhanced understanding and implementation of GMPs, with potential for scalable application to other regions and food sectors. This approach bridges the gap between regulatory expectations and practical implementation, fostering a culture of safety and compliance in the RTE food industry.

**Presentation Type:** Flash Talk

**Title:** Enhancing Experiential Learning in Food Science and Technology

**Author:** Assoumpta Umwali Ujeneza

**Faculty Advisor:** Dr. Byron Chaves-Elizondo

**Affiliations:** ¹University of Nebraska-Lincoln, Department of Food Science and Technology, Nebraska USA

Experiential learning is a critical component of Food Science and Technology education, serving to bridge the gap between theoretical knowledge and practical, real-world applications. As the food industry increasingly demands graduates with hands-on skills and problem-solving abilities, understanding how experiential learning is implemented in academic programs becomes essential. This study aims to examine how food science and technology faculty across the United States and Canada define, value, and integrate experiential learning into their curricula.

Through a comprehensive survey targeting faculty members at diverse institutions offering undergraduate and graduate programs, the project will investigate the types of experiential learning activities currently in use—such as lab-based instruction, industry partnerships, product development projects, internships, and service learning. The survey will also explore faculty perspectives on the effectiveness of these approaches and the barriers they encounter in designing and delivering experiential learning experiences, including issues related to resources, institutional support, and curriculum constraints.

By capturing a wide range of practices and viewpoints, this research will provide valuable insights into how experiential learning is shaping the next generation of food scientists. The findings will inform strategies for strengthening food science curricula to better align with industry expectations and student needs.

**Oral Presentations Session II, 1:00-1:45, room 277**

**Characterizing differences in adherence to host mucins across**

***Clostridium perfringens* strains**

**Thi Van Thanh Do1**, Kurt H. Piepenbrink1, Jennifer Auchtung1

1Department of Food Science and Technology, University of Nebraska Lincoln, Lincoln, Nebraska

*Clostridium perfringens* is an extremely versatile pathogen and has been associated with various systemic and enteric diseases in both humans and livestock, including gas gangrene, food poisoning and nonfoodborne diarrhea, enteritis/enterocolitis, and enterotoxemia. This bacteriumis currently divided into 7 toxinotypes (A-G) and each *C. perfringens* toxinotype is associated with specific diseases with host specificity. Bacterial adherence is the first important step in the pathogenesis of infection of most pathogens. Understanding interactions between *C. perfringens* and intestinal mucins is crucial to mitigate many enteric diseases in humans and animals. The objective of our research is to investigate how the difference in binding ability across *C. perfringens* strains from 4 toxinotypes (A, C, E, and F) to human intestinal mucins derived from HT-29 and mucin-producing HT-29 MTX cell lines. Our findings indicate that duration influences adherence to HT-29 and HT-29 MTX cells. Across all tested strains, adherence was higher in HT-29 MTX cells than in HT-29 cells at 14 and 18 days of culture while no significant difference was observed at 8 days. Adherence ability varies among strains, 65% of strains exhibited greater adherence to mucin-producing HT-29 MTX cells for 14 days. The presence of *nanI* does not lead to higher adherence level across *C. perfringens* toxinotypes. *cnaA* and *fimA* detected only in the toxinotype F strain F5603 may contribute to its higher adherence to HT-29 MTX cells. Next, we will perform comparative genomic analyses to identify genes involved in adherence and assess the impact of key candidate proteins on binding.

**Outgrowth of *Clostridium perfringens*during thermal stabilization of cooked pork sausages with nitrite removers**

Priya Biswas

**Introduction:** Improper thermal stabilization of meat products can lead to C. perfringens outbreaks, posing health risks. Nitrite removers and replacers are gaining popularity in clean-label meat formulations.

**Objective:** To determine *C. perfringens* outgrowth during thermal stabilization of cooked, uncured meat sausages with nitrite removers.

**Methods:** Ground pork samples (10 g) were inoculated with C. perfringens B-23847, vacuum-sealed, and heat-shocked at 75°C for 20 min to inactivate vegetative cells and activate spores, followed by 6.5 h dynamic cooling. Eight treatments were evaluated, with each timepoint consisting of six samples including four nitrite removers and two control samples were enumerated at 48-minute intervals, with two independent trials.

**Results:** Initial *C. perfringens* levels for NR1, NR2, NR3, NR4, positive control, and negative control were 4.08±0.25, 4.39±0.02, 4.31±0.02, 3.31±0.08, 3.20±0.16, 3.52±0.06 log CFU/g, respectively. After the 6.5-hour cooling process, NR1 exhibited a population of 4.01±0.07 log CFU/g with a growth reduction of 0.07 log CFU/g, while NR2 showed a growth of 4.18±0.05 log CFU/g, showing a reduction of 0.21 log CFU/g. NR3 and NR4 showed growths of 4.15±0.11 and 3.15±0.07 log CFU/g, with reductions of 0.16 and 0.16 log CFU/g, respectively. The positive and negative controls exhibited growths of 2.77±0.20 and 3.48±0.10 log CFU/g, with reductions of 0.43 and 0.04 log CFU/g, respectively. All nitrite remover treatments effectively prevented the outgrowth of *C. perfringens* and reduced the microbial population.

**Conclusion:** The nitrite removers and replacers evaluated effectively prevent *C. perfringens* outgrowth below 1 log CFU/g during cooling, making them suitable for clean-label meat products.

**Condensed tannins have a transient prebiotic effect on *Faecalibacterium duncaniae* in mice**

**Xiaohan Wu\*1**, David Gomez Quintero1, Kristin Beede1, Sedoten Ogun1, Robert Schmaltz1, Jeff Price1, Kaustav Majumder1, Andrew Benson1, Amanda Ramer-Tait1.

Affiliations: 1Department of Food Science and Technology, University of Nebraska-Lincoln, Lincoln, Nebraska.

