



Title: Beliefs related to food waste reduction

Topic: NUTRITION AND SOCIETY

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Summary: Background: Environmental protection is an important contemporary goal for the health of populations and the planet. To date, factors that influence behaviors related to food waste (FW) reduction remain insufficiently explored in the scientific literature.

Objective: This exploratory study aims to identify beliefs regarding FW reduction among adults.

Methodology: Data was collected using a self-administered online questionnaire from 47 adults aged 18 to 65. Based on the Theory of Planned Behavior, this questionnaire documented behavioral beliefs (advantages/disadvantages), normative beliefs (support or lack of support from significant others), and control beliefs (barriers/facilitators) related to FW reduction. Beliefs were identified using a quantitative content analysis performed by two independent coders.

Results: The most frequently identified advantages of FW reduction by the participants are money saving, perception that it would be good for the environment, perception that it would limit overproduction and overconsumption, and waste reduction, while disadvantages include meal planning efforts, perception that meals would be less interesting, the need to search information on alternatives, food monotony, and time required for cooking. Participants identified few significant others: children, friends, and groups of interest (e.g., shops) who would disapprove of the behavior of reducing FW, while family and romantic partners were often identified as significant others who would approve. The most frequent barriers to reduce FW are lack of time, household dynamics, lack of skills or knowledge, and lack of motivation. The most frequently cited facilitators include practical anti-waste tools, meal planning, change in usual purchases, management of food reserves, and time management.

Discussion: Identified beliefs towards FW reduction can be targeted by persuasive messages aiming to promote anti-waste practices. A larger-scale study with a representative sample would help to identify which beliefs should be prioritized in communication campaigns targeting Quebec households or specific groups of the population.



Title: Exploring the Impact of Harvest Maturity Stage on the Nutritional Value of Four Pulses

Topic: NUTRITION AND SOCIETY

Author: Piché, Sofia Ricci - Ben-Fadhel, Yosra - Perreault, Véronique - Duarte-Sierra, Arturo - Doyen, Alain

Summary: Despite pulses' having high protein and fibre contents, the limiting amount of sulfur-containing amino acids and the presence of antinutritional compounds have negative impacts on their nutritional quality and consumers' perception. Regarding specifically the protein fraction, an equilibrium of the albumin and globulin ratio must be achieved, as albumins are abundant in essential amino acids (EAA) and protein inhibitors whereas globulins are rich in non-essential amino acids (NEAA). Additionally, it is well known that the proximate composition of pulses can vary depending on various parameters including the harvest maturity stage. Surprisingly, there is limited research studying the impact of the harvest maturity stage on the nutritional properties of pulses, particularly regarding their protein, amino acid and antinutritional content.

In this project, the proximate composition, the EAA and NEAA profiles and the antinutritional compounds concentration (trypsin inhibitor (TI) and α -galactosides) of borlotti, red and black beans and chickpeas harvested at two stages of maturity i.e., fresh (FMS) and dry (DMS) were compared. Moreover, the calculation of the albumin: globulin ratio as a function of the harvest maturity stage for beans and chickpeas was also investigated.

Results showed that the FMS borlotti beans contained more proteins (25.8% dry matter (DM)) and α -galactosides compared to the DMS, whereas similar mineral, lipid, EAA, and TI contents were obtained, regardless of the maturity stage. In addition, similar mineral, protein, lipid, TI and EAA contents as well as protein profiles were noticed for red beans, regardless of the maturity stage. However, FMS red beans exhibited higher α -galactosides content compared to the DMS. The FMS black beans contained higher mineral, EAA and α -galactosides contents and lower lipid (0.9% DM) compared to the DMS. Conversely, its protein and TI contents as well as protein profiles were similar. Finally, FMS chickpeas exhibited higher albumin: globulin ratio (1.33) and TI content (26.9 TIU/mg DM) but lower α -galactosides whereas no changes were found for mineral, protein, lipid, and EAA contents. These findings indicate that the harvest maturity stage influences the nutritional profile of pulses and could be used as an interesting tool to optimize their nutritional values.



Title: Economic and environmental impacts of cheese by-product valorization pathways

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Castaneda Sanchez, Juan Esteban - Pouliot, Yves - Doyen, Alain - Chamberland, Julien

Summary: The dairy and cheese industries generate significant by-products, such as whey and ultrafiltration permeate, with considerable economic loss and environmental impact. In this context, the overall objective of this study is to create, specifically for the industry of Quebec, a decision support tool identifying optimal valorization pathways for dairy non-fat solids (NFS) from whey and ultrafiltration permeates. Valorization pathways will be modeled at different scales and characterized for their economic and environmental performances in different Quebec regions.

The production of by-products was mapped into four sub-regions based on volumes of milk processed. Three types of companies are considered based on annual milk processing volume. Three by-product valorization pathways are considered: biogas production, whey (and permeate) ingredients production for human consumption, and animal feed. The ongoing tool development will consider company-specific factors for optimal by-product valorization (e.g., distances between plants, driers or biomethanization plants), and potential incomes for all the valorization pathways tested. It will aid companies in selecting by-product valorization, considering regional specifics and business scales. This study seeks to enhance Quebec's cheese industry's economic and environmental performance by optimizing by-product management.



Title: Formulation of a hybrid-vegetable spreadable cheese analogue with the aim of reducing dairy food waste

Topic: FOOD SUPPLY AND WELL-BEING

Author: Waglay, Amanda - LeContellec, Lisa - Karboune, Salwa

Summary: Plant-based diets are increasing in trend for consumers as they are associated with being a more sustainable and healthier option. As an example, the vegan cheese market is currently on target to be a \$4 billion dollar industry by 2024 . Plant proteins are associated with an undesirable aftertaste, lower content of essential amino acids, fatty acids, vitamins, higher amount of salt, and reduced functionalities. In addition, the food industry is constantly facing sustainability scrutiny throughout the supply chain, particularly the dairy industry as they are associated with large green house gas emission, terrestrial acidification, large water consumption, and large amount of food waste. To overcome these drawbacks, the development of hybrid formulations involving both animal and plant-based proteins is desirable.

Nine plant-based proteins from various suppliers and sources namely, vegetable, seed, legumes, and algae were explored in the development of a hybrid cheese analogue product containing unsold brie cheese (30% of the formulation). The plant-based proteins were substituted at 1 and 10% of the formulations resulting in hybrid spreadable cheese formulations that varied according to their protein content and water holding capacity. Moreover, the cheese formulations resulted in various spreadability as determined by firmness (633- 5872 g) and consistency (4362. 34 gsec-1 – 37770.91 gsec-1) using a Texture Analyzer (TA-XTPlusC). Less spreadability is linked to elevated firmness and consistency . Our results show that spirulina, chickpea, and fava bean resulted in the highest spreadability. Visual interactions of the ingredients were determined by scanning electron microscope (500X magnification), and most formulations were characterised by dense structures with large air pockets dispersed. The formulations were analyzed by a sensory evaluation panel, using a 9-point Hedonic scale for visual: colour and graininess, ingestion: saltiness, vegetable flavour, hardness, graininess, and overall liking. The hybrid cheese with the highest overall liking contained 10% (w/w) potato protein, while the protein resulting in the most preferred texture of cheese was from mushroom with incorporation of 1% (w/w). The interactive effect of plant-based protein content and the proportion of unsold brie cheese on the quality attributes of hybrid cheese was optimized.



Title: Understanding the impact of several physicochemical factors on protein-polyphenols complexes with response surfaces and chemometrics

Topic: FOOD SUPPLY AND WELL-BEING

Author: Galarneau, Julie - Cordella, Christophe - Brisson, Guillaume

Summary: Polyphenols are natural substances with high nutraceutical potential. They are also very sensitive to their physicochemical environment. Oxygen, pH, and light can affect their structure, frequently in an irreversible way. During digestion, polyphenols are exposed to conditions that can lead to a loss in bioavailability. Polyphenols tend to create miscellaneous interactions with other macromolecules, impacting their digestibility. This study aims to use the natural affinity of proanthocyanidins (PACs) with several whey proteins. The goal of the research is to understand the fundamental chemistry behind the digestibility and assimilation of PACs by complexing them with proteins that have been treated in a specific way. Therefore, predicting the complex's behavior in each condition will be possible. A multifactorial approach is being used to explore different conditions, such as pH, ionic strength, and dynamic high homogenization pressures (HHPs) on the complex's characteristics. Particle size, infrared spectra, complexation ratio, and aggregates are being evaluated in a 3-way response surface. The study's hypothesis is that the treatments applied to the proteins will enhance the exposition of hydrophobic pockets, encouraging reversible interactions to form and upgrading the bioaccessibility of PACs. The methodological approach allows a broad screening of physicochemical conditions, treating data in an innovative manner for the field.



Title: Conventional and naked oat cultivars: macronutrients, atherogenicity and thrombogenicity indices and avenanthramide composition amidst environmental changes

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Germain, Isabelle - Turcot, Sophie - Goulet, Jean

Summary: Oats (*Avena Sativa* L.) is cultivated for numerous purposes such as feed, human consumption or pharmaceutical components. The popularity of oats is rooted in its well-balanced nutritional composition. In Canada, oat bran, rolled oats, whole oat flour and oat products presenting specific concentrations can display a health claim for beta-glucan oat fibre capacity to lower blood cholesterol. Also, oats provides valuable phenolic compounds such as avenanthramides. Changes in environmental conditions are suspected to impact future production of oats due to rise in temperatures and changes in precipitations. In 2021, Statistic Canada reported that total oat production declined by 43 per cent nationally, mainly due to dry conditions in Western Canada. Harvested oat acres diminished by 15.4% and yields dropped 32.6 % bushels per acre. Nutritional composition of naked oats (*Avena Nuda*) and conventional oats are suspected to be similar. However, naked oats produces less crop related residues but is sold to be used in feeds for race horses. Given the impact of climate change on crops and knowing that naked oats have good drought resistance, perhaps naked oat cultivars should be considered for foods. In this study, Canadian naked oat cultivars were characterized for their nutritional content: total protein, amino acid profile, carbohydrate, lipids, fatty acid profile, fibre and beta-glucan, Atherogenicity and thrombogenicity indices were calculated. Total phenolic content, beta-glucan, antioxidant activity and avenanthramides compositions were also measured. The values were compared to conventional Quaker cultivar and breakfast cereals to assess the impact of processing methods. Results to date suggest that naked oats might have an enhanced nutritional composition profile and health benefits compared to conventional oats. In times of climate changes and productivity challenges, nutrient profiles and bio-compounds of various crops should be systematically monitored and selection of crops for human consumption might be best supported by factoring in the nutritional profile as well as the yield factor. More food processing tests are required to compare naked oats to conventional covered oats in products offered to consumers. [Funded by Semican Canada and Agriculture and Agri-Food Canada]



Title: Effects of blueberry-derived polyphenol metabolites on the blood-brain barrier in a brain-chip model of Parkinson's disease

Topic: NUTRITION AND SOCIETY

Author: Arevalo, Océane - De rus Jacquet, Aurélie

Summary: INTRODUCTION. The human brain is composed of glial cells and neurons working in synergy to ensure cerebral homeostasis. However, over the course of neurodegenerative diseases such as Parkinson's disease (PD), a main pathological event is the loss of neuronal subpopulations. It is a slowly progressing age-related disorder characterized by the loss of dopaminergic neurons in the substantia nigra, leading to motor symptoms characteristic of PD. The cause of PD is still unknown, but factors leading to disease onset include age, genetics, and certain environmental factors. Among the genetic factors implicated in the development of familial PD, a substantial number of mutations are located on the leucine-rich repeat kinase 2 (LRRK2) and the SNCA genes. At present, there is no cure for PD, but there are treatments that can alleviate symptoms. In addition, certain foods could also help restore brain health, such as those rich in antioxidants, vitamins and minerals. Medicinal plants have been used for millennia, but in recent years they have once again become part of our daily lives for their beneficial properties to the human body. Among these pro-health plants, blueberries have anti-inflammatory and antioxidant properties, and research suggests promising neuroprotective properties in PD.

