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Non-targeted Analysis of Virgin Coconut Oil Adulteration using High-field and Low-field ${}^1\!\mathrm{H}$ NMR

Ruiya Bao¹, Fenfen Tang¹, Cam Rich¹, Emmanuel Hatzakis^{1,2} ¹ Department of Food Science and Technology, The Ohio State University, Columbus, OH 43210, USA for Health Discovery Theme, The Ohio State University, Columbus, OH 43210, USA bao.320@buckeyemail.osu.edu

Coconut oil is a product obtained from the fruit of coconut palm trees. It gained popularity recently due to its unique aroma and certain properties, such as the higher melting point which makes it solid at room temperature. The two main extraction methods used in the production of coconut oil are wet and dry methods. Virgin coconut oil (VCO) is produced by the wet method, which requires higher cost and has lower yields, but leads to a product with higher value. Refined coconut oil (RCO) relies on the dry process which has a lower cost and is subject to more intensive processing, which results in a lower value. Therefore, given the difference in prices and similarity in composition, VCO is subject to adulteration by RCO. However, only a few studies have focused on its authentication, leading to the urgent need for rapid and reliable detection methods.

Nuclear magnetic resonance (NMR) spectroscopy has been previously applied for food authentication studies. It is reproducible, non-destructive, and requires minimal sample preparation. High-field (HF) NMR provides higher spectral resolution and sensitivity, while lowfield (LF) NMR results in lower resolution and sensitivity. However, LF NMR is also reproducible and has major advantages—low cost and user friendly, so it fits well in an industrial environment. In this study, VCO, RCO, and oil blends were analyzed with HF and LF NMR. Both enabled the differentiation of VCO and RCO when coupled with chemometrics techniques such as Principal Component Analysis and Partial Least Square-Discriminant Analysis.

In conclusion, ¹H NMR combined with chemometrics approach has the potential to be a powerful tool to differentiate between VCO and RCO, as well as detect RCO adulteration in VCO products. This can further improve our arsenal of powerful analytical methods for the quality control of coconut oil.

Identification of Volatile Compounds that Impact Consumer Liking of Roasted Hybrid American Hazelnuts: Part A - Nontargeted and Targeted GC/MS Flavoromics

Megan Booth¹, Devin Peterson¹

¹ Department of Food Science and Technology, 317 Parker Food Science & Technology Building, The Ohio State University, 2015 Fyffe Rd., Columbus, OH 43210 <u>peterson.892@osu.edu</u>

American hazelnuts (Corylus americana) are being developed by breeding programs in the Upper Midwest for the purpose to enhance ecological and economic sustainability. Locally grown hazelnuts provide an environmentally beneficial crop and US consumers with healthy, local food rich in monounsaturated fatty acids, vitamin E, fiber, protein, and antioxidants. Beyond improving agronomic traits (e.g., yield), breeding efforts have also sought to improve flavor quality, a key driver of food choice. However, this progress has been limited by a lack of information regarding the flavor of current hybrid varieties and targets for improving consumer liking. Therefore, the overall aim of this project was to identify key aroma compounds that impact consumer liking in American hazelnuts. Thirty-four aroma compounds in a top-liked hybrid variety were identified using gas chromatography/mass spectrometry/olfactometry and then used for targeted GC/QQQ-MS chemical profiling. In parallel untargeted GC/QTOF-MS chemical profiling analysis was also conducted. Both chemical profiles were modeled against consumer liking scores by orthogonal partial least squares (OPLS). By relating aroma liking scores to volatile chemical data through orthogonal partial least squares regression (OPLS), predictive models were constructed with good fit ($R^2Y \ge 0.98$) and predictive ability ($Q^2 \ge 0.67$, RMSE_{CV} ≤ 0.26 on 9-point liking scale). Thirteen volatile compounds that were highly correlated to sensory results were selected as putative markers of aroma liking, of which 3 are currently level 4 unknowns. These compounds will be investigated in future work to validate their sensory relevance. This work will provide new understanding of the sensory attributes and chemistry driving consumer liking in roasted hybrid hazelnuts and facilitate the development of breeding and post-harvest processing strategies for flavor optimization.