Inflammatory bowel diseases (IBD) are characterized by chronic and relapsing inflammation of the gastrointestinal tract. The gut microbiota has gained increasing attention as a key factor influencing IBD outcomes. In particular, the commensal gut microbe *Faecalibacterium duncaniae* decreases in abundance in IBD patients compared to healthy individuals, suggesting that *F. duncaniae* may protect against IBD. Here, we investigated the ability of dietary tannins to support the growth of *F. duncaniae* in the human gut microbiota. Germ-free (GF) mice were colonized with a human fecal microbiota lacking *F. duncaniae* and fed either a diet enriched in or depleted of condensed tannins. Nine days later, half the mice receiving each diet were maintained as controls and the other half were administered one oral gavage of *F. duncaniae*. Fecal samples were collected at multiple time points to quantify *F. duncaniae* abundance using qPCR. By 6 hours post-gavage, mice consuming tannins exhibited a significant increase in fecal *F. duncaniae* abundance compared to mice not fed tannins, with peak levels observed at 12 hours. However, by 24 hours, the presence of tannins had no effect on the abundance of *F. duncaniae*, nor was it detectible in most mice, indicating that tannin supplementation was not sufficient to support colonization of this gut microbe. Altogether, our results show that condensed tannins have a transient prebiotic effect on *F. duncaniae* *in vivo*. Future research will investigate the effects of continuous administration of *F. duncaniae* and condensed tannins as a synbiotic preparation on intestinal inflammation during IBD in mice.

**Conference Oral Presentation 15min**

**Flash Talks II, 1:45-2:00, room 277**

**Quality attributes of cumin seeds after treating with radiofrequency over storage.**

Rachana Police1, Dr Rossana Villa Rojas1

University of Nebraska Lincoln, 2025

Abstract

Cumin seeds are integral to global culinary practices and have been recognized for their distinct flavor and medicinal properties. Over the past few decades, the demand for safe and quality food has increased due to outbreaks of foodborne illness. Developing innovative technologies that effectively reduce microbial load while minimizing the negative effects on the quality of spices is crucial for food safety and quality. The purpose of this project is to understand the changes taking place in the quality attributes of cumin seeds after treatment with radiofrequency during storage. The experiment will be performed on separate batches from three different lots which are obtained from McCornick and Company. The study involves measuring moisture content, water activity, color, total phenolics, antioxidant activity, volatile compound analysis, and microbial quality before and after treatment with radiofrequency to see the change in the quality of the cumin seeds. During storage only aw, moisture content, and volatile compound analysis will be measured.

The findings of this study are expected to contribute valuable insights into the efficacy of radiofrequency treatment as a method for preserving the quality and safety of cumin seeds over time. Understanding these changes is crucial for both the food industry and consumers, as it may impact the utilization of radiofrequency technology in enhancing the shelf life and safety of cumin seeds, ultimately influencing the overall quality of cumin-based products in the market.

Keywords: cumin seeds, water activity, moisture content, radio frequency, antioxidant activity, total phenolic, volatile compound analysis, microbial quality.

Subfamily Classiﬁcation of Glycosyl transferase 2 (GT2) Family Ananya Roy1, Yanbin Yin1

Aﬃliations: 1University of Nebraska-Lincoln, Lincoln, Nebraska USA

Glycosyltransferase Family 2 (GT2) enzymes are among the most functionally diverse Carbohydrate Activated Enzymes (CAZymes), playing essential roles in bacterial cell wall biosynthesis, glycoprotein formation, and polysaccharide assembly. GT2 is the largest CAZyme family having currently over 400,000 sequences listed in the CAZy database but only a fraction of them (<0.1%) are biochemically characterized. Despite their widespread biological signiﬁcance, GT2 enzymes remain challenging to classify due to their broad sequence diversity, overlapping substrate speciﬁcities, and the lack of universally accepted classiﬁcation criteria. The consensus method for subfamily classiﬁcation of CAZyme families having large number of members is Sequence Similarity Network (SSN) analysis, which clusters highly similar sequences based on the BLAST e-value threshold. At present dbCAN has nine hidden Markov models (HMMs) collected from the Pfam database to classify GT2 sequences to its designated family but the challenging aspect to subclassify the family based on SSN is that over 50% of the sequences are being lost as singletons even at a very lenient e-value threshold. The variety of sequence length, large multimeric structure of the members with various associated domains adds layers of complexity to the classiﬁcation problem. The goal of our project is to develop a methodology and build new HMMs to delineate a more reﬁned and compact subfamily division which would enable better understanding of substrate speciﬁcity and expand our knowledge on the taxonomic, structural, and functional diversity of GT2.

**Workshop, 2:00-2:45, room 106**

Root Cause Analysis & CAPA Workshop

Presented by Ashley Cunningham

Abstract:

Environmental monitoring for pathogens plays a vital role in maintaining food safety and protecting consumer health within food manufacturing environments. This presentation will examine how routine sampling and testing of facility surfaces, equipment, and environmental zones can aid in detecting harmful pathogens, such as Listeria monocytogenes and Salmonella spp. before they reach the final product. We’ll discuss practical strategies for designing an effective monitoring program, selecting sampling sites, interpreting results, and taking corrective actions. Attendees will gain a clear understanding of how environmental monitoring supports regulatory compliance, enhances sanitation practices, and ultimately strengthens food safety systems. The workshop portion will include a hands-on food safety team investigation for further understanding of root cause analysis and vectoring.

**Oral presentations Session III, 2:00-3:00, room 277**

Validation of Neogen® Molecular Detection System of *Salmonella, Listeria* and STEC in pet foods

**Allie K. Fowle1**, Byron D. Chaves1

Affiliations: 1University of Nebraska-Lincoln, Lincoln, Nebraska USA

Pet food safety is an increasingly important concern due to its role in the transmission of zoonotic diseases. With most United States households owning at least one pet, microbial contamination in pet food represents a significant risk to both animal and human health. Pet foods are usually labeled not safe for human consumption as they do not have the same microbial safety specifications as human foods, and although *Salmonella* is considering an adulterant in pet foods, challenges regarding risk mitigation and detection in pet food matrices persist. Different types of pet food—including dry, semi-moist, wet, raw, and treats—pose distinct microbiological challenges. Factors such as water activity, pH, processing methods, and storage conditions all influence the survival and proliferation of pathogens, making contamination control more complex. Detection of these pathogens can also be difficult. While traditional culture-based methods remain the gold standard, they are time-consuming. Molecular techniques, such as the Neogen® Molecular Detection System (MDS), which uses loop-mediated isothermal amplification (LAMP), provide rapid, sensitive detection and offer valuable tools for routine monitoring and improved food safety. The goal of this project is to validate the use of the MDS platform for the detection of Salmonella, Listeria monocytogenes, and Shigatoxigenic Escherichia coli (STEC) in pet food matrices with different physicochemical characteristics.