METHODS. We used induced pluripotent stem cell (iPSCs)-based models to reproduce PD-related features in a dish. We performed directed differentiation of iPSCs into glial and neuronal cells derived from healthy donors or people with PD (e.g. LRRK2 G2019S and SNCA triplication mutations). Then, we established 3D models such as microfluidic brain-chips that recapitulate the blood-brain barrier with brain (astrocytes, neurons, pericytes) and bloodstream (brain microvascular endothelial cells) channels, thus reproducing the complex exchanges between these compartments. Using these models, blueberry-derived polyphenols metabolites are perfused in the bloodstream compartment to quantify and characterize the profile of metabolites crossing the BBB, and determine their potential effects on PD-related pathology.

RESULTS AND CONCLUSIONS. Previous research has found that the BBB is impaired in people with PD. Our preliminary data show the selective passage of blueberry metabolites across the BBB. In addition, we observe restoration of the BBB, attenuation of inflammation and neuroprotection. If the results are confirmed, blueberries could play a role in the prevention and treatment of PD, as well as in the development of treatments for other forms of neurodegenerative disease



Title: Dietary meat protein aggravates the deleterious metabolic effect of high fat and high sucrose diet through changes in hepatic lipid and amino acid metabolism in mice

Topic: NUTRITION AND SOCIETY

Author: Bégin, Frédéric - Marette, André

Summary: We recently reported that dietary proteins (DP) modulate diet-induced obesity and insulin resistance in mice (Nat Commun 12: 3377, 2021). We posit that these metabolic alterations are caused by differential activation of the hepatic urea cycle in response to different amino acid (AA) compositions and total nitrogen load. Objective: To test whether DP sources alter hepatic metabolism and insulin resistance through the urea cycle. Methods: Metabolic phenotypes, hepatic urea cycle and insulin resistance were measured in mice fed low-fat, low-sucrose (LFLS) or high-fat, high-sucrose (HFHS) diets containing either pork (PP), soy (SP) or casein (CP) protein for 12 weeks. Based on their AA composition, PP had the highest nitrogen load, followed by SP and CP. Results: When compared to SP and CP, feeding PP to HFHS mice induced more glucose intolerance which was correlated with higher post-prandial AA-derived nitrogen load in the portal vein. PP feeding in HFHS mice induced hepatic insulin resistance, revealed by impaired insulin-induced Akt phosphorylation on Ser473. Mice fed the LFLS diet were, however, protected from PP-induced glucose intolerance and insulin resistance, and this was associated with robust increase in the protein levels of urea cycle enzymes (CPS1, OTC) in the liver. In starked contrast, induction of urea cycle enzymes was blunted in the liver of PP-fed HFHS mice. PP feeding also increased the expression of inducible nitric oxide synthase (iNOS) and reactive oxygen species (ROS) as showed by DHE staining of liver sections. Conclusion: Dietary PP increases total nitrogen load activating the urea cycle, which may protect against metabolic dysfunction and hepatic insulin resistance in LFLS mice. This protective mechanism is lost in PP-fed HFHS mice, likely by downregulation of urea cycle activity, when the liver is overloaded with dietary fat. iNOS induction could be acting as an alternative nitrogen handling pathway, causing a build-up of mitochondrial ROS.



Title: Acute impact of high-fat high-sucrose diet on inflammation and metabolic health in mice: the potential role of the gut microbiota

Topic: NUTRITION AND SOCIETY

Author: Rossi Perazza, Lia

Summary: The impact of dietary choices on metabolic health has been extensively investigated, with a majority of studies focusing on the long-term effects of diets. It is well documented that chronic consumption of an obesogenic diet leads to obesity, inflammation, and impaired glucose metabolism, culminating in Type 2 diabetes. However, limited information is available regarding the immediate consequences of acute high-fat high-sucrose (HFHS) feeding on metabolism. This study explores the acute effects of an HFHS diet intake on glucose intolerance, adiposity, inflammation, and gut microbiota using a murine model of obesity.

Within just 24 hours of being fed an HFHS diet, mice displayed impaired glucose homeostasis as revealed by elevated fasting glycemia and insulinemia, as well as glucose intolerance. This rapid development of dysmetabolism in response to the HFHS diet emphasizes the relevant impact of dietary choices on metabolic processes. Furthermore, 24h HFHS diet feeding increased overall adiposity, as well as elevated plasma and liver triglycerides and cholesterol. These early indicators of metabolic dysfunction suggest that even short-term exposure to an HFHS diet can set the stage for long-term health complications. In addition to metabolic changes, animals exposed to the obesogenic diet for only 24 hours demonstrated a significant rise in several inflammatory markers, including NOS2 (nitric oxide synthase 2), an enzyme that has been largely associated with the pathophysiology of diet-induced obesity and Type 2 diabetes. Moreover, acute HFHS feeding compromised intestinal permeability and modulated the composition of the intestinal microbiota in both the small intestine and fecal samples. These alterations in gut microbiota within such a short timeframe suggest that dietary choices can rapidly influence the gut ecosystem, which plays a crucial role in metabolic processes.

Importantly, both male and female mice displayed similar phenotypes, suggesting that the observed immuno-metabolic impairments are relevant to both sexes. Thus, this study emphasizes the urgency of addressing the mechanisms by which short-term HFHS feeding impacts the gut microbiome, inflammation to impair metabolic health.



Title: **Caenorhabditis elegans: Exploring the links between gut microbiota and aging**

Topic: NUTRITION AND SOCIETY

Author: Alonzo de la Rosa, Claudia Miriam - Miard, Stéphanie - Taubert, Stefan - Picard, Frédéric

Summary: Introduction: The mutual relationship between the intestinal microbiota and biological aging is not yet fully characterized and it is difficult to study it on a large scale in mammals.

Objectives: To compare the energetic and symbiotic contributions of the intestinal microbiota of young and old mice on the biological aging of the nematode *Caenorhabditis elegans*.

Methodology: The faeces of male and female C57BL/6J mice aged 3, 6, 12 and 18 months were freshly collected. The microbiota was extracted and quantified by DNA analysis. Half of each microbiota extract was inactivated with paraformaldehyde (used primarily as an energy source) and the other half remained alive (to assess symbiosis impacts). In an experimental matrix model, the worms were placed with the different microbiota extracts at similar concentrations. Next, we assessed the worms' food choice, lifespan, and fat accumulation.

Results: The worms showed a stronger preference for the living microbiota of 3-month-old mice than for that of older mice, while the aged microbiota was preferred when inactive. Inactivation of the microbiota reduced longevity in all groups studied. Worm longevity was increased by live microbiota of 3-month-old male mice and 18-month-old female mice. The worms accumulated less fat by feeding on the living microbiota of 3-month-old male and female mice than on that of older mice. This effect was not observed when the microbiota was inactive.

Conclusion: The microbiota of aged mice induces significant changes in the aging and energy reserves of worms. Several effects are lost by inactivation of the microbiota, suggesting that symbiosis plays an important role. The mechanisms at the heart of this symbiosis between the microbiota and the biology of the host *C. elegans* remain to be elucidated.



Title: Plant-based natural products to treat Parkinson's disease-related symptoms: prevalence, interest, awareness and determinants

Topic: NUTRITION AND SOCIETY

Author: Diadiou, Sandra

Summary: Natural health products (NHP) have emerged as a potential complementary approach to the treatment of people with Parkinson's disease (PwP). The objective of this study is to quantify the prevalence of ever use of NHP, interest in plant-based NHP, awareness of potential herb-drug interactions, and the prevalence of discussing NHP use with PD healthcare professionals among PwP. We addressed these objectives by embedding a cross-sectional 4-item survey in a subsample of a population-based cohort of PwP (PRIME-NL) Sixty-five percent (n=367) of the 566 participants who were contacted, completed the survey. Of those participants, 132 (36%) reported having used NHP to alleviate PD-related symptoms, with cannabis, coffee and turmeric being the most popular. This included 12% (n=44) of PwP who had used at least one other NHP than coffee or cannabis. Furthermore, 259 (71%) participants expressed an interest in exploring the use of NHP. 51 (39%) of NHP users were aware that these products can interact with PD medication. 51 (39%) of NHP users had discussed their use of NHP with their neurologist or PD nurse specialist. In a sensitivity analysis, we conservatively assumed that all non-responders to the survey had never used NHP and had no interest in exploring NHP. This rendered an estimated prevalence of NHP of 23% and estimated interest in exploring NHP of 46%. In conclusion, in this study, over one in three PwP has used NHP to alleviate symptoms of PD and the majority of PwP is interested in exploring the use of plant-based NHP. The majority of users has not discussed the intake of NHP with their PD healthcare professional and are unaware that these products can interact with PD medication. This study supports the need for sustained evidence-based research on the properties of plant-derived therapeutics.



Title: Exploring the ex vivo effects of stearidonic acid (SDA)-rich Ahiflower oil on the gut microbiota of individual humans and their capacity to produce SDA-derived N-stearidonoyl ethanolamine

Topic: PERSONALIZING NUTRITION

Author: Roussel, Charlène

Summary: The seed oil from *Buglossoides arvensis* (Ahiflower™) is the richest source of the ω -3 PUFA stearidonic acid. Within the palette of mechanisms potentially explaining the beneficial effects of dietary PUFAs, the bidirectional interaction between dietary PUFAs and the gut microbiome is of great interest. Dietary PUFAs may in fact exhibit prebiotic properties, by positively modulating resident microorganism populations and their metabolic activities, while the gut microbiota can impact the metabolism, biotransformation, and absorption of dietary PUFAs. However, such studies on the effects of Ahiflower oil on the gut microbiota and its metabolic functions are lacking, warranting further investigations.

In this context, we utilized the TWIN-M-SHIME®, which mimics both the ileum and proximal colon lumen and mucosal microbiome ecosystems, as an ecological framework to characterize the compositional and metabolic (in terms of SCFA, targeted lipidomic) responses of the human gut microbiota to 14-days of Ahiflower oil supplementation. This exploratory investigation utilized a mini cohort of four unique fecal donors to elucidate the personalized spatial-temporal fermentation effects using 16S rRNA sequencing and LC-MS/MS approaches.

Cluster analysis revealed two distinct groups (cluster 1 and 2) in response to Ahiflower oil supplementation at the microbial community composition level. Cluster 2 exhibited an increased abundance of potential second-generation probiotics like *Akkermansia muciniphila* with an increased metabolic response with higher propionate production in both the ileum and proximal colon. Spearman correlation analysis identified the potential role of bacteria utilizing the succinate pathway in propionate production. Additionally, our findings indicated the ability of gut bacteria, particularly in the ileum of both clusters, to produce N-stearidonoyl ethanolamine, SDEA. Relevance network analysis to predict SDEA biosynthesis by bacterial taxa is currently ongoing. Further research in this field will help deepen our understanding of the intricate interactions between dietary PUFAs, the gut microbiota, and human health.