Pharmacokinetics of tomato steroidal alkaloids in healthy adults following consumption of two doses of tomato juice

Daniel Do¹, Maria Sholola¹, Jessica Cooperstone^{1,2}

¹Department of Food Science and Technology, The Ohio State University, United States ²Department of Horticulture and Crop Science, The Ohio State University, United States <u>do.226@osu.edu</u>

Steroidal alkaloids derived from tomatoes are gaining traction as a potentially health beneficial class of phytochemicals based on a growing number of in vitro and in vivo studies. Prior to investigating the bioactivity of tomato steroidal alkaloids (TSAs) in humans, understanding their pharmacokinetic behavior after absorption is important. The objective of this study is to elucidate the pharmacokinetics, bioavailability, and metabolism of TSAs following a single tomato juice containing meal. Healthy subjects (n = 11, 6M/5F) participated in a randomized crossover trial where they consumed 94 g juice (low dose) and 505 g juice (high dose) with a two-week washout period in between doses. Blood samples were collected at 11 time points over 12-hours following test meal consumption, and plasma was isolated to be analyzed using UHPLC-QTOF-MS. Alpha-tomatine and tomatidine, two of the most studied TSAs in literature and those with existing authentic standards, were found to be present in plasma from both the low and high doses indicating absorption. Bioavailability for alpha-tomatine was estimated using baseline-corrected area under the curve (AUC) values (low dose: 0.50 +/- 0.11 (nmol·h)/L, high dose: 4.74 +/- 1.33 (nmol·h)/L). The concentration over time curve for tomatidine revealed three distinct peaks within the 12-hour collection period potentially indicating multiple metabolic events of glycosylated TSAs that contribute to its observed absorption pattern. MS/MS fragmentation was used to annotate additional analytes where authentic standards are not available, revealing the presence of hydroxylated and sulfonated metabolites not endogenously present in tomato suggesting phase I and phase II metabolism. This study reports the first pharmacokinetic data for TSAs which agree with previous observations of their presence in biological fluid and provides valuable data to understand their metabolic fate after consumption of a tomato containing meal.

Diets with carbohydrate intake below recommendations and high in fat are associated with increased prevalence of metabolic syndrome

Dakota Dustin, B.S¹; Corina Kowalski²; Meredith Salesses²; Acree McDowell, B.S²; Penny Kris-Etherton, PhD, RD³; Martha Belury, RD, PhD¹; LuAnn Johnson, M.S⁴; Zach Conrad, PhD, MPH²

¹Program of Human Nutrition, Department of Human Sciences, The Ohio State University, Columbus, OH ²Department of Kinesiology, William & Mary, Williamsburg, VA ³Department of Nutritional Sciences, Pennsylvania State University, University Park, PA ⁴Independent Contractor, Warren, MN dustin.8@buckeyemail.osu.edu

Background: Over one-third of adults in the United States have metabolic syndrome, and many report using popular diets for weight loss and other health benefits. Despite their popularity, there is a lack of consistent evidence supporting the long term effectiveness of diets with carbohydrate intake below recommendations. Not accounting for differences in fatty acid classes of diets with carbohydrate intake below recommendations may be a reason for inconsistent findings.

Objective: This study evaluated the association between diets with carbohydrate intake below recommendations and metabolic syndrome stratified by fat quantity and fatty acid classes in a nationally representative sample of U.S adults.

Design: This cross-sectional study acquired data on food and nutrient intake and markers of metabolic syndrome from respondents in the National Health and Nutrition Examination Survey (NHANES) 1999-2018.

Participants/setting: This study included 19,078 respondents who were ≥20 y, had reliable and complete data on food and nutrient intake and markers of metabolic syndrome; and were not pregnant or breastfeeding.

Main outcome measures: The main outcome was prevalent metabolic syndrome.

Statistical analyses performed: Usual dietary intake was estimated using the National Cancer Institute's usual intake methodology. Multivariable logistic regression models assessed the relative odds of prevalent metabolic syndrome between those that consumed diets with carbohydrate intake below recommendations and those that met macronutrient recommendations.

Results: Compared to individuals that met all macronutrient recommendations, those that consumed a diet with carbohydrate intake below recommendations were 1.110 (95%CI: 1.103-1.117) times more likely to have metabolic syndrome compared to those who met all DRI macronutrient recommendations (P<0.001).

Conclusions: The likelihood of prevalent metabolic syndrome was moderately higher (11%) among individuals that consumed diets with carbohydrate intake below recommendations compared to individuals that met all macronutrient recommendations. High intake of fat of any class was associated with increased likelihood of metabolic syndrome in those consuming a diet below carbohydrate recommendations.