**Evolutionary history of *Camellia sinensis* crop varieties: Insights into comparative chloroplast genomics and phylogenetic relationship**

**Khurram Shahzad**

Abstract

Tea, produced from *Camellia sinensis,* the most widely consumed nonalcoholic beverage worldwide, has numerous health benefits attributed to its richness in characteristic compounds such as catechins, theanine, and caffeine (Pastoriza et al., 2017). With over two billion cups consumed daily, tea is an essential crop economically and globally, yielding an annual global harvest of ~5 million tons, worth about US $5.7 billion. Global tea planting area and production exceeded 5.31 million hectares and 6.30 million tons, respectively, with an economic value reaching approximately US$17 billion. Tea is classified into three major varieties, *C. sinensis var. sinensis* (CSS), *C. sinensis* *var. assamica* (CSA), and *C. sinensis var. publimba* (CSP) with several distinct features, such as leaf size. CSS and CSA are two main varieties; CSS is characterized by smaller leaves, cold tolerance, and a shrub or semi-shrub growth habit, whereas CSA has larger leaves and an arborous or semi-arborous habit. These main varieties contain flavorful leaves that carry health-promoting bioactive compounds and have been domesticated for commercial tea production. However, since tea plant taxonomy generally lacks comprehensive genomic evidence, further analyses using population resequencing are required to optimize taxonomic assignments at the whole genome level. Here, I have constructed a geographical-based pangenome of cpDNA representing a wide range of genetic diversity of *Camellia sinensis's* three varieties.

I explored phylogenetic relationships, evolutionary history, and genetic structure among geographically distinct tea varieties based on cpDNA by integrating extensive information regarding geographical areas and genetic variations between tea varieties. Results provide insight into the origin of tea, the subsequent routes of expansion, and the mechanism of divergence that remains to be clarified. Through deep analyses of the cpDNA genome, comparative genomic and gene variations analysis followed to identify candidate gene variations and genomic regions associated with tea diversification, domestication, and evolution.

Cadmium has differential effects on the human gut microbiome by composition

**Carmen E. Perez Donado**,1,2 Sujun Liu, 1,2 Devin J. Rose1,2,3, Jennifer M. Auchtung1,2

Affiliations: 1 Department of Food Science & Technology, University of Nebraska-Lincoln, Lincoln NE, USA; 2 Nebraska Food for Health Center, University of Nebraska-Lincoln, Lincoln, NE USA; 3 Department of Agronomy & Horticulture, University of Nebraska-Lincoln, Lincoln, NE USA

Cadmium (Cd) is a toxic heavy metal primarily ingested through food and water in non-smoking populations. Cd disrupts redox balance across multiple organs and interacts with the gut microbiota, which may trigger gut microbial disruptions, compromise intestinal barrier integrity, and promote increased Cd absorption. Previous studies have shown variations in microbiome responses to Cd, with differences in microbial composition affecting the extent of Cd disruption and reduction in production of short chain fatty acids. We investigated how differences in initial microbiota composition alter the compositional and functional effects of Cd exposure on human gut microbiotas. We conducted 24-hour in vitro cultures from twenty-one healthy adult donors as sources of gut microbiota under conditions that mimic the nutrient availability of the human colon. Regression analysis of log2-transformed butyrate at 0 vs. 20 ppm Cd identified three categories of microbial response (R = 0.61, p = 0.003): sensitive, intermediate, and tolerant. Two-thirds of microbiomes showed reduced butyrate production when exposed to Cd; highly sensitive microbiomes exhibited larger decreases and elevated lactate, consistent with lower levels of *Lachnospiraceae*, a family that contains many butyrate-producing bacteria. In contrast, tolerant microbiomes did not show these metabolic shifts and maintained *Lachnospiraceae* levels, potentially through *Erysipelotrichaceae* support. No significant differences in free Cd levels were found between tolerant and sensitive microbiomes (p > 0.2). These findings highlight distinct gut microbial responses to Cd exposure and provide a foundation to investigate microbiota features underlying Cd sensitivity or tolerance.

Title: CAZyme Gene Cluster Diversity in Human Gut Microbiome

Yi Xing1, Yanbin Yin1

Affiliations: 1 Department of Food Science and Technology, University of Nebraska-Lincoln, Lincoln, Nebraska, USA

The human gut microbiota plays a critical role in dietary carbohydrate metabolism, primarily via polysaccharide utilization loci (PULs), which facilitate the production of short-chain fatty acids (SCFAs) that modulate host metabolic health. Carbohydrate-active enzyme gene clusters (CGCs), computational analogs of PULs, are physically co-localized genomic regions encoding enzymes and transporters required for complex glycan degradation. Despite their recognized importance, the diversity, prevalence, and functional relevance of CGCs—particularly in the context of metabolic disorders such as obesity—remain inadequately characterized. To address this gap, we are developing an automated and scalable bioinformatics workflow to systematically identify and profile CGCs from publicly available human gut metagenomic datasets. Using reference CGCs curated from the dbCAN-seq database, we employ Bowtie2 for metagenomic read alignment and inStrain for quantifying gene cluster abundance and diversity in fecal metagenomes derived from both obese and non-obese individuals. By linking compositional differences in CGCs to substrate-specific glycan utilization patterns and microbial metabolic pathways, this study aims to elucidate how gut microbial fiber degradation capacity correlates with host metabolic status. Moreover, incorporating host metadata—such as age, sex, and body mass index (BMI)—enables the investigation of host–microbiome interactions and the modulatory effects of demographic variables on microbial carbohydrate metabolism. Collectively, our findings will enhance understanding of CGC-mediated functions in the human gut microbiome and their implications for metabolic health and disease, while informing the development of microbiome-based therapeutic strategies targeting carbohydrate metabolism.