Title: Validation of the mice as a research model for investigating the potential of bile acid glucuronidation as a therapeutic target for the treatment of cholestatic autoimmune liver

Topic: PERSONALIZING NUTRITION

Author: Haddad, Elena Maria - Grondin, Jordan - Béji, Sarra - Chouinard, Justine - Mouchiroud, Mathilde - Verreault, Mélanie - Trottier, Jocelyn - Caron, Alexandre - Barbier, Olivier

Summary: Background: Glucuronidation is a phase II conjugation reaction involved in the detoxification of numerous exogenous and endogenous compounds such as bile acids (BAs). These acids play important roles for cholesterol, lipids and glucose metabolism and absorption. But their accumulation, as it occurs in cholestatic diseases such as primary biliary and sclerosing cholangitis (PBC and PSC), is toxic for liver cells and promotes inflammatory processes ultimately leading to liver failure, if not pharmacologically prevented. While the mechanisms governing human BA glucuronidation are well understood, this process occurring in mice has received less attention, thus limiting the access to well-known animal models for studying BA-glucuronidation formation in vivo.

Methods: Glucuronidation assays were conducted using recombinant Udp-glucuronosyltransferase (Ugt) enzymes and tissue homogenates from male and female CD1-Elite mice (n=4/group). The enzymatic assays were performed at 37°C in presence of the UDP-glucuronic acid co-substrate with various BA substrates, and the formation of BA-Glucuronides (BA-G) was quantified using LC-MS/MS. LC-MS/MS was also used to profile BA-G in murine feces, intestinal contents, liver, and plasma. How environmental factors affect BA glucuronidation were investigated by exposing male C3H/HeJ mice (n=8/group) fed with control or high fat diets to different temperatures (10°C and 30°C).

Results: The β -muricholic acid (β -MCA)-24G was the most frequently detected BA-G in mice, while the murine Ugt2b34, 2b35 and 2b37 were the most reactive enzymes for BA-G formation. The most reactive tissues were the liver and colon, and female organs exhibited higher activity levels than male ones. HFD-fed mice livers exhibited significantly higher rates of glucuronidation of β -MCA. In contrast, the same diet caused a significant reduction in β -MCA-24G formation in the colon.

Conclusion: These experiments revealed the BA-, Ugt-, tissue- and sex-dependent manner in which bile acids are glucuronidated in mice. We also demonstrated that the BA glucuronidation activity is regulated in a tissue- and stimuli (i.e diet or temperature factor)-dependent way. Overall, these observations support the idea that mice could be an adequate model for studying the role of BA glucuronidation in the context of PBC and PSC treatment.



Title: Interplay of Gut Microbial Pathways and Circulating Metabolites in Response to Short-term Dietary Interventions in Humans

Topic: PERSONALIZING NUTRITION

Author: Bourdeau-Julien, Isabelle - Castonguay-Paradis, Sophie - Plante, Pier-Luc - Lamarche, Benoît - Flamand, Nicolas - Di Marzo, Vincenzo - Veilleux, Alain - Raymond, Frédéric

Summary: Introduction : The contribution of diet to metabolic health is well recognized, but the gut microbiota is also thought to have an important effect. Since gut microbiota composition depends on the host's diet and metabolism, metabolic health is not determined by single specific factors, but by a complex network of interactions between diet, microbiota and metabolism. The aim of this project is to gain a better understanding of this dialogue.

Method : In a longitudinal study, 21 participants received a Mediterranean diet (MedDiet) for 3 days, a 13-day lead-in controlled diet reflecting the average Canadian dietary intake (CanDiet), and once again a MedDiet for 3 consecutive days. Fecal and blood samples were taken for analysis at each change of diet. Untargeted metabolomics with UHPLC-MS was performed to identify and quantify blood metabolites. Metagenomic sequencing of fecal samples was processed with HUMAnN 3.0 to determine enrichment of microbial pathways.

Results: We observed significant effects of dietary interventions on both circulating metabolites and the gut microbiota. Among the 1261 detected circulating metabolites, 92 displayed an immediate and reversible response to the dietary intervention, while 55 metabolites exhibited non-reversible changes after three days of MedDiet following CanDiet after FDR correction. Functional analysis using the KEGG database highlighted the significant impact of dietary interventions, particularly on the histidine metabolic pathway. Out of 801 microbial pathways identified in the gut microbiota samples, 36 pathways displayed immediate and reversible response as 1 displayed non-reversible change after FDR correction. Specifically, gluconeogenesis and amino acid pathways were markedly affected by the dietary interventions. Notably, inter-individual variation was observed in both the overall metabolic and microbiota functional profiles, indicating significant differences among participants. We found significant spearman correlations between the gut microbiota and metabolites. Out of the 64 bacterial genera comprising over 1% of the gut microbiota in at least one sample, 56 genera exhibited significant correlations with an average of five metabolites each after FDR correction. Metabolites from the histidine pathway exhibited noteworthy changes, with histidine blood levels increasing during the MedDiet intervention and positively correlating with numerous pathways from *Eubacterium eligens*. Conversely, levels of imidazole propionate, a microbially produced histidine metabolite known to impair glucose tolerance, decreased with MedDiet and negatively correlated with several pathways from *Bacteroides uniformis*. **Conclusions :** This study highlights the importance of considering the diet in research exploring the relationship between the gut microbiota and metabolism. Moreover, metabolic profile analyses must consider the uniqueness of metabolites.



Title: Fast and accurate quantification of proanthocyanidins metabolites by combining enzymatic hydrolysis and high-throughput mass spectrometry

Topic: PERSONALIZING NUTRITION

Author: Lessard-Lord, Jacob - Plante, Pier-Luc - Auger, Serge - Picard, Pierre - Desjardins, Yves

Summary: To study the inter-individual variability associated with the metabolism of proanthocyanidins (PACs), absolute quantification of phase II PACs metabolites in urine is crucial. However, the accurate quantification of these molecules requires expensive or non-commercially available conjugated standards. This issue can be overcome by the use of enzymatic hydrolysis associated with the quantification of unconjugated metabolites using commercially available standards. Although widely used, β -glucuronidase and arylsulfatase from *Helix pomatia* have limited efficacy for polyphenols hydrolysis. Additionally, the high volume of samples resulting from large cohorts requires high-throughput methods for metabolite quantification. We aim to demonstrate that conjugated PACs metabolites in urine can be fully hydrolyzed by enzymes from bacterial sources and that Luxon-MS/MS, a high-throughput MS ion source, is a fast and effective tool to quantify these metabolites.

To compare the performance of the two enzyme sources and to cross-validate the Luxon-MS/MS method, 24 urine samples from a clinical trial where 12 healthy subjects were given a cranberry PACs supplement for 4 days were used. Urine samples were collected at the end of each period. Samples were analysed by UPLC-QToF and Luxon-MS/MS to quantify PACs metabolites following enzymatic hydrolysis.

Bacterial enzymes fully hydrolyzed 12 conjugated PACs metabolites out of 14 measured, while enzymes from *Helix pomatia* fully hydrolyzed only 8 conjugated metabolites. In general, bacterial enzymes were more efficient than enzymes from *Helix pomatia*, and they greatly reduce the hydrolysis time from 360 to 30 minutes.

Luxon-MS/MS was used to quantify phenyl- γ -valerolactones in the 24 urine samples following enzymatic hydrolysis. Analysis time was reduced from 22 minutes (UPLC) to less than 10 seconds. Passing-Bablok regression was used to cross-validate quantification results of hydroxyphenyl- γ -valerolactone ($r=0.992$) and dihydroxyphenyl- γ -valerolactone ($r=0.957$).

In combination with bacterial enzymes, Luxon-MS/MS is a promising innovative method to study PACs inter-individual variability in large cohorts.



Title: Identifying a nutrient profiling model to characterize and monitor the healthfulness of the food supply: a validation study in the Canadian context.

Topic: NUTRITION AND SOCIETY

Author: Vézina, Annie - Corriveau, Alicia - Harrison, Stéphanie - Turcotte, Mylène - Kayigire, Ange Cédric - Nadeau, Magalie - Provencher, Véronique - Labonté, Marie-Ève

Summary: Background: Nutrient profiling (NP) models aim to prevent diet-related chronic diseases and to promote health by classifying foods and beverages based on their nutritional composition. NP models can be used to characterize the healthfulness of the food supply in an objective, transparent and reproducible way. Most existing NP models have been developed outside Canada. Thus, it is important to ensure that they are appropriate for use in the Canadian context by testing their validity using population-based data. Objective: This study aimed to test the validity of three NP models by analyzing the NP-derived nutritional quality of foods consumed by individuals in a Canadian sample and comparing it to an index which measures overall adherence to the 2019 Canada's Food Guide recommendations on healthy food choices. Methods: The Health Star Rating system (HSR), the Nutri-Score, and the Nutrient-Rich Food Index (NRF) 6.3 were tested in the 2015 Canadian Community Health Survey-Nutrition. Data from a single 24-h recall completed by 9627 adults were used to calculate energy-weighted NP-derived individual scores for each model. Associations between individual scores and diet quality as measured by the Healthy Eating Food Index (HEFI)-2019 were assessed using multivariate linear regression models while adjusting for age, sex, province, and reporting status. Results: For all three NP models, consumption of higher quality foods was associated with a higher HEFI-2019 (all p-values<0.05). The HSR explained most of the variability in the HEFI-2019 (adjusted R²=0.46), closely followed by the Nutri-Score (adjusted R²=0.43), and the NRF6.3 (adjusted R²=0.33). Conclusions: These results show that the HSR and Nutri-Score performed better than the NRF6.3 while assessing their associations with overall diet quality in Canadian individuals, suggesting that these two NP models would be better suited to the Canadian context. Results from other types of validity testing and additional criteria, such as ease of use of a given model, should be considered to determine which single NP model should ultimately be used to characterize and monitor the healthfulness of the food supply in Canada, particularly as part of the work conducted by the Food Quality Observatory (<https://offrealimentaire.ca/en>).



Title: In Vitro Investigation of Phage Targeting *E. coli* K1 in Pregnant Donors' Intestinal Microbiota

Topic: PERSONALIZING NUTRITION

Author: Antoine, Céline - Laforêt, Fanny - Goya-Jorge, Elizabeth - Gonza, Irma - Lebrun, Sarah - Douny, Caroline - Duprez, Jean-Noël - Scippo, Marie-Louise - Taminiau, Bernard - Daube,

Summary: Extra-intestinal *E. coli* (ExPEC) have a high potential for transmission through diet and poultry is the food source that has the strongest association with human ExPEC. Avian pathogenic *E. coli* (APEC) serogroup O18:K1 share many similarities with those responsible for neonatal meningitis in humans. The asymptomatic carriage of these strains in the maternal intestinal microbiota constitutes a risk of vertical transmission to infant at birth. Phage therapy is a promising alternative to antibiotics and previous work has enabled the selection of the phage vB_EcoP_K1_ULINTec4, active against avian and human O18:K1 strains. This work aimed to evaluate the efficacy of phage therapy against *E. coli* O18:K1 in an intestinal environment and its impact on the intestinal microbiota. For this purpose, three independent experiments were conducted on the SHIME® system, the first one with only the phage vB_EcoP_K1_ULINTec4, the second experiment with only *E. coli* K1 and the last experiment with both *E. coli* K1 and the phage. Microbiota monitoring was performed using metagenetics, qPCR, SCFA analysis and the induction of AhR. The results showed that phage vB_EcoP_K1_ULINTec4, inoculated alone, was progressively cleared by the system and replicates in the presence of its host. *E. coli* K1 persisted in the microbiota but decreased in the presence of the phage. The impact on the microbiota was revealed to be donor dependent, and the bacterial populations were not dramatically affected by vB_K1_ULINTec4, either alone or with its host. In conclusion, these experiments showed that the phage was able to infect the *E. coli* K1 in the system but did not completely eliminate the bacterial load.