Chemical drivers of vanilla flavor liking

Paola Forero¹, Devin Peterson¹

¹ Department of Food Science and Technology, 317 Parker Food Science & Technology Building, The Ohio State University, 2015 Fyffe Rd., Columbus, OH 43210 <u>peterson.892@osu.edu</u>

Vanilla owes its popularity to its highly desirable characteristic flavor and is an established staple ingredient all over the world. Vanilla beans are the fruit of a climbing orchid that requires extensive care and manual labor to produce. After development on the vine for 9 to 10 months, the beans are harvested and subjected to a lengthy curing process of up to 9 months that enables the generation of the highly prized flavor. Therefore, several quick curing methods have been developed; however, the flavor quality does not match those of traditionally cured beans. Hence, the complexity of vanilla flavor opens an opportunity for further discovery by identifying flavor actives to understand differences in the entire chemical composition and discover drivers of vanilla liking. This work adopted an innovative research approach named flavoromics to identify new compounds that impact vanilla flavor perception and vanilla flavor liking by the obtention of highly predictive models followed by selection and characterization of key markers. Understanding the chemical drivers of vanilla liking and their impact on flavor perception will improve our ability to tailor vanilla quality and value. Further, these findings will give tools to the entire vanilla supply chain (from farmers to manufacturing) including strategies for breeding and harvesting to develop sustainable high-quality products to increase consumer acceptability by monitoring the key compounds.

Identification of Non-volatile Compounds that Impact Consumer Liking of Roasted Hybrid American Hazelnuts: Part B - Untargeted LC/MS flavoromics

Zoey Fu¹, Devin Peterson¹

¹ Department of Food Science and Technology, 317 Parker Food Science & Technology Building, The Ohio State University, 2015 Fyffe Rd., Columbus, OH 43210 <u>peterson.892@osu.edu</u>

The non-volatile compounds that impact the acceptability of 14 roasted hazelnut pastes were investigated by untargeted LC/MS flavoromics analysis. Chemical profiles for the hazelnuts were modeled against consumer liking scores by orthogonal partial least squares (OPLS) with good fit ($R^2Y \ge 0.99$) and predictive ability ($Q^2 \ge 0.99$). Twelve non-volatile compounds, among which six negatively correlated and six positively correlated to sensory results were selected as putative markers of flavor liking. All selected compounds were subsequently isolated and purified by multi-dimensional preparative LC-MS to >90% purity and validated for their sensory relevance. Sensory characteristics of negatively correlated compounds were identified as bitter and astringent. The threshold value of each compound was determined to be within the corresponding concentration range in hybrid hazelnuts, indicating the contribution of these compounds to the bitter and astringent perception of hybrid hazelnuts and the overall negative impact on flavor liking. Current work is on-going to define the sensory relevance of the positively correlated compounds on nut liking. This work will provide new understanding of the impact of nonvolatile compounds driving consumer liking in roasted hybrid hazelnuts and facilitate the development of breeding and post-harvest processing strategies for flavor optimization.

Characterization of intestinal immune responses to coccidiosis in chicken

Shaimaa K. Hamad¹, Shuja Majeed¹, Ali Nazmi^{1,2} ¹Department of Animal Sciences, The Ohio State University, Wooster, OH 44691 USA ²Food for Health Discovery Theme, The Ohio State University, Columbus, OH, USA <u>hamad.70@osu.edu</u>

Coccidiosis is one of the most important diseases that threatens the poultry industry. It is an economically dangerous disease caused by different species of Eimeria parasites. Eimeria infection leads to intestinal damage, low feed consumption, poor growth, and subsequently high rates of mortality. Thus, the objective of this study is to characterize the intestinal intraepithelial lymphocytes (IELs) during the Eimeria infection. In the current study, at 14 day of age, SPF chicks were divided into 3 groups (n=30 each): non-infected control, and 2 infected groups (low-dose and high-dose). The low-dose group was challenged orally with 10000 oocysts/ml per bird, while the high-dose group was challenged with 20000 oocysts/ml per bird of *Eimeria acervulina*. A single cell suspension was prepared from duodenums collected from 8 bird/group at 2-days post-infection (dpi), 7dpi and 14dpi. Cells were stained with antibody cocktail and acquired with a flow cytometry. The number of IEL subpopulations including, TCR $\gamma\delta$, TCR β , TCR β ⁺CD4⁺, TCR β ⁺CD4⁺, TCR β ⁺CD8 α ⁺, TCR β ⁺CD8 $\alpha\alpha$ ⁺, and iCD8 α were significantly increased in the infected groups at 14dpi compared control group. However, there was no difference among groups at 2dpi and 7dpi. In addition, more challenge experiments with other Eimeria species will be tested.