**Poster Session II, 2:45-3:45, Fourth Floor**

2. Evaluation of 1% fat mozzarella cheese for pizza Eli Wills and Qinwen Zheng (FDST 132)

4. Evaluation of 2% fat mozzarella cheese for pizza Emily Frain, Ella Glliam, and Fatima Madero (FDST 132)

6. Evaluation of lactose-free mozzarella cheese for pizza Srimathi Balakrishnan, Riley Maldonado, Elijah Reazor (FDST 132)

8. Developing a Human Biobank to Investigate the Interactions Between Diet, Gut Microbiota, and Health

Corina Grimaldo1,2, Jiayu Tang1,2, Lisa Wisenhenhunt2, Daren L. Knoell4, Derrick R. Samuelson3, Edward C. Deehan1,2

1Department of Food Science and Technology, 2Nebraska Food for Health Center, University of Nebraska, Lincoln, NE; 3 Department of Internal Medicine, 4 Department of Pharmacy Practice and Science, University of Nebraska Medical Center, Omaha, NE

Diet strongly influences the relationship between the gut microbiota and human health, yet many aspects of these interactions remain not well defined. To enable further preclinical research on diet-microbiota-health interactions across the University of Nebraska system, there is a need for a collection of well-characterized fecal microbiomes from healthy individuals in Nebraska. The objective of this project is to develop such a well-characterized biobank of human fecal and peripheral blood mononuclear cell (PBMC) samples at the University of Nebraska-Lincoln (UNL). To achieve this objective, we are actively recruiting healthy adults (Target *N*=70) who are ≥19 years of age and from Lincoln and the surrounding communities. Each participant will provide a fecal and blood sample, which will be carefully processed and frozen for use in future *in vitro* and preclinical studies. To evaluate dietary habits, participants will complete a zinc-specific Food Frequency Questionnaire (FFQ), the Harvard Willett FFQ, and three 24-hour dietary recalls. Other relevant host factors such as alcohol intake, physical activity, bowel-related habits, immune and metabolic markers, and body composition measures will also be evaluated. Overall, establishing a Nebraskans biobank at UNL will enable future studies that aim to investigate how gut microbiota impact human health and disease. Providing such a foundational resource will enable future research on diet, lifestyle, host genetics, and microbiome interactions and will support the improved efficacy of dietary interventions that aim to promote health and prevent or treat chronic diseases.

**10.** Tree nut peptides selection for a quantitative multi-allergen mass spectrometry method

**Jerry Kahu1**, Philip Johnson1, Melanie Downs1

**Affiliation:** Food Allergy Research and Resource Program (FARRP), Department of Food Science and Technology, University of Nebraska-Lincoln, Nebraska, USA1

**Abstract**

Food allergies are immunological reactions resulting from consumption of proteins from specific foods, known as food allergens. In the U.S. nine major food allergens including tree nuts are regulated. While regulations require mandatory labeling of intentional use of allergens in food, unintentional presence due to cross-contact remains a hidden threat, underscoring the need for sensitive, specific, and robust analytical methods. Immunoassays can face challenges with detection and quantification due to factors like thermal processing and matrix complexity, leading to false negatives. Mass spectrometry (MS) offers potential solutions. This study aims to select peptides from six tree nuts to develop a single multi-target MS method for allergen quantification in incurred food matrices. As tree nuts are typically used in roasted forms, an assessment was conducted to optimize roasting conditions and evaluated for soluble protein profiles. Proteins of the unroasted and selected roasted nuts (179 0C, 10 minutes) were extracted, digested, and desalted for untargeted LC-MS/MS analysis. MS data were analyzed for peptide identification using commercial software, incorporating label free quantification (LFQ). Protein recovery for unroasted tree nuts exceeded 80%, with acceptable ranges for most roasting conditions. Electrophoretic profiling indicated the presence of major seed proteins. Roasting lowered the number of identifiable protein groups and peptides. LFQ showed that the most abundant peptides were from 11S legumins, 7S vicilins and 2S albumins. Target peptides which are abundant, unique to a tree nut species and relatively unchanged by roasting were selected as potential targets for the development of the multi-targeted MS method.

**12. Evaluating the Reuse of Greywater for Irrigating Ground-Level Fresh Produce: A Microbiological Risk Assessment of Generic *E. coli* Contamination on Lettuce**

**Andrew Stiven Ortiz Balsero1,** Constanza Avello Lefno2, and Bing Wang1

Affiliations: 1Food Science and Technology Department, University of Nebraska-Lincoln, Lincoln, NE; 2Chilean Agency for Food Safety and Quality (ACHIPIA), Chile

Chile's water crisis, driven by drought and rising agricultural demand, calls for innovative solutions like greywater reuse. This study applied a Quantitative Microbial Risk Assessment (QMRA) model to assess *Escherichia coli* contamination risks on raw-consumed lettuce. The QMRA incorporated modules for microbial dynamics at each stage, from production to retail. Baseline scenarios simulated contamination risks from three irrigation sources: untreated greywater, surface water, and groundwater. Treatment scenarios evaluated the efficacy of wetland-based and microfiltration primary systems combined with secondary disinfection methods (ClO2, ozone, and UV). Additionally, sensitivity analyses identified other key risk factors, from soil contamination to post-harvest practices.

Findings revealed that untreated greywater posed significant risks, with 85.06% and 82.10% of cases exceeding *E. coli* safety threshold of 3-LogCFU/gin fresh produce in Spring/Summer and Fall/Winter, respectively. However, integrated primary and secondary treatments reduced microbial loads by over 5-log, meeting international safety standards. In addition to irrigation water, soil contamination presents another major risk factor, particularly with insufficient manure application intervals. Inadequate cold chain control accelerated post-harvest contamination, with lettuce exceeding safe *E. coli* levels within 30 hours post-harvest at ambient temperatures.

This study highlights the feasibility of greywater reuse when supported by effective treatment while emphasizing contamination risks from irrigation, soil, and post-harvest practices. The findings will be used as the scientific basis for the development of potential new legislation in Chile on the safe reuse of greywater in agricultural settings and offering a framework for policies promoting sustainable water management and public health protection.

16. Inactivation of *E. faecium* NRRL B-2354 in whole black pepper by fluidization with hydrogen peroxide vapor

**Daniela Segura1** and Rossana Villa-Rojas1

Affiliation:1 Departmentof Food Science and Technology,University of Nebraska-Lincoln, Lincoln, Nebraska, USA.