Title: Characterisation of GUS enzymes from the intestinal microbiome: a translational approach for a novel therapeutic target in cholestatic auto-immune liver diseases

Topic: PERSONALIZING NUTRITION

Author: Dzanouni, Salma - Gagnon, William - Verreault, Mélanie - Trottier, Jocelyn - Redinbo, Mathiew R. - Barbier, Olivier

Summary: Background: High bile acids (BAs) levels exacerbate the liver damage and inflammation in cholestatic auto-immune liver diseases. Glucuronidation converts toxic BAs into non toxic glucuronide derivatives (BA-G) and favors their elimination . However, our group has recently discovered that BA-G can be retoxified into BAs by microbial β -glucuronidases enzymes (GUS) from the intestine. This study aimed at quantifying GUS activity toward BAG, and investigating how this activity is altered by pharmaceutical and nutritional interventions.

Methods:Enzymatic GUS assays were performed at 37°C for 30 minutes in the presence of 50 μ M of BA-G and 5 μ g of human or murine fecal proteins. BA formation was then resolved using LC-MS/MS. For enzymatic screening, 11 BA-G species were assayed with human (5':5') or CD1-Elite mice feces (2':2'). For inhibition assays, the enzymatic reaction was performed with a pools of human (5': 5') or murine (4':4') feces in the presence of 200 μ M amoxapine, a known GUS inhibitor. Finally, GUS assays were also performed using feces from human donors harvested before and after consumption of either 280g/day of frozen raspberries (16':7') or 50g/day of freeze dried blueberry powder (13':11') for 8 weeks, and incubated with BA-G as described above.

Results: All tested BA-Gs were reactive with human and murine feces, with deconjugation percentages ranging from 0.8 \pm 0.5%(mean \pm SEM)for HDCA-6G to 41.4 \pm 11.0% for CDCA24G in women's feces. Compared to vehicle alone, the inhibition rate caused by amoxapine was higher in pool of women's feces than in men's (68.3% for LCA-3G to LCA conversion and 49.6% for LCA-24G to LCA vs 66.4% and 33% respectively for the same glucuronides).

Similar experiments performed with the murine-specific acid, β -MCA-24G and pool of mice feces revealed sexual dimorphism with amoxapine being more efficient in female samples. Interestingly, in human volunteers, the consumption of blueberry extracts caused a significant ($p < 0.01$) reduction of LCA-3G deconjugation, while the GCDCA-3G to GCDCA conversion remained unaffected after an 8-week raspberry-enriched diet.

Conclusion: These data, show that bacterial GUS enzymatic activity toward BA-G can be modulated by pharmacological and diet interventions, , suggesting that its modulation could be targeted to ensure an optimal BA detoxification in cholestatic liver diseases.



Title: Investigating the role of the gut in fructose induced glucose intolerance

Topic: PERSONALIZING NUTRITION

Author: Sellami, Eya - da Silva Lima, Francielton - Jordão Teixeira, Caio - Forato Anhô, Fernando

Summary: Background: Obesity and type 2 diabetes (T2D) are global health challenges linked to the consumption of ultraprocessed foods high in sucrose. The latter is one key source of excess dietary fructose. Although evidence indicates that excess fructose can negatively impact metabolic health and blood glucose regulation, the mechanisms are ill-defined. Excess dietary fructose overwhelms enterocyte absorption in the small intestine and spills over the distal gut. Interestingly, excess fructose has been linked to an expansion of the gut's absorptive surface and increased fat absorption. However, it remains uncertain whether excess dietary fructose impairs glucose tolerance by increasing gut absorptive surface and gut glucose absorption (GGA).

Aims and Hypothesis: We hypothesized that dietary fructose impairs glucose tolerance by expanding gut surface and upregulating glucose transport machinery, which promotes increased GGA and glucose intolerance. We aim to (i) map the onset of altered glucose tolerance, plasma insulin, and altered GGA in mice fed a high-fructose diet, (ii) investigate whether fructose driven increase in GGA correlates with an expansion of absorptive surface, and (iii) evaluate whether glucose transporters are upregulated upon high-fructose feeding.

Methodology: C57BL6J male mice were fed a fructose-free (Fru-free) or a high-fructose diet (17% Kcal sucrose, Fru-rich). Oral glucose tolerance tests (OGTT) and 3-O-methyl-glucose (3-OMG) tests were conducted in tandem 1, 4, and 7 weeks after introduction of diets.

Preliminary results and future analysis: We found that 4 weeks, but not 1 week, on a Fru-rich diet is sufficient to cause glucose intolerance. This phenotype persists, but is not aggravated, in week 7. We are evaluating insulin and 3-OMG levels in samples collected during OGTTs to determine the temporal relationship between the onset of hyperinsulinemia, altered GGA, and glucose intolerance. We will assess changes in glucose transports by qPCR and perform morphometric analysis in the small intestine to assess changes in absorptive surface. This time-course study will uncover novel mechanisms by which dietary fructose contributes to impaired blood glucose control and elevates the risk of T2D. The findings from this work will lay the groundwork for novel approaches to address the growing burden of metabolic disorders worldwide.



Title: Deciphering the interaction between the gut microbiota and type 2 diabetes risk factors

Topic: PERSONALIZING NUTRITION

Author: Amzil, Loubna - Deschênes, Thomas - Plante, Pier-Luc - Di Marzo, Vincenzo - Veilleux, Alain - Couillard, Charles - Marette, André - Vohl, Marie-Claude - Raymond, Frédéric

Summary: Objective: The gut microbiota plays an increasingly evident role in the development of certain metabolic diseases such as type 2 diabetes (T2D). However, the specific bacteria and microbial genes involved in these diseases are still to be determined. The objective of this project is to identify bacterial genes associated with insulin resistance and glucose intolerance.

Method: This project combines several existing studies, including healthy individuals and those with pre-diabetes, for whom complete metagenomic sequencing data is available ($n = 275$). A method to classify healthy and diseased phenotypes based on the gene content of bacteria using machine learning has been validated on publicly available data. Briefly, proteins encoded in the metagenomic sequences are identified and then grouped based on their similarity, enabling comparison of study samples. These data are then used for sample classification using machine learning approaches, including algorithms generating interpretable models. This approach will be used to classify samples from our group of clinical studies based on metabolic parameters and clinical criteria.

Results: This approach has established a link between genetic markers and metabolic elements. Our findings reveal a negative correlation between bacterial enzymes potentially involved in surface polysaccharides biosynthesis, and metabolic parameter associated with the onset of T2D. This discovery suggests that bacterial enzymes could play an important role in regulating metabolic levels in the studied individuals.

Conclusion: These initial results are particularly promising. They reinforce the notion that our protocol, which combines genetic and metabolic analyses, holds promise in elucidating the complex mechanisms underlying the onset of T2D.



Title: Supplementation with a cranberry extract rich in PAC and oligosaccharides favours the establishment of a butyrogenic guild in the human fermentation SHIME system

Topic: PERSONALIZING NUTRITION

Author: Cattero, Valentina - Roussel, Charlène - Lessard-Lord, Jacob - Roy, Denis - Desjardins, Yves

Summary: Les proanthocyanidines (PAC) ont montré des bienfaits sur la santé dans des études in vitro, précliniques et cliniques, en particulier dans la prévention des maladies chroniques et le traitement des infections urinaires. Une fois consommées, en raison de leur structure complexe, elles atteignent le côlon intactes où elles rentrent dans une relation bidirectionnelle avec le microbiote. Les (poly)phénols comme les PAC peuvent agir à la fois comme antibiotiques contre certains pathobiontes et comme prébiotiques, modifiant ainsi la composition du microbiote. Cette interaction bidirectionnelle n'a toutefois pas été décrite de façon exhaustive et la modulation du microbiote par les (poly)phénols est encore mal caractérisée. Pour élucider l'impact d'un extrait de canneberge riche en PAC sur le microbiote intestinal luminale et mucosale, le modèle in vitro M-TWIN-SHIME a été inoculé avec des échantillons fécaux de 6 individus sains (n=6) pour simuler le côlon ascendant et transverse pendant une semaine de témoin et deux semaines de supplémentation standardisée à 86mg/jour/individu de PAC. La supplémentation a engendré une modification du microbiote et un changement dans le profil de production d'acides gras à chaîne courte, les deux plus marquées dans le colon ascendant. Un effet bifidogénique spécifique sur *B. adolescentis* a été observé dans le mucus du colon ascendant et une croissance des genres producteurs de butyrate et de probiotiques de deuxième génération comme *Faecalibacterium prausnitzii* a été remarqué dans le colon transverse à la suite des deux semaines de supplémentation. Certaines espèces impliquées dans le métabolisme des PAC ont été stimulées, mais cela dépend de la composition initiale du microbiote des différents sujets. Un consortium d'espèces bactériennes clés (keystones) comme *Akkermansia muciniphila*, essentielles à l'équilibre de l'écosystème intestinal, a été identifiées grâce à l'analyse des réseaux de co-occurrence : ces espèces clés, localisées principalement dans le mucus, sont probablement impliquées dans l'augmentation significative en butyrate engendrée par la supplémentation. Les résultats démontrent l'impact de la supplémentation avec un extrait de canneberge riche en PAC sur le microbiote intestinal, son activité butyrogénique, ainsi que la capacité de moduler l'équilibre de l'écosystème intestinal en favorisant un nouveau consortium de bactéries potentiellement bénéfiques.



Title: Evaluating the protective effects of lactoferrin-osteopontin complex (LF-OPN) on cardiometabolic disorders in a murine model fed with high-fat, high-fructose diet

Topic: PERSONALIZING NUTRITION

Author: Baumel Tagharist, Sarah - Spahis, Schohaya - Sané, Alain - Normandeau, Chloé - Bélanger, Véronique - Marcil, Valérie - Lévy, Émile

Summary: Background: There is a growing interest in bioactive peptides derived from human and bovine milk proteins due to their potential health benefits against the development of the metabolic syndrome (MetS) and its components. Lactoferrin (LF) and osteopontin (OPN) are two multifunctional milk proteins that have an affinity for each other and together naturally form a protein complex (LF-OPN). While the benefits associated with their administration have been evaluated in vitro, animal studies are necessary to assess their effects in vivo.

Aim: The main purpose of this study is to examine the capacity of the LF-OPN complex to mitigate cardiometabolic disorders including lipid abnormalities, glucose disturbances, and oxidative stress induced by a high-fat, high-fructose diet (HFHS) in a murine model.

Methods: Thirty-six C57BL6/J mice were treated and divided into 3 groups: (1) control: standard diet + vehicle; (2) placebo: HFHS diet + vehicle; and (3) LF-OPN: HFHS diet + LFOPN complex (20 mg/kg bw/day). After 8 weeks of treatment, animals were weighed, oral glucose tolerance test was performed and sacrificed. Detailed analyses of lipid profile (triglycerides and cholesterol) and glycemic parameters will be measured in plasma (glucose and insulin levels). Protein expression implicated in the mechanisms of these cardiometabolic disorders (lipogenesis [FAS, ACC, and SREBP1c] and insulin resistance marker [Akt, p38, AMPKa]) will be semi-quantitatively measured by Western blot. The results will be compared between each group using analysis of variance (ANOVA) test.