Keywords: Coccidiosis, Eimeria, flow cytometry, immune response, IELs.

Determining a method to monitor the effect of a growth substrate on bacteria found in the gut

Jennifer Janovick¹, Justin North², Seema Nath³, Joshua Blakeslee³, & Emmanuel Hatzakis¹

¹Department of Food Science and Technology, The Ohio State University, USA, Janovick.3@buckeyemail.osu.edu ²Department of Microbiology, The Ohio State University, USA ³Department of Horticulture and Crop Science, The Ohio State University, USA

Prebiotics are non-digestible compounds that stimulate the growth of beneficial bacteria in the gut and provide benefits to the host¹. Some of these benefits include, but are not limited to, inhibiting the growth of pathogens² and are largely due to the production of short chain fatty acids (SCFA). Because of these benefits, it is important to investigate compounds that could act as prebiotics and understand their mechanism of action. In vitro experiments which utilize a single microorganism are important to elucidate the bacteria-prebiotics interactions at the molecular level. Those experiments are often conducted for 24 hours^{3,4}, which can be problematic because bacterial growth rates and the optimal fermentation times may differ. Given that metabolite concentrations can vary between different growth stages, ensuring bacteria are assayed at the appropriate time is a crucial step when performing metabolomics. Additionally, it can be difficult to culture gut bacteria under anaerobic conditions and there are currently no well-established protocols. Because of this, we aimed to develop a method to yield growth curves and optimal growth conditions for our bacterium of interest that will allow us to choose the most practical fermentation time to examine the effect of a potential growth substrate on the growth and metabolism of certain bacteria. This method allowed us to optimize the media composition and determine the optimal fermentation time for our bacterium of interest, Lactobacillus *gasseri*. We will perform a pilot NMR based metabolomics experiment examining the metabolites produced by bacteria after being treated with various carbohydrates in addition to a SCFA analysis. This will allow us to better understand the growth and metabolism of a bacterium after it has been treated with a growth substrate that could potentially act as a prebiotic.

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Investigation of pectin interactions in blueberry and galacto-oligosaccharide confections

Jennifer Jordan, Yael Vodovotz²

¹ Department of Food Science and Technology, The Ohio State University, United States ² Department of Food Science and Technology, The Ohio State University, United States, <u>jordan.1286@osu.edu</u>

Confections rich in blueberries and galacto-oligosaccharides (GOS) were developed as a delivery vehicle for a future dietary intervention trial. Pectin has been shown to interact individually with GOS and anthocyanins, yet its effect on the combined ingredients in a whole food has not been studied. It was hypothesized pectin-GOS-anthocyanin interaction will improve anthocyanin stability and texture qualities in a confection made from whole fruit. The objectives of the study were to 1) determine blueberry anthocyanin stability and release rate over a 2-week storage period 2) assess texture properties, and 3) describe physical differences in confection's matrix. Two GOS formulations were prepared at 0% and 1% of high-methoxy (HM) pectin. Another confection designed with sucrose and 1% HM pectin and served as a comparison between saccharide and pectin ingredient effects. Prepared confections were separately stored at 4°C in light protective bags. Analysis was completed on days 1, 8, and 15. Simulated gastric fluid dissolution was performed to measure the impact of the physical matrix on anthocyanin release. High pressure liquid chromatography evaluated the bioactive retention in the different matrices. Physical properties including texture (Instron Testing Machine) and freezable and unfreezable water (Differential Scanning Calorimeter) were assessed. Pectin increased anthocyanin stability in a 2-week period and decreased release rate *in vitro* compared to confections without pectin. This is likely due to the noncovalent interactions between anthocyanins and soluble components in pectin. The slower release rate is predicted to enable intact anthocyanins to reach the colon for fermentation. The pectin and GOS combination increased hardness and decreased adhesiveness compared to confections without pectin. The weaker matrix in GOS-pectin confections resulted in less unfreezable water compared to sucrose-pectin confections. Future clinical trials will use confections formulated with HM pectin to determine the synergistic role of the ingredients on the gut-brain relationship.