Abstract:

In 2024, pepper represented 25% of U.S. spice imports. Despite its low water activity (less than 0.7), which is traditionally considered safe, there have been several *Salmonella*-related outbreaks and recalls over the years. A recent recall in 2024 highlights the need for improved decontamination technologies. While thermal treatments are effective for inactivation, they often degrade spice quality. Gaseous technologies provide an alternative, but most leave chemical residues. Hydrogen peroxide vapor (HPV) is advantageous as it decomposes into water and oxygen without harmful byproducts.

A previous study explored HPV fluidization for *Salmonella* inactivation in black peppercorns, but the efficacy of *Enterococcus faecium* NRRL B-2354 under the same conditions remains unverified. This study evaluated microbial inactivation, hydrogen peroxide residue levels, and quality parameters (water activity, moisture content, and color) before treatment, immediately after treatment, and at 24 and 48 hours post-treatment. At a treatment temperature of 60°C for a dwell time of 60 minutes, *Salmonella* exhibited a 2.94 ± 0.16 log CFU/g reduction after 48 hours, while *E. faecium* showed a significantly greater reduction of 4.63 ± 0.55 log CFU/g, indicating it is not a suitable surrogate under these conditions.

HPV treatment significantly reduced water activity and moisture content, with no further changes during storage. Residual hydrogen peroxide levels decreased over time but did not reach safe levels even after 48 hours. These findings provide insights into HPV’s potential for decontaminating spices and emphasize the need for alternative surrogates in process validation to ensure consumer safety.

**18. Exploring the Impact of Different Dietary Pulse Market Classes on Host Health and the Gut Microbiota**

Jiayu Tang1,2, Lisa Whisenhunt2, Devin J. Rose1,2, Kaustav Majumder1,2, Edward C. Deehan1,2

1Department of Food Science and Technology, University of Nebraska–Lincoln

2Nebraska Food for Health Center, University of Nebraska–Lincoln

Dietary pulses such as dry beans, peas, lentils, and chickpeas are rich in fiber, protein, and polyphenols, offering a promising approach to support host health via gut microbiota modulation. However, current evidence evaluating the impact of pulse consumption is scattered, and market class-specific effects remain underexplored. Emerging in vitro evidence suggests that different dry bean market classes and cultivars elicit distinct gut microbial responses, potentially linked to varied health outcomes. For example, great northern beans selectively increased *Bacteroides* species, while pink beans promoted the growth of butyrate-producing *Faecalibacterium* species. To evaluate these findings in a broader context, we conducted a systematic review of human and preclinical studies examining the impact of specific pulse market classes on gut microbiota composition and health-related biomarkers. The review followed PRISMA guidelines and leveraged AI-based tools (ASReview and SR-Accelerator) to enhance study identification and screening efficiency. Although the literature supports beneficial effects of pulse consumption on cardiovascular and metabolic health—including cholesterol reduction, improved insulin sensitivity, and blood pressure control—few studies differentiated between pulse types or included microbiota endpoints. Our findings highlight a critical gap in understanding how the genetic diversity within pulses translates into functional differences in host physiology and microbial ecology. Our next step will be to conduct a randomized crossover pilot trial to test the microbiota and health effects of 5 different bean market classes in 12 adults.

20. Mucin Degrading Cellulosome Systems in Limousia

Jerry Elorm Akresi1,2, Xinpeng Zhang1, Yuchen Yan1, Yi Xing1, Yanbin Yin1,2

Affiliations: 1 Nebraska Food for Health Center, Department of Food Science and Technology, University of Nebraska-Lincoln, Lincoln, Nebraska, USA; 2 Complex Biosystems, University of Nebraska-Lincoln, Lincoln, Nebraska, USA

Bacteria feeding on plant cell walls have evolved different molecular mechanisms for polysaccharide degradation. One mechanism is the use of the cellulosome-like multienzyme complexes by anaerobic bacteria on their cell surfaces for highly efficient lignocellulose degradation. Proteins in cellulosomes contain the signature protein domains: cohesins and dockerins, which are key structural modules for forming the lego-like multi-enzyme complexes through cohesin-dockerin interactions. CAZymes (carbohydrate active enzymes) such as cellulases, hemicellulases, and other glycoside hydrolases (GHs), dock onto scaffoldin proteins (cohesin-containing structural proteins) through dockerin-cohesin interactions, and together form a highly organized swissknife-like structure (i.e., cellulosome) for synergistically degrading complex carbohydrates such as lignocelluloses and amyloses. Prior cellulosomal-like system research has mostly focused on the degradation of polysaccharides associated with plant cell walls. As such this research was focused on the expansion of the bioinformatics discovery of cellulosome-like systems (i.e., dockerin and cohesin modules) in bacterial MAGs of various environmental microbiomes that could potentially utilize the system for the degradation of non-plant cell wall polysaccharides.

**22. Influence of condensed tannins on in vitro fermentation of maize and potato starches using diverse human microbiomes.**

Valeria Pineda1, Bo Peng2,3, Tricia King2,3, Tieling Zhang2,3, and Andrew K. Benson2,3

1Department of Food Science and Technology, Zamorano University, Honduras

2Department of Food Science and Technology, University of Nebraska

3Nebraska Food for Health Center, University of Nebraska

**Abstract**

Tannins, which are polyphenolic compounds produced by several different food crops, are known to have significant bioactivities, including effects on the human gut microbiome. One family of non-hydrolyzable tannins, the condensed tannins, is also known for strong effects on the gut microbiome, particularly their stimulatory effects on beneficial organisms such as *Faecalibacterium*. Condensed tannins are also recognized for their anti-nutritional properties due to their ability to bind a wide range of proteins as well as starch, reducing their bioavailability to the host. Little is known, however, about the interaction effects of condensed tannins and resistant starches and how they may influence the digestibility of resistant starches by the gut microbiome. In this study, we are using an in vitro digestion/fermentation strategy to examine how condensed tannins influence the bioavailability of resistant starches to degradation by the gut microbiome. The study includes purified resistant starches from maize and potato, as well as whole grains from three different maize lines that vary in amylose and resistant starch composition (K55 parental, K55AE—high amylose, and K55WX—low amylose), alone or in combination with condensed tannins. Digestion and fermentation patterns of these substrates are being examined for interaction effects across 9 diverse human microbiomes. Outcomes being measured include qPCR for *Bifidobacterium* and *Faecalibacterium*, two organisms known to respond to resistant starch (*Bifidobacterium*) and condensed tannins *(Faecalibacterium*). Short-chain fatty acids (SCFAs) are also being measured to determine whether condensed tannins affect metabolic end-product levels of resistant starch fermentation. Ultimately, these interactions will inform sorghum breeding, predicting whether high-amylose, high-condensed tannin sorghum lines would have desirable combinatorial effects on bioavailability and fermentation by the human gut microbiome.