Preliminary results: Compared to placebo mice, LF-OPN mice had lower body weight (mean \pm SEM : 24.9 ± 2.2 g vs. 22.8 ± 1.8 g; $p < 0.001$) and total adipose tissue weight (3.4 ± 0.2 g vs. 2.3 ± 0.3 g, $p < 0.01$). Based on the OGTT, lower plasma glucose levels (area under the curve) were observed in LF-OPN mice compared to placebo at all time points.

Conclusions: These preliminary results suggest a protective effect of the LF-OPN complex against increased body fat and glucose intolerance induced by a HFHS diet in mice. This research project will contribute to describe the effects of the LF-OPN complex as a promising intervention in MetS management.



Title: Effects of dietary Iron in mice reshaping the gut microbiome and host endocannabinoid mediators

Topic: PERSONALIZING NUTRITION

Author: Guevara Agudelo, Fredy Alexander - Leblanc, Nadine - Bourdeau-Julien, Isabelle - Martin, Cyril - Flamand, Nicolas - Veilleux, Alain - Di Marzo, Vincenzo - Raymond, Frédéric

Summary: The endocannabinoid system (eCB), or endocannabinoidome (eCBome) in conjunction with the gut microbiota, has been involved in impaired metabolism. The interaction of these biological systems has arisen as a key modifier of human health that may affect the development and progression of obesity, due in part to their involvement in the regulation of food intake and metabolism. Iron (Fe) is a fundamental micronutrient required in a wide variety of metabolic processes. Here, we identify the implications of dietary variations of Fe may affect on the composition of the intestinal microbiota and the eCBome during the establishment of diet-induced obesity. We sequenced by 16S rRNA metataxonomics the intestinal contents of mice fed with Fe-depleted and -enriched, combined with low- and high-fat/sucrose, diets and correlated the levels of circulating and intestinal eCBome mediators (ileum and caecum) with the microbial species found for each condition. Overall, the intestinal microbiota composition showed a remarkable differentiation between the segments of the intestine ($P < 0.01$, PERMANOVA). Individual differences of microbial taxa were more pronounced in the caecum than in the ileum, and the two segments reacted differently to dietary Fe treatments. In the caecum, *Eubacterium coprostanoligenes* group showed an increase in its relative abundance associated with the interaction of Fe-depletion with the LFLS diet, while *Streptococcaceae* exhibited higher relative abundance under the interaction between the Fe-depletion and the HFHS formulation. Regarding the eCBome, circulating levels of anandamide and N-oleoylethanolamine were associated with the interaction between depletion of Fe and LFLS. Moreover, circulating levels of anandamide and N-oleoylethanolamine were higher with the HFHS and LFLS diet, respectively. In the intestine, a statistically significant modulation was observed for N-stearoylethanolamine, associated with the interaction of Fe enrichment with LFLS. Our study shows that a Fe-enriched diet induces a slight intestinal inflammation, and remodels the intestinal microbiota as well as the circulating and intestinal eCBome. The role of this remodeling in Fe status-induced inflammation needs to be further explored.



Title: Oral fructose increases inflammation without modifying exercise inflammatory response in men with type 2 diabetes: a randomized crossover study

Topic: PERSONALIZING NUTRITION

Author: Tremblay, Xavier - Maelle, Blais - Sarthou, Julienne - Prémont, Chloé - Mathieu, Marie-Anne - Auclair, Audrey - Pettigrew, Myriam - Piché, Marie-Ève - Poirier, Paul

Summary: Background: Type 2 diabetes (T2DM) is associated with chronic inflammation which increases insulin resistance and cardiovascular risk. Fructose consumption as well as exercise increase inflammation in the short term in the general population. The combined effect of fructose consumption and exercise on inflammation in T2DM is unknown. The objective of this study is to assess the impact of fructose ingestion on the exercise related acute inflammatory response in adults with T2DM.

Methods: Ten men (age: 55 ± 12 years, BMI: 29.8 ± 5.1 kg/m²) with T2DM (HbA1C: 0.059 ± 0.006) without insulin treatment or cardiac conditions completed five 60-min moderate-intensity (60% VO₂max) exercise sessions in a single-blind crossover design under the following conditions: 1) fasted state and, 2h after an equal calorie counts meal enriched in; 2) glucose, 3) fructose, 4) fat, and 5) aspartame. Blood samples were taken 15 minutes prior to exercise (i.e. 2 hours after the standardized meal), and every 15 minutes until 30 minutes into post-exercise recovery (time 90) for C-reactive protein (CRP). Other markers, interleukin 6 (IL-6), macrophage inflammatory protein-1 alpha (MIP-1 α), and monocyte chemoattractant protein 1 (MCP-1) were measured at the start of exercise (time 0) and after the exercise session (at 60 and 90 min).

Results: CRP levels were higher during the exercise session following ingestion of fructose compared with glucose (2.93 vs 1.66 mg/L, $p=0.005$). No significant differences were observed between time points. MCP-1 levels increase after the ingestion of fructose compared to the fasted state (161.1 vs 117.0 pg/L, $p=0.003$). There was no changes in IL-6) and MIP-1 α , No interaction was found between exercise and meal content (Figure).

Conclusion: Our results suggest that fructose leads to an increased inflammatory response when compared to other macronutrients. The lack of interaction between time and meal condition suggests that the pre-exercise meal does not modulate the potential acute exercise inflammatory response. Further studies are needed to evaluate whether exercise intensity or different exercise type leads to distinct results, as well as the possibility of a sex-specific response.



Title: Effect of the addition of maple syrup on the phenolic profile of local wine

Topic: PERSONALIZING NUTRITION

Author: Potvin, Maxime - Corminboeuf, Anne - Perillous, Océane - Drainville, Louis - Cardinal, Sébastien

Summary: In some regions of Quebec, the culture of vine is submitted to harsh weather. Consequently, the sugar content of the grapes may vary when comes harvest time and might end up insufficient for winemaking. Therefore, it is sometimes necessary to add sugar to the must to be able to have a successful alcoholic fermentation and reach a minimal alcohol level of 12%. This process, called chaptalization, is traditionally performed using white sugar. However, maple syrup could potentially be used as an alternative to sugar for producing a purely local wine, while also valorizing a trademark of Canada's craftsmanship and food industry. The Ferme Expérimentale Terre-Eau (FETE), with its sugar bush and its 10 km of vines composed of 13 different hybrid grape varieties, is working since 2016 to explore this possibility. So far, three vintages of various wines chaptalized with maple syrup have been produced and many of them showed pleasant organoleptic properties. More importantly, this new type of wine may also offer a higher added value in terms of nutritional value. Indeed, studies suggest that a moderate consumption of wine and/or maple syrup may bring some health benefits due, notably, to the presence of phenolic compounds in these two foodstuffs. Recently, our group has established a collaboration with FETE to investigate the impact of the addition of maple syrup on the phenolic profile of the resulting wine. First, the total phenolic content of wines produced at the FETE with and without the addition of maple syrup will be determined. Then, quantitative, and qualitative HPLC studies will be carried out to establish a more detailed phenolic profile for those two types of wine. This presentation will focus on describing this methodology with further details. Some preliminary results will be shown as well.



Title: FIGHTING INFLAMMATION AND CARDIOMETABOLIC DISEASES BY COMBINING THE IMMUNOMETABOLIC PROPERTIES OF MARINE OMEGA-3 FATTY ACIDS AND PLANT

Topic: PERSONALIZING NUTRITION

Author: Navarro, Pauline - Agrinier, Anne-Laure - Marcotte, Bruno - Mitchell, Patricia - Marette, André

Summary: Background: Obesity is associated with a chronic-low grade inflammation known to promote insulin resistance leading to type 2 diabetes and cardiovascular diseases. Studies have indicated that gut microbiota plays a critical role in obesity and metabolic diseases. Objective: To study extracts from various marine biomasses, rich in omega-3 (ω -3), and plant extracts, rich in polyphenols and terpenes to develop bioactive ingredients with strong anti-inflammatory and anti-diabetic potential. Method: LPS (lipopolysaccharides, 5ng/ml) induced inflammation in J774 macrophages was co-incubated with indicated treatment compound for 21h. Nitric oxide (NO) production was assessed using the Griess reaction and pro-inflammatory cytokines (IL-6 and TNF- α) assessed by ELISA. Results: Treatment with marine oils (ω -3 sources), lignin extract (polyphenols source) and essential oil (terpenes source) induced a dose-dependent inhibition of the pro-inflammatory mediator NO (-30% for 100 μ g/mL of ω -3 oils; -69% for 100 μ g/mL of lignin extract and -60% for 100 μ g/mL of essential oil). The production of pro-inflammatory cytokines was significantly decreased by the treatments at 100 μ g/mL (-60% IL-6 and -30% TNF- α for ω -3 oils; -40% IL-6 for lignin extract; -30% IL-6 and -25% TNF- α for essential oil). Differently, lignin extract increased TNF- α production (+60% at 100 μ g/mL). Conclusion and perspectives: These results indicate that ω -3, polyphenol or terpene rich biomasses may have the potential to act on immuno-metabolic targets. Further validation in vivo will be necessary. To advance our understanding of these biomasses on the gut microbiota we will employ a bioreactor (artificial colon system) to investigate metabolite production, which will provide insight into potential mechanisms of action.



Title: Sucralose and maltodextrin affect differently the gut microbiota of healthy individuals and IBD patients

Topic: NUTRITION AND SOCIETY

Author: Gonza, Irma - Goya-Jorge, Elizabeth - Douny, Caroline - Scippo, Marie-Louise - Louis, Edouard - Delcenserie, Véronique

Summary: Intestinal fibrosis is a long-term complication of inflammatory bowel diseases (IBD). Changes in microbial populations have been linked with the onset of fibrosis and some food additives are known to promote intestinal inflammation facilitating fibrosis induction. Most of these studies have been performed using murine models or healthy donors while the effects of food additives on intestinal microbiota of patients suffering from IBD is less understood. The aim of this work was therefore to determine how food additives affect intestinal microbiota of both healthy and “IBD” donors. Two food additives, sucralose (SUC) and maltodextrin (MDX), were tested in a short-term (72h) in vitro model of the human intestinal microbiota. Three groups of donors were investigated: healthy persons (H), patients in remission of IBD (R) and patients with an active period of IBD (A). Short-chain fatty acid production was assessed using SPME-GC/MS while the evolution of microbial populations positively or negatively correlated with health, inflammation and/or fibrosis was assessed using qPCR. MDX and SUC increased propionate and butyrate production in H and R donors. In addition, MDX increased butyrate in A donors and decreased the butyrate-producer genus *Roseburia* in H and R donors. Both, SUC and MDX decreased the beneficial bacteria *F. prausnitzii* in A donors. Moreover, in R and A donors, SUC and MDX decreased *A. muciniphila*. MDX promoted the growth of *Enterococcus* in H and R groups and *Streptococcus* in the three groups of donors, both genus being associated with intestinal inflammation. SUC induced increases of *Escherichia/Shigella* in H and *Enterococcus* in H and R groups. *Ruminococcus*, correlated with higher risk of fibrosis, was increased in the three groups of donors treated with MDX while SUC increased *Ruminococcus* only in IBD donors. *Oscillospira*, correlated with reduced risk of fibrosis, was decreased in the three groups of donors with MDX and in H and A donors with SUC. This study demonstrates how strongly the human microbiota can be affected by some food additives. In addition, to our knowledge, this is the first human in vitro study focusing on the impact of food additives on microbiota of IBD patients.