Using metabolomics to study how novel processing technologies alter the composition of mango juice and orange juice

Ziqi Li¹, Jin Hong Mok², Sudhir K Sastry^{1,2}, Rachel E Kopec^{1,3,4}

¹Department of Food Science and Technolog ²Department of Food, Agricultural and Biological Engineering ³Interdisciplinary Nutrition Graduate Program, Department of Human Sciences ⁴Foods for Health Discovery Theme, The Ohio State University, Columbus, Ohio, USA Li.11396@buckeyemail.osu.edu

Background: The effects of novel processing technologies on food metabolome profiles remains understudied, and could help to identify how these technologies better conserve a number of favorable attributes of these food products relative to traditional processing techniques, to provide a superior product. To use metabolomics to study the effects of shear stress (SS) and shear stress + moderate electric field (SS+MEF) treatments on the composition of mango juice and orange.

Methods: Mango juice and orange juice were treated with either SS or SS+MEF at 3 temperatures (27°C, 40°C and 50°C) over 10 min. Each condition was tested in triplicate. Samples were vortexed and extracted using a bi-phasic liquid-liquid approach. The aqueous phase was separated using HILIC and C18 columns, interfaced with an Agilent 6545 quadrupole time-of-flight mass spectrometer with electrospray ionization (operated in positive mode for both HILIC and C18, and in negative mode for C18), over 50-1700 m/z, and iterative fragmentation used to produce MS2 spectra. Features which did not meet quality control cutoffs were removed from the datasets. A variety of statistical approaches including t-test and linear modeling were used to compare the most extreme treatments, and to better elucidate the roles of time, temperature, and treatment type on metabolome changes. Identities of metabolites of greatest difference between treatments were further assessed via FooDB, GNPS and METLIN.

Results and Conclusions: A total of 681 metabolites were observed in the treated mango juice and 1047 metabolites were observed in the treated in orange juice. The greatest difference between SS and SS+MEF was observed under the most extreme treatments (i.e. at 50°C for 10 min). Higher intensities of (S)-abscisic acid was found in SS-treated mango juice relative to SS+MEF. In orange juice, the SS group had lower intensities of pyridoxine relative to MEF+SS treatment.

Chicken immune responses to wooden breast myopathy

Shuja Majeed¹, Shaimaa K. Hamad¹, Ali Nazmi^{1,2} ¹Department of Animal Sciences, The Ohio State University, Wooster, OH 44691 USA ²Food for Health Discovery Theme, The Ohio State University, Columbus, OH, USA, Majeed.34@osu.edu

The wooden breast myopathy is one of the global poultry industry critical issues that impacts the fast growing broiler chickens and causes condemnations and consumer dissatisfaction and leads to loss of up to \$200 million per year. It can reduce the nutritional quality of meat through higher levels of fat, collagen, moisture, and lower levels of protein and ash. Additionally, the wooden breast causes less water-holding capacity and undesirable textural changes in the breast meat tissue. The wooden breast can be diagnosed by both gross and microscopic lesions. The gross lesions are observed after three weeks, while the microscopic lesions can be observed as low as 1-2 weeks. As for the gross lesions, it can be observed as hard, swollen, and pale breast muscle tissue accompanied by edema and hemorrhages occasionally. While microscopic lesions can be detected through muscle fiber degeneration, regeneration, necrosis, lymphocytic vasculitis, lipidosis, and fibrosis. Although various metabolic and live production factors are often associated with wooden breast, the exact etiology is not well known yet. Previous studies have reported that a wooden breast causes lymphocyte infiltration in the breast and increases total intraepithelial lymphocytes in the ileum. However, the exact immune cells and their role in the progression of wooden breast is not studied yet. The objective of this proposed research is to characterize immune-cell subpopulations in the local muscles and in the intestinal mucosa of the affected birds to understand their immunological role. In addition, we are interested in elucidation of the metabolic functions for some intraepithelial lymphocytes that might be associated with wooden breast myopathy. This research might help to develop preventive strategies that could mitigate wooden breast disease in chickens.

Integrating genomics and multi-platform metabolomics enables metabolite QTL detection in breeding-relevant apple germplasm

Emma A. Bilbrey¹, Kathryn Williamson², Emmanuel Hatzakis², Diane Doud Miller³, Jonathan Fresnedo-Ramírez³, and Jessica L. Cooperstone^{1,2,}

¹Department of Horticulture and Crop Science, The Ohio State University, Columbus, OH, USA

²Department of Food Science and Technology, The Ohio State University, Columbus, OH, USA ³Department of Horticulture and Crop Science, The Ohio State University, Wooster, OH, USA

Apple (Malus × domestica) has commercial and nutritional value, but breeding constraints of tree crops limit varietal improvement. Marker-assisted selection minimizes these drawbacks, but breeders lack applications for targeting fruit phytochemicals. To understand genotype–phytochemical associations in apples, we have developed a high-throughput integration strategy for genomic and multiplatform metabolomics data.