24. Isolation and identification of *Faecalibacterium duncaniae* strains for murine colonization

***Sam Koebernick1,2****, Lucas Townsend2,3, Xiaohan Wu2, Kristin Beede2, Jeff Price2, Amanda Ramer-Tait2,3*

Affiliations:*1Department of Biochemistry, University of Nebraska-Lincoln; 2Department of Food Science and Technology, University of Nebraska-Lincoln; 3Complex Biosystems, University of Nebraska-Lincoln*

The human gut microbiota comprises a diverse range of microbes essential to human health. Changes in gut microbiota composition have also been linked to diseases such as Inflammatory Bowel Disease (IBD). IBD presents commonly as Ulcerative Colitis (UC) and Crohn's Disease (CD) and is characterized by chronic relapsing colonic inflammation. IBD patients often have microbiomes devoid of beneficial bacteria in the *Faecalibacterium* genus. One species, *F. duncaniae*, is known to produce butyrate, a short-chain fatty acid that enhances intestinal barrier function and promotes anti-inflammatory immune responses. Our lab seeks to increase *Faecalibacterium* abundance in IBD microbiomes. We currently work with the *F. duncaniae* type strain A2-165 in our preclinical mouse model but have found that it does not persist in mice harboring human microbiomesdevoid of *Faecalibacterium*. However, we have identified a human fecal microbiome sample that naturally contains *F. duncaniae,* and this strain persisted in mice for up to 28 days, suggesting that it can colonize mice. This study aims to isolate and identify the strain of *F. duncaniae* from the fecal sample for use in future mouse studies. We are screening isolates based on colony morphology, cell morphology, aerobic tolerance. We are also isolating DNA and performing qPCR tests for *F. duncaniae.* Whole genome sequencing will be performed on isolates identified as *F. duncaniae* via qPCR, and eventually these strains will be tested for their ability to colonize mice. Currently, we have not identified any candidate isolates but are refining our protocol for more precise screening.

26. **Background Microflora and Characterization of Mold Species in**

**Buckwheat Flour**

**1Chenfengjia Wang,** 1La Fontaine Bahatsi, 1Andreia Bianchini, 1Jayne Stratton

1Department of food Science and Technology, University of Nebraska Lincoln, Nebraska, USA

Abstract

Grains including rice, wheat, and corn have been used as major staple food and source of daily nutrients for humans for several thousands of years. However, global population growth has led the food industry to use other alternative crops, including buckwheat, to meet increased food demand. Buckwheat is a traditional crop that has gained popularity due to its nutritional value and gluten-free nature. However, like other grains, buckwheat is susceptible to microbial contamination, including mycotoxin-producing mold species, during processing and storage. This study aimed to conduct a general microbial profiling of buckwheat flour to assess their quality and characterize isolated mold species. Buckwheat flour samples (n=20) were enumerated using 3M PetrifilmTM and culture-based media followed by incubation at appropriate temperature and time. Microbial counts of 6.3 logs, 4.9 logs, and 4.8 logs were observed for aerobic plate count (APC), *Enterobacteriaceae* (*EB*), and molds, respectively. Mold growth was supported by DRBC and strains were purified/identified using PDA, CYA, MEA, and DG18. Mold identification was performed based on the phenotypic characteristics, including colony diameter size, presence or absence of septa, and maturity of spores. The most predominant types of molds identified were xerophilic and zygomycetes, with *Aspergillus* identified in one sample. This study indicates that microbial contamination can occur during the processing of buckwheat from groats to flour, stressing the need for effective mitigation strategies such as proper storage, processing, and packaging, to ensure buckwheat flour quality and consumer safety.

Poster

**28. Creating an *in vitro* model to evaluate the potential anti-adipogenic activity of *Gordonibacter***

**and *Lactobacillus* species**

**Elizabeth Andersen1,2**, David Gomez Quintero2, Ashley Toney2, Kristin Beede2, Jeff Price2, Robert Schmaltz2, Amanda E. Ramer-Tait2

Affiliations: ¹Microbiology Program and Department of Biochemistry, University of Nebraska, Lincoln, NE; ²Department of Food Science and Technology, University of Nebraska, Lincoln, NE

More than 40% of adults in the United States have obesity, and obesity rates are rising. Previous studies have shown that people with obesity possess a distinct gut microbial composition compared to healthy individuals. Therefore, novel approaches to treating obesity have focused on modifying the gut microbiome. Probiotics have been shown to mitigate obesity-related symptoms such as adipose mass accumulation, elevated blood glucose levels, and increased bodyweight. Studies from our lab have shown that mice receiving the gut bacterium *Gordonibacter urolithinfaciens* (*G. uro*) gained less weight compared to controls in a diet- induced obesity mouse model*.* Additionally, *G. uro* treatment increased the abundance of

*Lactobacillus* species and decreased adipose tissue accumulation compared to the control treatment. These results suggest a potentially beneficial relationship between *G. uro* and the *Lactobacillus* species in the mouse gut microbiome. To properly assess these potential anti- adipogenic effects, we are developing an *in vitro* cell culture model using the 3T3-L1 preadipocyte cell line and bacterial culture supernatants. First, we will optimize the dosage of supernatants administered to the preadipocytes to ensure cells viability. Next, the preadipocytes will be treated with supernatants from various co-culture combinations of *G. uro* and the *Lactobacillus* species we observed providing benefits in during our previous studies.

Differentiation will be assessed through imaging and optical density measurements following Oil Red O staining. The results from this systematic *in vitro* screening will help guide the design of future mouse studies to identify the specific combinations of *G. uro* and *Lactobacillus* that provide anti-adipogenic effects.

30. Comparative Analysis of Six Commercial Sesame ELISA Methods

**Janine L. Merkle1**, Shyamali Jayasena1, and Joseph L. Baumert1

Affiliations: 1University of Nebraska-Lincoln, Lincoln, Nebraska USA

The information on commercial testing methods for sesame as an allergen is scarce. Six commercial sesame ELISAs were evaluated on their efficacy on recovering sesame flour spiked into buffer and sesame flour, extract, and seeds spiked into crackers.