Title: Exploring the Role of Tissue Microbiota in the Development of Type 2 Diabetes

Topic: FOOD SUPPLY AND WELL-BEING

Author: Scapino, Ilaria

Summary: Obesity, and more particularly visceral obesity, represents a major risk in the development of glucose intolerance leading to type 2 diabetes. A recent discovery has made it possible to identify a very different bacterial signature in the tissues of healthy obese subjects compared to that of obese diabetic subjects [1]. The first objective of the project will be to characterize the bacterial activity of metabolic tissues and to understand its role in the development of type 2 diabetes. We thus hypothesize that live bacteria are found in the liver and adipose tissue of diabetic or non-diabetic subjects and thus play a role in the regulation of the metabolism of these subjects. Thus, the second objective of this project will consist in testing in mice the metabolic impact of the different strains thus cultured from human tissues. For this second objective, we hypothesize that the bacteria isolated from the tissues of diabetic subjects cross the intestinal barrier and cause metabolic disorders in the recipient mice and that conversely, those isolated from non-diabetic subjects are not harmful or protect against metabolic disorders associated with obesity. This highly innovative project will provide a better understanding of the importance of tissue microbiota in the development of type 2 diabetes. On the other hand, by discovering strains specific to subjects resistant to diabetes, this project could lead to the discovery of new probiotics protective against the development of the disease.

1. Anhê, F.F., B.A.H. Jensen, T.V. Varin, F. Servant, S. Van Blerk, D. Richard, S. Marceau, M. Surette, L. Biertho, B. Lelouvier, J.D. Schertzer, A. Tchernof, and A. Marette, Type 2 diabetes influences bacterial tissue compartmentalisation in human obesity. *Nat Metab*, 2020. 2(3): p. 233-242. PMID: 32694777



Title: Cranberry proanthocyanidins modulate intestinal epithelial function and differentiation in mouse intestinal organoids

Topic: NUTRITION AND SOCIETY

Author: Tinoco Mar, Briscia Anaid - Mayer, Thomas - Di Marzo, Vincenzo - Desjardins, Yves - Veilleux, Alain

Summary: Cranberry proanthocyanidins (PACs) possess a distinctive polyphenol profile associated with various health benefits, including antidiabetic and antioxidant properties. Due to their high degree of polymerization, PACs are poorly absorbed but can be metabolized by the gut bacteria into 5-(3',4'-dihydroxyphenyl)- γ -valerolactone (DHPVLT) and other metabolites. In the small intestine, PACs can therefore directly interact with the intestinal epithelial cells, including enterocytes, goblet cells, enteroendocrine cells, Paneth cells, and stem cells. This study aims to investigate the impact of cranberry PACs, on intestinal epithelial functions, such as metabolism, mucosal barrier protection, and organogenesis.

Methodology: Mouse duodenal intestinal epithelial organoids were subjected to cranberry proanthocyanidin (PAC) extract in a dose- and time-dependent manner. The expression of genes associated with epithelial barrier function, lipid metabolism, endocrine and cell differentiation was analyzed through by qPCR.

Results: Cranberry PACs increase mRNA expression of the transcription factors Hes1 and Atoh1, involved in intestinal absorptive and secretory epithelial cell differentiation. Cranberry PACs upregulated the expression of genes involved in mucosal defense, such as Muc2 and Reg3A and Defa20. We also observed several changes in the expression of genes involves in glucose homeostasis (Gip, Gcg) and endocannabinoidome signaling (Gpr55) following organoid exposure to cranberry PACs. These changes were mostly cumulative in dose and time, but some genes show transient response which culminates within 2–6 hours after exposure to PACs.

Conclusions: These results suggest that cranberry PACs enhance intestinal barrier function by promoting the differentiation of intestinal stem cells into the secretory lineage, including the Goblets cells. These results also suggest that PACs promote antibacterial effects and mucin secretion. Further experiments are needed to determine the molecular mechanisms by which PACs exert their beneficial effects in the epithelial cells.



Title: A unique model to assess the oral transfer of dietary microRNAs

Topic: FOOD SUPPLY AND WELL-BEING

Author: Husseini, Zeinab - Benmoussa, Abderrahim - Gilbert, Caroline - Provost, Patrick

Summary: The horizontal transfer of dietary microRNAs, especially milk-derived microRNAs, has been the focus of many studies in the previous 10 years and is gaining more attention in the field of oral route-based RNA therapeutics. The study of the bioavailability and bioactivity of dietary microRNAs upon oral food ingestion has many limitations and challenges, to mention of which microRNA sequence homology across species, which hinders the ability to distinguish between exogenous and endogenous microRNAs. In our lab, we employed a unique cow model which exhibits mammary gland-controlled expression of unique microRNA sequences. Upon small RNA sequencing of milk RNA, we found that these microRNAs are highly enriched in this model's milk. Additionally, the majority of these microRNAs were associated with milk extracellular vesicles (EVs) which are hypothesized to protect these microRNAs from harsh conditions in the digestive tract and RNase-rich environment in the blood. Further in vivo studies showed the transfer of these microRNA species into mice upon oral ingestion of concentrated milk EVs. Further work is on the way to elucidate potential gene regulatory functions of these orally transferred microRNAs.



Title: Automation of a nucleic acid extraction platform: its potential for foodborne viruses on berries, romaine lettuce and oysters

Topic: FOOD QUALITY

Author: Trudel-Ferland, Mathilde - Collard, Marie-Ève - Jubinville, Éric - Hamon, Fabienne - Jean, Julie

Summary: Introduction: Each year, approximately 23% of foodborne illnesses across the world are attributed to human noroviruses (HuNoV) and hepatitis A virus (HAV). In recent years, these viruses have been under surveillance by several government bodies to determine their prevalence in mollusks and fresh or frozen produce. Consequently, it is crucial to develop rapid and automated detection methods to facilitate efficient surveillance of these at-risk food matrices.

Purpose: An automated nucleic acid extraction platform was optimized for the detection of viruses in at-risk food matrices. This protocol was then validated in comparison to a semi-automated method already on the market and using the extraction principle required in the reference method ISO 15216-1:2017.

Methods: Target viruses (HuNoV GII.4, GI.7 and HAV) were spiked on fresh or frozen raspberries (25 g), frozen blackberries (25 g), romaine lettuce (25 g) and oyster digestive glands (2 g) at either 10^2 , 10^3 or 10^4 genome copies/samples. Different elution, recovery and purification of the samples were done according to the ISO method depending on the food matrices tested. Viral RNA was extracted using the optimized automated protocol or semi-automated method. For the comparison between the two platform, results were analyzed in a qualitative detection (presence/absence of signals). All experiments were replicated three times.

Results: On fresh raspberries, romaine lettuce and oysters, target viruses were detected on all samples at medium and high concentrations (10^3 or 10^4 copies/samples) but some negatives were seen at low concentration (10^2 copies/samples); nonetheless, the two extraction methods were considered equivalent ($p > 0.05$).

For frozen raspberries and blackberries, some negative samples were seen at medium and low concentrations. The optimized automated extraction method led to a better detection than the semi-automated method ($p = 0.0488$) for frozen raspberries. As for frozen blackberries, less inhibition was seen with the automated method compared to the semi-automated method, 56.5% (95% CI 25.6-63.2%) and 95.0% (95% CI 76.4-99.7%) respectively.

Significance: These results show that the automated extraction platform can be effortlessly operated by users without continuous oversight yielding comparable or even superior results to the semi-automated method. This highlights its potential for routine analysis during food processing and surveillance.



Title: Effect of pulsed light for the inactivation of foodborne viruses on frozen fruits

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Kim, Hyo Jung - Jubinville, Éric - Goulet-Beaulieu, Valérie - Jean, Julie

Summary: Introduction: The rapid growth of the frozen food market has raised concerns regarding the incidence of outbreaks linked to frozen fruits. Notably, frozen fruits serve as significant vectors for transmitting foodborne viruses, like human noroviruses (HuNoV) and hepatitis A virus (HAV). Recent outbreaks continue to be a problem, requiring further research and control measures to ensure food safety. For example, in Canada, five recalls involving norovirus-contaminated frozen raspberries have been observed since May 2022. Also in 2021, an outbreak related to the hepatitis A virus caused by frozen mangoes was recorded. Therefore, the evaluation of innovative control strategies such as pulsed light (PL) are essential to reduce the risk associated to foodborne viruses in frozen fruits and improve overall food safety.

Purpose: This study aims to assess the efficacy of pulsed light (PL) in inactivating foodborne viruses directly applied on several at-risk frozen fruits, including blueberry, raspberry, strawberry, blackberry, frozen cranberry, cherry, mango, and pineapple.

Method: Fresh fruits were artificially contaminated with 30 μL of murine norovirus 1 (MNV-1) or HAV suspension (106 PFU/mL) and subjected to freezing for 48 h. Subsequently, pulsed light (PL) treatment, consisting of 16 pulses (11.52 J/cm²), was applied to the frozen fruits. Post-treatment, viruses were recovered using Earle's Balanced Salt Solution (EBSS) and titer was determined through plaque assay. The visual characteristics and temperature profiles of samples were examined pre-and post-PL treatment to confirm any alterations induced by PL exposure.

Results: Frozen cranberries showed more than 3.5 log reduction in MNV-1 and HAV titer after PL treatment. In contrast, most other frozen fruits showed 1-2 log reduction, like what was observed in previous studies with fresh fruits. However, the frozen fruits did not change color or darken after PL treatment unlike fresh fruits, and they remained frozen. PL process had significant effect (2-way ANOVA, Sidak $p > .0001$) to the log reduction against target viruses.

Significance: The viral decontamination effect of PL observed in various frozen fruits during this study can offer a promising strategy to mitigate foodborne virus outbreaks originating from frozen fruit consumption.



Title: Characterization of chicken cruor-derived hydrolysates produced through enzymatic hydrolysis and evaluation of the feasibility of their use as natural antimicrobials

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Rahimi, Delasa - Thibodeau, Jacinthe - Fliss, Ismail - Mikhaylin, Sergey - Bazinet, Laurent

Summary: Chicken blood is a rich protein source that can be upgraded to generate value-added products. Annually, 48 million liters of blood are produced in Canada during chicken slaughter. 40% of the total volume of blood is composed of cruor, which is a solid substance in the blood. Upon hydrolysis of cruor after its separation from blood, bioactive peptides may be obtained. It has been shown that bioactive peptides can provide health benefits such as antimicrobial (antibacterial and antifungal), antioxidant, antihypertensive, and antihyperglycemic properties. Bioactive peptides as bio-preservatives have gotten significant attention in the past years in developed countries where people demand healthier foods without chemical or synthetic preservatives. In this project, after collecting chicken blood from slaughterhouses and separating the cruor part by centrifugation then peptic hydrolysis conditions (pH 2, 3, 4 and 5) and duration (30 and 180 minutes) were applied. Following this, the antifungal and antibacterial effects of the hydrolysates against 3 main pathogenic bacteria of concern for the consumer of poultry meat (*Listeria ivanovii* HP B28, *Campylobacter Coli* ATCC 33559, *Salmonella enterica* ssp Newport ATCC 6962), one yeast (*Rhodotorula mucilaginosa* 27,173) and one mold (*Paecilomyces* spp. 5332-9a) were evaluated. Then, the minimum inhibitory concentration (MIC) of hydrolysates, as well as their minimum bactericidal concentrations (MBC) or minimum fungicidal concentrations (MFC) were determined. Also, peptide population, sequence, enzyme mechanism, and degree of hydrolysis (DH%) were determined to evaluate the hydrolysates generated during the process. The greatest inhibitory effect against *Paecilomyces* and *R. mucilaginosa* was observed in hydrolysates obtained at pH 2 after 30 min of hydrolysis. However, no antibacterial activity was observed in all the hydrolysates produced. The highest DH% was recorded at pH 2, which was not significantly different from pH 3. Further, the enzyme's mechanism of action at pH 2 and 3 was a zipper mechanism, while at pH 4 and 5, it was a one-by-one mechanism. Following this, to increase the functionality, the hydrolysates with the best antimicrobial activity will be purified using electro dialysis with filtration membranes (EDFM), then it will be used as a natural preservative in the food model. This project aimed to valorize blood waste as a source of peptide fractions with effective antimicrobial properties. Indeed, besides reducing waste, a natural preservative was produced in the context of a circular economy.