Here, 124 apple genotypes, including members of three pedigree-connected breeding families alongside diverse cultivars and wild selections, were genotyped and phenotyped. Metabolite genome-wide association studies (mGWAS) were conducted with c. 10 000 single nucleotide polymorphisms and phenotypic data acquired via LC–MS and 1H NMR untargeted metabolomics. Putative metabolite quantitative trait loci (mQTL) were then validated via pedigree-based analyses (PBA).

Using our developed method, 519, 726 and 177 putative mQTL were detected in LC–MS positive and negative ionization modes, and NMR, respectively. mQTL were indicated on each chromosome, with hotspots on linkage groups 16 and 17. A chlorogenic acid mQTL was discovered on chromosome 17 via mGWAS and validated with a two-step PBA, enabling the discovery of novel candidate gene–metabolite relationships.

Complementary data from three metabolomics approaches and dual genomics analyses increased confidence in the validity of compound annotation and mQTL detection. Our platform demonstrates the utility of multiomic integration to advance data-driven, phytochemical-based plant breeding.

Discovering biomarkers of tomato consumption using animal studies, human clinical trials, metabolomics, and targeted analyses

Maria Sholola¹, Jenna Miller¹, Mallory Goggans¹, Michael Dzakovich², and Jessica Cooperstone^{1,2}

¹Department of Food Science and Technology, The Ohio State University, USA, <u>Sholola.1@osu.edu</u> ²Department of Horticulture and Crop Science, The Ohio State University

Background: Interest in understanding the relationship between tomato intake and potential health benefits has necessitated an accurate measurement of tomato consumption. Using plasma lycopene as an indicator is challenged by variation in lycopene content in tomato products, and differences in absorption across foods and between individuals.

Objective/Hypothesis: Our objective was to investigate key markers of tomato consumption across organisms (mice, pigs, humans) and biofluids (plasma and urine) to discover metabolites associated with tomato consumption.

Methods: Mice (n=36) were fed control (AIN93G), 10% orange tomato, or 10% red tomato containing diets for 12 weeks. Pigs (n=20) were fed 10% red tomato diets or a macronutrient matched control for 2 weeks. Subjects (n=11) were fed a single dose of either 100 mL or 500 mL tomato juice in a crossover design, and urine was sampled over the subsequent 24 hours. Plasma was extracted from the mice and pigs using methanol, and urine was volumetrically normalized according to osmolality and equivalently diluted. All samples were chemically profiled using UHPLC-QTOF-MS in positive and negative ionization modes, fragmentation data was collected, and spectra were deconvoluted using MZmine.

Results: A combination of multivariate and univariate statistical approaches were used in prioritizing features for identification. Matching to authentic standards when available and referencing/interpretation of MS/MS spectra yielded ~70 peaks attributable to tomato steroidal alkaloids were found in mouse and pig plasma. Urine analysis in humans found phase II metabolites of naringenin and imidazole alkaloids along with metabolites still undergoing structural elucidation.

Conclusions: Distinct metabolic profiles pertaining to tomato intervention were observed across multiple and provide targets for validation in studies of individuals consuming more typical and varied diets.

13

Chemical and physical stability of EPA and DHA fortified plant milk analogs

<u>Abigail Sommer¹</u>, Yael Vodovotz¹

¹Department of Food Science and Technology, Ohio State University, USA <u>Sommer.155@osu.edu</u>

Eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) have demonstrated health benefits including reducing cardiac death risk. Fish is the primary source of EPA and DHA, yet the environmental impact of overfishing/aquaculture and dietary restrictions call for an alternative. Additionally, challenges with oxidative stability and bioavailability must be overcome. Our objective was to incorporate EPA and DHA from non-fish sources into plant milks, creating a sustainable and accessible beverage with enhanced oil stability and bioavailability. It was hypothesized that stability of fortified plant milks would differ by beverage and oil type due to varying macro and micronutrient compositions and physical properties. Four beverages (water, oat milk, soymilk, and almond milk) and four oil conditions (no oil, sunflower oil, fish oil, and yeast oil plus algae oil) were assessed. The beverage physical and chemical properties were monitored over 15 days at 4°C and 55°C. The impact of oil addition on beverage turbidity, viscosity, and color were examined. Oil droplet size was measured using dynamic light scattering (DLS) and observed using light microscopy. Peroxide value, thiobarbituric acid reactive substances, and nuclear magnetic resonance assessed oxidation. Oil addition did not significantly influence beverage viscosity or turbidity. Only algae oil affected beverage color, imparting a green hue. Beverage type influenced mean DLS particle size (soy < water < oat < almond), yet microscope observations showed reduced droplet size and increased droplet stability in plant milks over water. Beverages with no oil or sunflower oil had approximately 50% lower levels of oxidation compared to those with fish oil and yeast/algae oil. Soymilk attenuated oxidation with 25-140% lower levels than other beverages. Ongoing work includes sensory evaluation and clinical assessment of bioavailability, safety, and compliance. The collective analyses will help determine the optimal EPA/DHA source and vehicle, ultimately yielding a commercially viable and accessible beverage.

Polyphenol-rich Nutrition Intervention Significantly Changed Gut Microbiome and Their Metabolic Landscape in a Human Colonic Model

Shiqi Zhang¹, Mengyang Xu², Xiaowei Sun¹, Haifei Shi², Jiangjiang Zhu^{1,3}

¹Human Nutrition Program, Department of Human Sciences, The Ohio State University, Columbus, OH 43210, USA, zhang.6517@osu.edu

²Department of Biology, Miami University, Oxford, OH 45056, USA ³James Comprehensive Cancer Center, The Ohio State University, Columbus, OH 43210, USA

Human gut microbiota is critical for human health, as their dysbiosis could lead to various diseases such as irritable bowel syndrome and obesity. Polyphenol-rich nutrition intervention (e.g., black raspberry extract (BRB) and green tea extract (GTE)) has been increasingly studied recently for its impact on gut microbiota as a rich source of phytochemicals (e.g., anthocyanin). To investigate the effect of polyphenol-rich intervention on the gut microbiota composition and their metabolism, an in-vitro human colonic model (HCM) was utilized to study the direct interaction between nutrition intervention and gut microbiome. Conditions (e.g., pH, temperature, anaerobic environment) in HCM were closely monitored and maintained to simulate the human intestinal system. Donated fresh fecal samples were used for gut microbiota inoculation in the HCM. 16S ribosomal DNA sequencing and liquidchromatography mass spectrometry (LC/MS) based metabolomics were performed to study the impact of polyphenol-rich nutrition intervention on gut microbiota characteristics and their metabolism (fatty acids, polar metabolites, and phenolic compounds). Our data suggested that polyphenol-rich nutrition intervention modulated gut microbiota at the genus level. Among top 10 most abundant gut microbes in gut microbiota from MetS patients, GTE induced significant change in the abundance of Escherichia, Klebsiella, Bilophila, Clostridium, Bacteroides, Sutterella, Phascolarctobacterium, Citrobacter, unknown genus in Planococcaceae, and Enterococcus. Meanwhile, significant changes in the metabolic profile of gut microbiota related to fatty acids (e.g., isovaleric acid and isocaproic acid), endogenous polar metabolites (e.g., N-Acetylasparagine and dopamine), and phenolic compounds (e.g., protocatechuic acid and gallic acid) were detected. In summary, HCM creates a stable environment for gut microbiota culture and enables in vitro studies of gut microbiota composition and metabolism change after nutrition intervention. The impact of polyphenol-rich nutrition intervention on gut microbiota composition and metabolism change may exert further physiological change to host metabolism and host health.

Associations of dietary intake and cognitive function in breast cancer survivors

Zihan Zhang¹, Kellie Weinhold¹, Darrin Aase², Bridget Oppong³, Nicole Williams³, Erin Stevens³, Patrick Schnell⁴, Stephanie Gorka², Martha Belury¹, Rachel Cole¹, Tonya Orchard¹

¹ Human Nutrition Program, Department of Human Sciences, College of Education and Human Ecology, The Ohio State University, Columbus, OH 43210 USA,

² Department of Psychiatry & Behavioral Health, College of Medicine, The Ohio State University, Columbus, OH 43210 USA,

³ The James Comprehensive Cancer Center, The Ohio State University, Columbus, OH 43210 USA, ⁴Division of Biostatistics, College of Public Health, The Ohio State University, Columbus, OH 43210 USA, zhang.6648@osu.edu