10, 50, and 100 ppm sesame flour spikes prepared in buffer were evaluated using Veratox (Neogen), R-Biopharm, Romer, Morinaga, BioFront, and 3M (Neogen) sesame ELISAs. 10, 50 and 100 ppm sesame flour and sesame extract spikes were spiked into crackers. A sesame seed was spiked into a 15 g homogenized or whole cracker sample before homogenization with either a benchtop blender or freezer. The R-Biopharm and BioFront Sesame ELISAs were used to evaluate these samples. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and Western Blots were conducted on all six extracts.

Recovery of sesame varied among the six kits. The R-Biopharm and BioFront kits were the most consistent in recovering sesame from the buffer spikes (~90% recovery). For the sesame extract and flour samples, R-Biopharm and BioFront had average recoveries of 102% and 72%, respectively, and 81% and 146%, respectively. Spiking a sesame seed into homogenized crackers was more consistent than spiking into cracker pieces. With the exception of the 3M kit, the extracted protein profiles only differed in the amount of soluble protein extracted. The conjugated antibodies of the six kits differed in the proteins recognized. Sesame ELISA kits differ in recovery and quantification capacity across different spiking materials and type of sesame residue used for spiking, as do the antibody specificities.

32. nf-core/dbcan: A Comprehensive Pipeline for CAZyme Analysis in Metagenomic Data

Xinpeng Zhang1, Haidong Yi2, Jinfang Zheng3, Yanbin Yin1

Affiliations: 1University of Nebraska-Lincoln, Lincoln, Nebraska, USA; 2 St. Jude Children's Research Hospital's High Performance Research Cluster, Memphis, TN; 3 Zhejiang Lab, China.

The advancement of sequencing technologies and decreasing costs have significantly enhanced the accessibility of metagenomic sequencing in microbiome research. Carbohydrate active enzyme (CAZyme) is the predominant component in the microbiome but remains hindered by a lack of standardized analytical methods. Here, we propose a complete nextflow-based computational process from raw reads to downstream CAZyme analysis. Our pipeline establishes a standardized protocol for CAZyme annotation, promoting efficiency and enabling researchers to rapidly explore the relationships between CAZymes and the microbiome.

34. Toxin production in *Conocybe apala*

Qinwen Zheng, Heather Hallen-Adams

Conocybe apala, also referred to as the milky cone cap, is a common lawn mushroom known to produce low levels of phallotoxins. Unlike the related amatoxins—highly toxic peptides found in several Amanita, Galerina, Lepiota, and Conocybe species—phallotoxins typically do not cause severe poisoning in mammals because they are poorly absorbed in the digestive tract. Nonetheless, investigating the genomic basis of phallotoxin production offers valuable insights into the broader context of fungal toxin biosynthesis and evolution. In this project, total genomic DNA was extracted from C. apala using standard eukaryotic protocols to ensure high yield and purity. The DNA was then subjected to Illumina-based whole genome sequencing, generating sufficient coverage for the identification of potential toxin biosynthesis gene clusters.

Our primary focus was on putative secondary metabolite genes, particularly MSDIN (amatoxin and phallotoxin) gene families and prolyl-oligopeptidases (e.g., POPB), which are known to encode or process cyclic peptide toxins in other fungi. To explore possible evolutionary relationships, these sequences were compared to genomes of other amatoxin- and phallotoxin-producing species, highlighting patterns that may indicate horizontal gene transfer or convergent evolution. Early analyses suggest that C. apala may share key biosynthetic features with its toxic relatives, thereby raising intriguing questions about how toxin genes evolve and spread within the fungal kingdom. By clarifying the genetic and molecular underpinnings of phallotoxin production, this study contributes to our growing understanding of fungal secondary metabolism and the evolutionary dynamics of toxin diversity.

### **Afternoon Keynote, 4:00-5:00, room 277**

### Food Ingredient Innovations to meet changing consumer needs and government regulations.

John Sweeney, Director, Food Technology, Gräńde Custom Ingredients Group

ABSTRACT

Delivering ingredient solutions that deliver health or functional benefits with a clean label, at an economic price is a challenge for large ingredient companies and start up entrepreneurs. Ingredient companies need to innovate in order to add value to agricultural ingredients, stay competitive with changing consumer trends and adjust to changing regulations and processing technologies.

Many important questions must be answered to justify an investment. Is an ingredient new to the world or new to a geography or product category? What benefits does it bring and what value must be created to justify the cost. What other ingredients will it compete with? What capacity is needed to supply customers?

 The ingredient development process will be reviewed, and examples of  ingredient innovation to meet changing consumer needs, regulations and adoption of new technologies will be discussed, providing useful context for future UNL Food Science innovators.

**Videos – running throughout day in room 111**

**EatHealthier: A Digital Solution for Personalized Nutrition Guidance**

**Wensheng Ding**

In an era where diet-related health concerns are on the rise, leveraging technology to promote healthier eating habits is essential. **EatHealthier** is an innovative mobile application designed to help individuals make informed food choices based on their dietary needs, preferences, and health goals. This app integrates evidence-based nutrition science with user-friendly technology, offering personalized meal recommendations, real-time food analysis, and behavior-tracking features.

EatHealthier serves three primary functions: **(1) Daily Nutrition Tracking**, allowing users to log their meals, monitor nutrient intake, and receive personalized feedback to support long-term dietary improvements; **(2) Research Study Integration**, where researchers can collect anonymized dietary data to study trends, assess interventions, and analyze the impact of food choices on health outcomes; and **(3) Diabetes Management Support**, offering specialized tools for individuals with diabetes, including blood sugar tracking, carbohydrate counting, and meal recommendations tailored to glycemic control.

This presentation will discuss the app's development process, its potential impact on public health, and preliminary user feedback. As a graduate researcher in food science, my aim is to explore how digital nutrition interventions can bridge the gap between scientific knowledge and everyday eating behaviors. EatHealthier represents a step forward in making personalized nutrition accessible, scalable, and effective in fostering long-term dietary improvements.