Title: Deposition of viral aerosols on surfaces and food: the factors involved

Topic: FOOD QUALITY

Author: Sanka, Linda Amayeale - Jubinville, Eric - Turgeon, Nathalie - Goulet-Beaulieu, Valérie - Duchaine, Caroline - Jean, Julie

Summary: In Canada, the incidence of foodborne illnesses is 4 million cases per year. The majority of these are associated with viral infections. Among the viruses involved, human norovirus (HuNoV) is the leading cause of viral gastroenteritis worldwide, followed by hepatitis A virus (HAV), which poses enormous health problems. In addition, hepatitis E virus (HEV) is an emerging zoonotic virus. Infection with hepatitis A and E viruses manifests as fever, unusual tiredness and weakness, headache, jaundice and, in some cases, nausea and vomiting. HuNoV infection is characterized by diarrhea, nausea and jet vomiting. During an episode of vomiting, aerosols that may contain viral particles are produced. Depending on their size, these viral aerosols may contribute to the spread of the disease, either directly when inhaled or indirectly when deposited on a surface or food that can be in contact with humans. Over a short distance, aerosols composed of large particles settle under the influence of various forces. Despite numerous studies on natural airborne viruses, very little is known about the conditions that influence the deposition and persistence of foodborne viruses on surfaces and food after aerosolization. The aim of this project is to study the deposition of aerosolized viruses on surfaces found in the food sector and on high-risk foods. It will thus constitute a reference for studies concerning foodborne viruses and aerosols.

The first step is to fine-tune the technique. To this end, an initial aerosolization test will be carried out on the phage Phi X-174, which is used here as a model. The phage will be aerosolized using the TSI 9602 nebulizer in a small experimental chamber containing stainless steel, polypropylene, glass disks and fruits samples. Parameters such as nebulization time and dilution rate will be determined during this study. Based on these initial results, the deposition of the above viruses under optimal conditions will be evaluated.

These data will provide more precise guidelines for restaurant managers and manufacturers on how to manage and respond to aerosol-generating incidents, thus limiting the risk of viral propagation.



Title: LC-MS Application in Food Safety: Food Thermal Labels are a Source of Dietary Exposure to Bisphenol S and Other Color Developers

Topic: FOOD QUALITY

Author: XU, Ziyun - Tian, Lei - Goodyer, Cindy Gates - Liu, Lan - Bayen, Stephane - Hales, Barbara

Summary: Bisphenol A (BPA) has been widely used in plastic food packaging and as a color developer in thermal paper. The European Union (EU) prohibited BPA usage in thermal paper above 0.02% by weight in 2020, leading to the adoption of substitutes such as bisphenol S (BPS). Several reports have flagged potential human health risks associated with chronic exposure to such structural analogues of BPA. In earlier research, we identified BPS in packaged fresh food in Canada, yet its source remained unknown.

In this study, liquid chromatography quadrupole time-of-flight mass spectrometry (LC-Q-TOF-MS) was used to detect and quantify a suite of bisphenol compounds. We collected 140 packaging samples from Montreal stores, including thermal weighing label stickers (40), films (39), trays (18), meat absorbents (14), and other label stickers (29). Thermal labels (40) were shown to be a major source of bisphenols (up to 214 $\mu\text{g}/\text{cm}^2$). Although BPA was not detected in thermal label samples, BPS (frequency: 29/40), D-8 (4/40), D-90 (8/40), TGSA (7/40), and PF-201 (8/40) were found at significant levels.

Bisphenol migration from thermal labels to food was then explored using twenty-four packaged fish samples from Canada and the USA. Important levels of migration were recorded for BPS (up to 1140 ng/g wet weight), D-8 (up to 230 ng/g ww), D-90 (up to 3.41 ng/g ww), and PF-201 (up to 1.87 ng/g ww) in fish wrapped in film with a thermal label sticker (4°C) for 5 days. The BPS migration significantly exceeded the European Union Specific Migration Limit (50 ng/g ww).

Dietary exposure to BPS was assessed to be significantly higher than dermal exposure. This study revealed that thermal label stickers are a substantial dietary source of bisphenols, necessitating a comprehensive risk assessment. Strategies to reduce the migration of bisphenols from food labels through films should also be investigated.



Title: Structure-activity study and optimization of the antimicrobial peptide Brevibacillin : A chemical approach for novel synthetic analogues with a low hemolytic activity

Topic: FOOD QUALITY

Author: Fliss, Omar - Guay, Louis-David

Summary: Introduction: The overuse of antibiotics in humans and farm animals has led to the emergence of antibiotic-resistant bacteria that are problematic from both a health and clinical standpoint. Face to this public health problem, the development of new antimicrobial agents has become a global priority. Antimicrobial peptides represent one of the most promising alternatives to antibiotics. Among them, the lipopeptide brevibacillin produced by *Brevibacillus larterosporus* is particularly attractive because of its inhibitory activity against several pathogenic bacteria, including many that are multi-resistant to antibiotics.

Objective: To better understand its mode of action and improve its pharmacological properties, structural analogues of brevibacillin were produced for a structure-activity study.

Methodology: Brevibacillin and 14 analogues were produced by chemical synthesis. Agar diffusion and microtiter tests against a dozen pathogenic strains were used to determine the minimum inhibitory and bactericidal concentrations, as well as the spectrum of action. The hemolytic activity of each peptide was also investigated.

Results and discussion: The results obtained show that most of the analogues have an inhibitory activity equivalent to the native brevibacillin. The structure-activity study showed that some amino acids can be modified without affecting antimicrobial activity. These positions can be used to increase production yields and improve pharmacological properties. In addition, hemolytic activity results showed that two synthetic analogues exhibited low hemolytic activity (6% and 8%) at a concentration 100 times higher than their MIC values.

Conclusion: The investigation provides evidence of the antimicrobial efficacy inherent in brevibacillin and highlights the feasibility of enhancing its production yields and antimicrobial properties through analogous compounds for uses in the food industry as well as veterinary and human medicine.



Title: Paving the Way for Next-gen Antibacterial Solutions: Unraveling Antimicrobial Peptides against Clinical Isolates of *Campylobacter* spp.

Topic: FOOD QUALITY

Author: Khaled, Abdallah - Phung, Ngyen - Fliss, Omar

Summary: Introduction : Antibiotics can be effective in killing bacteria or inhibiting their growth, but their misuse can lead to antibiotic resistance. Researchers are increasingly drawn by investigations about the possibilities of utilizing novel antimicrobial peptides (AMPs) as alternative therapeutic agents. One avenue of interest in these endeavors involves ongoing studies on bacteriocins and lipopeptides such as brevivacillin, for their potential antimicrobial properties.

Objective : The aim of the study was to evaluate the inhibitory activity of four microcins and brevivacillin against clinical multidrug resistant *Campylobacter* spp. isolates.

Methodology : Five peptides (MccJ25, MccB17, MccC and MccE492 and brevivacillin) were produced and purified. Their inhibitory activity was determined by microtitration assays against a number of well-characterized *Campylobacter* spp. through the determination of the minimum inhibitory concentrations (MIC) and minimum bactericidal concentrations (MBC). A comprehensive Genome-Wide Association Study (GWAS) was undertaken to elucidate the intricate relationship between genomic variants and phenotypic resistance.

Results : We first tested the antimicrobial resistance profiles of *Campylobacter* spp, part of our collection (n=44). The antibiotic susceptibility testing revealed significant resistance to ciprofloxacin, tetracycline, ampicillin, and gentamicin, with 68.7% of the strains displaying multidrug resistance. The analysis of the WGS data revealed a plethora of resistance genes and mutations. The results obtained from susceptibility assays using the five peptides demonstrated significant inhibitory activity against the tested strains. Specifically, MccJ25, MccC, and MccE492 exhibited considerable inhibitory effect, with minimum inhibitory concentrations (MICs) ranging from 125µg/ml to 500µg/ml. In comparison, brevivacillin displayed even greater efficacy, with MICs ranging from 8µg/ml to 64µg/ml against the same strains.

Conclusion : The results indicate a strong potential of microcins as antimicrobial peptides, providing a promising avenue to address the pressing issue of antibiotic resistance. Further exploration and development of these peptides could potentially open new avenues for combating bacterial infections. Additionally, the findings highlight brevivacillin as a particularly promising antimicrobial agent, showing potent activity with lower MIC values against *Campylobacter*.



Title: Ketone body transport across the blood-brain barrier by in situ cerebral perfusion in a mouse model of Alzheimer's disease

Topic: NUTRITION AND SOCIETY

Author: Seguin, Dominique - Leclerc, Manon Leclerc - Linhares, Sabine - Emond, Vincent - Calon, Frédéric

Summary: Background: β -hydroxybutyrate (BHB) is a ketone body that can be used by the brain as an alternative energy source to glucose. Since glucose utilization becomes deficient in Alzheimer's disease (AD), ketogenic interventions are under clinical intervention. Yet, the mechanisms of transport of BHB across the blood-brain barrier (BBB) and the relative role of the monocarboxylate transporters (MTC) remain unknown.

Methods: Intracarotid cerebral perfusion was used to quantify and characterize the transport of 3H-D- β -hydroxybutyrate (3H-BHB) through the BBB of non-transgenic and 3xTg-AD mice (modeling AD neuropathology). A high-fat diet (HFD) was used to induce obesity and metabolic disorders.

Results: First, we showed that 3H-BHB crosses the mouse BBB with a brain transport coefficient (Clup) of approximately $1 \mu\text{l.g}^{-1}\text{s}^{-1}$, similar to brain glucose transport. Competition with unlabeled BHB ($\times 200$) did not reduce the Clup, consistent with a non-saturable transport. However, blocking its putative transporter MCT1 with AZD3965 coperfusion resulted in a decrease of the Clup (-17%), suggesting that even if most 3H-BHB diffused freely across the BBB, it can be optimized from a more specific transport mechanism. The brain uptake of 3H-BHB remained similar in 3xTg-AD mice compared to non-transgenic, at different ages (14 and 21 months), independently of HFD consumption.