Chemotherapy may contribute to cognitive dysfunction. Previously we found that serum omega-3 and omega-6 fatty acids were associated with self-reported cognitive function in women undergoing chemotherapy for breast cancer. The objective of this project was to evaluate preliminary associations of diet quality, dietary fatty acids, and other specific nutrients with objective cognitive function scores in breast cancer survivors enrolled in an ongoing remote study 1-4 years after the initial cancer diagnosis. Self-reported dietary intake was assessed using an electronic food frequency questionnaire (eFFQ). Cognitive function was measured with a battery of validated cognitive tests and administered remotely by a trained researcher. Demographic and other self-reported cognitive and mental health data were completed using online questionnaires, including NeuroQoL. Linear regression models, adjusted for education, were used to quantify the association between dietary variables and objective cognitive tests [Hopkins Verbal Learning Test (HVLT), Wechsler Adult Intelligence Scale-IV Digit Span (WAIS), Oral Trail Making Test (Oral TNT), and Controlled Oral Word Association Test + Animals (COWAT+Animals)]. Preliminary statistically significant (p<0.05) results from the first 19 participants are presented.

Higher NeuroQoL scores, assessing self-reported cognitive function and QoL, were correlated with higher intake of the monounsaturated fatty acids C20:1n-9 and C22:1n-9. Better WAIS-IV scores, assessing working memory and attention, were associated with higher intake of the omega-3 fatty acids C18:4n-3, C20:5n-3, C22:5n-3, C22:6n3, and the monounsaturated fatty acid C22:1n-9. Better (shorter) Oral TMT times, assessing executive function and attention, were associated with lower dietary C18:3n-3. Better performance on COWAT+Animals, assessing verbal fluency and executive function, was associated with higher dietary fiber consumption and higher diet quality (i.e., Healthy Eating Index-2015) scores (p<0.05 for all). In conclusion, these data suggest that diet quality, unsaturated fatty acids, and fiber may be related to better cognitive performance in breast cancer survivors.

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The combination of bath-immersion and moderate electric field (MEF) treatments on iron concentrations in kale leaves (Brassica oleracea L. var. sabellica)

Siqiong Zhong¹, Jin Hong Mok², Ziqi Li³, Sudhir Sastry², Rachel E Kopec^{1,4}

¹Human Nutrition Program, Department of Human Sciences, The Ohio State University, USA
²Food, Agricultural and Biological Engineering, College of Food, Agricultural, and Environmental Sciences, The Ohio State University, USA
³Department of Food Science and Technology, The Ohio State University, USA
⁴Foods for Health Discovery Theme, USA, Zhong.198@osu.edu

Background: Due to anti-nutrients found in leafy greens and the physical-chemical properties of inorganic iron found in plant sources, iron bioavailability is lower relative to heme iron rich in red meat.

Objectives: We hypothesized that novel food processing techniques (i.e. vacuum treatment, bathimmersion, and moderate electric field (MEF) would increase iron delivery from plant foods.

Methods: A ferrous sulfate (FeSO4) solution was prepared and fresh kale samples (n=3 per treatment) were immersed in the solution alone (control), treated with vacuum alone, vacuum + water bath (30-50°C), or vacuum + water bath + MEF (15 V/cm at frequency of 60 Hz at 40-60 °C) for up to 15 min. Effects of immersion (24 h at 4 °C) after each treatment step were also tested. Concentrations of chlorophyll and iron chlorophyll derivatives were measured in both lipophilic and polar leaf extracts using ultra high liquid chromatography-diode array detection (UHPLC-DAD). Atomic absorption spectrometry was used to measure iron concentrations. Differences between treatment groups were analyzed with one-way ANOVA, followed by Tukey's posthoc testing for pairwise comparisons (P < 0.05 considered statistically significant).

Results: MEF-treated kale had the greatest increase in iron concentration (~4000x than control). Two novel metabolites, tentatively iron chlorophyllin derivatives, were observed in the lipophilic extracts of the MEF and immersed kale samples, and identifies are being pursued via UHPLC-high resolution mass spectrometry metabolomics.

Conclusions: The novel food processing techniques employed here produced kale with iron concentrations significantly higher than the kale control, as well as other iron-rich plant foods (e.g. ~40x times higher than black beans). Future testing will determine if this" iron-enhanced" kale has the potential to better deliver iron as compared to untreated kale, an FeSO4 supplement, or a heme-rich source.

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