**Introduction to starch-based aerogel formation process through supercritical carbon dioxide drying technology and its applications**

**Yidong Jiang1, Ozan Ciftci1**

**1Department of Food Science and Technology, University of Nebraska-Lincoln, Lincoln, Nebraska USA**

Aerogels are a synthetic porous, solid ultralight material delivered from a gel, which comprises a network of interconnected nanostructures. The process of making starch-based aerogels involves two steps: the formation of starch-based hydrogels and drying technology to make them as aerogels. During the formation of starch-based hydrogels, different types of starch are utilized: maize starch, potato starch, wheat starch. To enhance the mechanical strength, starch is always crosslinked via physical or chemical bonds. One of the major challenges to fabricate aerogels is the elimination of liquid solvent from the wet gel (hydrogel). Drying techniques are normally used during this process such as freeze-drying, air-drying and supercritical carbon dioxide drying. Among those methods, supercritical carbon dioxide drying technology is a simple and green method which is the most common and efficient way to fabricate starch aerogels. The key benefit of supercritical carbon dioxide drying technology is that it eliminates the use of toxic chemicals throughout the process. When the carbon dioxide is heated and pressurized above its critical points, which is 31.1℃ and 7.38MPa, carbon dioxide will enter the supercritical state and possess the properties of both gas and liquid, allowing it to penetrate materials efficiently, making aerogels porous structure which are ideal drug carrier materials with good drug loading and releasing mechanisms.

**(Video)**

Best Practices for Foreign Material Control and Management in Poultry Processing

**Molly Rosenthal**

Physical hazards or foreign material are common in food processing processes such as poultry processing. Processing steps such as grinding, improper use equipment or failure to follow procedure can lead to foreign material to contaminate poultry products. As normal practices can lead to contamination of product it is important to have mitigation steps in place to lower the risk of physical hazards. Some mitigation steps are simple such as following good manufacturing practices or monitoring the conditions and accountability of tools being used. Metal detection and x-ray devices are also helpful in poultry processes as most of the equipment used in poultry processing facilities are made of metal. Perhaps one of the greatest opportunities of foreign material is the use of rubber, plastic, or glass in the processing facilities because these items cannot be picked up by a metal detector or x-ray machine. Understanding the risk of each possible foreign material source is essential for establishing monitoring procedures to control physical hazards.

**Bioinformatic Trends in Glycan Substrate Inference via Microbiome Genomics**

**Yuchen Yan**1 & Yanbin Yin1

Affiliations: 1Nebraska Food for Health Center, Department of Food Science and Technology, University of Nebraska - Lincoln, Lincoln, NE, USA

Carbohydrates represent a significant part of the human diet and serve as primary energy sources for the gut microbiome. The composition of gut microbiota is largely influenced by both the type and quantity of dietary polysaccharides consumed. Exploring the genomic features related to carbohydrate utilization within the microbiome can provide valuable insights into how dietary preferences shape microbiome structure and influence host-diet-microbiome interactions. Within the microbiome, carbohydrate-active enzymes (CAZymes) and their neighboring genes form CAZyme gene clusters (CGCs), which specialize in degrading various glycan substrates. Experimentally validated CGCs, known as polysaccharide utilization loci (PULs), have characterized glycan substrates. Current computational approaches to predicting glycan substrates of CGCs typically rely on sequence similarity to the known PULs. The ongoing research aims to infer glycan substrates through unsupervised CGC classification and to provide comprehensive bioinformatic resources. Understanding which dietary glycans gut microbes specifically utilize will clarify their roles in host health and support the development of personalized nutrition and dietary therapies for treating human metabolic disorders.

**TED Talks – running throughout day in room 111**

*The Secret Language of Food: How Your Gut Talks Back***Bo Peng1**

Affiliations: **1**University of Nebraska-Lincoln, Lincoln, Nebraska USA

The gut microbiome, an intricate ecosystem of trillions of microbes, plays a crucial role in digestion, metabolism, immunity, and even mental health. However, the modern diet—high in processed foods and low in fiber—has disrupted this delicate balance, leading to widespread health issues such as inflammation, obesity, and gut-related disorders.

This talk explores how dietary choices influence the microbiome and, in turn, overall well-being. Using relatable stories and scientific insights, we examine the profound impact of fiber-rich foods, such as whole grains, fruits, and fermented products, in shaping microbial diversity and promoting health. The concept of "food as information" is introduced, demonstrating how nutrients interact with gut bacteria to regulate bodily functions, from energy production to neurotransmitter synthesis.

The take-home message is clear: by making simple, informed dietary changes, we can cultivate a healthier gut microbiome and, consequently, a healthier life. Attendees will leave with practical, science-backed strategies for enhancing gut health—starting with their next meal. This TED Talk aims to demystify the science of the gut microbiome and inspire a shift in the way we view food: not just as sustenance, but as a powerful tool for well-being.

**“TED-Tech” Talk**

**The science behind your grocery cart: How food science shapes what you buy**

**Liya MO**

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Food shopping is a routine activity, yet few consumers realize the extent to which food science influences their choices. From product formulation to packaging and marketing, scientific innovation shapes nearly every item in a grocery store. This talk explores how food science affects what we see, buy, and consume, with a focus on the differences between traditional supermarkets and health-focused grocery stores. The talk will examine the role of food processing in extending shelf life and enhancing texture, the impact of labeling strategies on consumer perceptions, and the psychology behind supermarket layouts. By highlighting real-world examples, this presentation will challenge common misconceptions and encourage critical thinking about food choices. Attendees will gain a deeper appreciation for the science behind their grocery cart and leave with a more informed perspective on navigating the modern food landscape.

“TED-Tech” Talk: Regulation of GMO crops in the United States food supply

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Genetically modified organisms (GMOs) are plants, animals, and microorganisms that have had their DNA altered through the use of bioengineering techniques. As of January 1st, 2022, food products containing bioengineered food ingredients that “contain detectable genetic material that has been modified through certain lab techniques and cannot be created through conventional breeding or found in nature”, as defined by the U.S. FDA, must be labelled according to new regulations. Such biotechnology has been in use and regulated in combination by the U.S. Food and Drug Administration, U.S. Department of Agriculture, and U.S. Environmental Protection Agency since 1986. This talk will explain what aspects of GMOs are regulated and by which agency, as well as examining the level of care and rigor committed to preserving human and environmental health while supporting advancements in food and agricultural technology.

1. [↑](#footnote-ref-1)