Conclusion: Our results indicate that (i) BHB brain uptake is similar to glucose with a facilitate diffusion transport across the BBB; (ii) partially dependent of the MCT1 transporter and (iii) unaffected by aging, AD neuropathology or HFD. This work supports the use of ketogenic interventions in AD by improving knowledge of the cerebral transport of ketone bodies. \AA



Title: Targeted and Non-targeted Identification of Phenolic Compounds as Markers for Authenticating Honey's Botanical Origin using LC-QTOF-MS

Topic: FOOD QUALITY

Author: Roginski, Alexandra - Tian, Lei - Bilamjian, Shaghig - Anumol, Tarun - Cuthbertson, Daniel - Bayen, Stéphane

Summary: Honey is a highly valued natural food product with superior nutritive value compared to other sweeteners. It contains essential minerals, vitamins, amino acids, proteins, enzymes, and bioactive compounds like phenolic compounds, which are recognized as the main compounds responsible for the antioxidant properties of honey. Studies suggest that phenolic compounds present in honey have various beneficial effects, including anti-cancer, anti-microbial, anti-fungal, anti-viral, anti-inflammatory, and antidiabetic effects. However, food fraud is a growing problem in the food industry, with honey being one of the most commonly affected products. The market value of honey is heavily influenced by its botanical origin, making it a lucrative target for fraudulent practices. Current strategies for studying the botanical origin of honey are either time-consuming or do not provide unambiguous markers, given the diversity of floral origins. This research delves into the utilization of advanced data processing tools in combination with high-resolution mass spectrometry (HRMS) for both targeted and non-targeted analysis to rapidly characterize phenolic compounds in honey as a means of authenticating their botanical origin. The phenolic fingerprint of >400 honeys from 19 different floral origins collected from the Canadian market was analyzed using a simple 'dilute-injection' LC-QTOF-MS method. This is the first study to analyze and compare the phenolic profile of Canadian honey from various botanical origins. This investigation revealed that the phenolic profile of honey may be used as a marker of honey's floral origin. This innovative approach has significant potential for food authenticity testing, and findings suggest that phenolic compounds in honey can be used as a powerful tool for combatting honey-related authentication challenges in the food industry.



Title: Applicability of CeresNano Viral Capture Kit for Foodborne Virus Detection

Topic: FOOD QUALITY

Author: Martel, Florence - Trudel-Ferland, Mathilde - Jubinville, Éric - Goulet-Beaulieu, Valérie - Jean, Julie

Summary: Hepatitis A virus (HAV) and human noroviruses (HuNoV) are known to be the most implicated viruses in foodborne diseases. Found in fresh and frozen berries and lettuce, their quick detection is necessary in these types of food matrices.

The optimization of the CeresNano method for the concentration of viruses in food matrices was performed. The virus recovery from this optimized and faster method was compared to the reference method ISO 15216 on fresh and frozen produce.

Concentration of viruses was performed using CeresNano kit and the ISO 15216 method. Samples (25g) of fresh and frozen raspberries, and romaine lettuce were spiked with HAV, NoV GII.4 and E. coli at either 10^3 or 10^4 genome copies/sample. The use of E. coli allowed to see the specificity of the methods under study. Mengo virus (MGV), as a process control virus, was also spiked in samples at 10^6 genome copies/sample. The extraction was performed to recover viral RNA. For raspberries, a column purification was applied after the extraction to remove inhibitors from this food matrix. Viral RNA was analyzed by RT-qPCR.

During optimization, capture of the viruses on magnetic beads was significantly improved by time ($P=0.0006$), 40 minutes of capture was chosen for the final experiments. The optimization of the CeresNano method reduced by more than 1 hour the total time of manipulations compared to the ISO method. While comparing the two methods, the ISO protocol led to better recovery ($P<0.05$) for HAV, NoV GII and MGV in the different food matrices, but similar results ($P>0.05$) were found for HAV on frozen raspberries at 10^3 genome copies/sample (26.79% vs. 15.08%, CeresNano and ISO, respectively) and lettuce at 10^4 genome copies/sample (13.24% vs. 7.15%, CeresNano and ISO, respectively).

While the CeresNano method provided lower or similar recovery for viruses in food matrices, the use of this method allows getting faster results which can be useful in industry to prevent the release of contaminated products and for routine surveillance programs. CeresNano could be a promising new detection tool for foodborne viruses. Further studies are required to reach the same recovery of the reference method.



Title: Comparison of Pretreatments to Distinguish the Infectious and Non-infectious Foodborne Viruses

Topic: FOOD QUALITY

Author: Lauzier, Anne-Marie - Douette, Émilie - Jubinville, Éric - Goulet-Beaulieu, Valérie - Jean, Julie

Summary: Introduction: Foodborne viruses, such as hepatitis A virus (HAV) and human norovirus (HuNoV) are responsible for multiple foodborne illnesses. To ensure food safety, it is important to apply specific, sensitive, and fast detection methods such as molecular methods. However, molecular methods, such as RT-qPCR, cannot discriminate between infectious and non-infectious viral particles. The application of specific treatments prior RT-qPCR could overcome this problem by only detecting RNA from infectious virus in food samples.

Goal: The aim of this project was to analyze the effectiveness of different RT-qPCR pretreatments applied to inactivated foodborne viruses.

Material and methods: HAV was inactivated partly and totally for each inactivation method. For heat inactivation, the virus was heated at 100 °C for 10 minutes or at 80 °C for one minute. For pulsed light inactivation, HAV was exposed to 7.2 J/cm² fluence in a single well plate or to 1.44 J/cm² fluence. Lastly, sodium hypochlorite at 500 ppm for 5 minutes or at 200 ppm for 1 min was used to inactivate HAV. Afterwards, inactivated viruses were treated with different pretreatments: PMA and PMAxx at 50 µM in 0.5 % triton, PtCl₄ at 500 µM, magnetic silica beads and Amicon centrifugal 100 KDa filter. Viral RNA was then extracted and amplified by RT-qPCR.

Results: Results show that PtCl₄ is the least effective pretreatment (< 0.1 log reduction) regardless of the type of inactivation tested with HAV compared to the untreated HAV samples. PMA and PMAxx were the most effective ones (> 1.2 log reduction) compared to untreated samples, especially during partial heat inactivation (2.4 log reduction) or during total heat inactivation (4.3 log reduction). Silica beads and Amicon were not as effective as PMAxx to reduce the viral titer of the infectious virus with a reduction of 0.8 log and 0.48 log, respectively.

Conclusion: Combinations of pretreatment and inactivation method showed interesting results. Based on the results, no universal pretreatment method can be applied for the detection of HAV following the three inactivation strategies tested. Further studies are required to confirm the results with human noroviruses and its application on food matrices.



Title: Human norovirus replication in zebra fish larvae and evaluation of antiviral treatments

Topic: FOOD QUALITY

Author: Plénière, Charlène - Goulet-Beaulieu, Valérie - Jubinville, Éric - Jean, Julie

Summary: Introduction : Human noroviruses (HuNoV) are the primary cause of worldwide foodborne gastroenteritis. Despite the virus being discovered in the 1970s, there is still limited knowledge regarding its biology and susceptibility to inactivation treatment. The lack of a robust, repeatable, and easily implemented viral replication system has hindered progress in these studies. HuNoV has been successfully propagated in cell cultures; however, maintaining these cultures is a challenging and very costly, often yielding low quantities of the virus. As an alternative approach, researchers have explored using surrogate models for studying norovirus behavior. While these surrogate studies offer valuable insights, the results are not always directly applicable to HuNoV due to several differences between the viruses. However, the use of zebrafish larvae for HuNoV replication appears to be a promising solution to these problems. Notably, various strains, including the highly epidemic GII.4 strain, have been successfully amplified through infection, resulting in an increase of approximately 3 log genome copies per 10 larvae.

Goal: In this project, the resistance of HuNoV should also be tested against heat, pulsed light, active chemical agents using the zebrafish larvae to identify the infectiousness of the virus.

Material and methods : First, a viral solution containing a minimum of 1×10^9 RNA copies per mL and derived from HuNoV-contaminated fecal samples will be microinjected into zebrafish larvae's yolk. The process will allow the replication for 3 days to generate viral stock. Then, HuNoV will be treated with physical (heat, pulsed light) and chemical treatments (grape seed extract, sodium hypochlorite). The viral inactivation will be evaluated by microinjecting those treated HuNoVs into the larvae : the objective is to determine their replication capability after the treatment. Additionally, in a parallel experiment, specific molecules of interest can be introduced into the larvae's environment during the replication process to further control viral proliferation.

Expected results : The production of larger quantity of same strains of HuNoV will facilitate studies and investigations on inactivation through physical or chemical treatments and detection methods. The results will provide more accurate and specific data on the viral resistance without HuNoV surrogates.



Title: ANTIMICROBIAL ACTIVITIES OF TURKEY CRUOR AFTER PEPSIC HYDROLYSIS: SLAUGHTERHOUSES BLOOD VALORISATION IN A CIRCULAR ECONOMY APPROACH

Topic: FOOD SUPPLY AND WELL-BEING

Author: Fliss, Houssine

Summary: Global pressure is growing to minimize the environmental impact of slaughterhouses. One way to answer this issue is to valorize by-products such as blood, by the production of bioactive peptides using enzymatic hydrolysis¹. To the best of our knowledge, no research has been previously performed regarding the pepsin hydrolysis of turkey cruor which contains, after blood centrifugation, hemoglobin, a protein not yet valorized since the main use of blood is focused on its colorless part (plasma)². This project aims to optimize the enzymatic hydrolysis conditions of turkey cruor and to evaluate the potential antimicrobial and antioxidant activities of peptides produced. Enzymatic hydrolysis of turkey cruor was carried out by pepsin (37°C, E:S ratio of 1:11 and pH 2, 3, 4, and 5). The kinetics of hydrolysis was evaluated by hydrolysis degree determination employing o-phthalaldéhyde (OPA) spectrophotometric assay and the peptide characterization was performed by reverse-phase high-performance liquid chromatography coupled with mass spectrometry (RP-HPLC-MS). A Gram+ bacterium (*Listeria ivanovi* HP B28) and a Gram- bacterium (*Escherichia coli* MP 4100), a filamentous fungus strain (*Mucor racemosus* LMA-722), and a yeast strain (*Rhodotorula mucilaginosa* 27,173) were tested to evaluate the antimicrobial activities of the time-dependant hydrolysates. This project is expected to take advantage of slaughterhouse blood by the production of bioactive peptides with the respect of circular economy principles, the adoption of which is currently being encouraged in the food industries.



Title: Probiotics in aquaculture : impact of *Pseudoalteromonas* strains on the flat oyster *Ostrea edulis*

Topic: FOOD SUPPLY AND WELL-BEING

Author: Leroy, Garance - Jégou, Camille - Baron, Sandrine - Beaulieu, Lucie - Fleury, Yannick

Summary: The global aquaculture production keeps on increasing since the 1990s, reaching 87.5 million tons of animals and 35.1 million tons of algae in 2020. 89% of the animal production was destined to human consumption (FAO, 2022).

This field encounters numerous infection events linked to different factors such as stress, dysbiosis or host genetics. The misuse and/or overuse of antibiotics have led to the emergence of antimicrobial resistance, which has become a major concern in aquaculture and a global public health threat. (Martínez Cruz et al., 2012; Preena et al., 2020; Quintanilla-Villanueva et al., 2023).

Probiotics are considered as a relevant tool to reduce the use of antibiotics. They are defined as "[...] a live microbial adjunct which has a beneficial effect on the host by modifying the host-associated or ambient microbial community" (Verschuere et al., 2000).

Five strains of *Pseudoalteromonas* bacteria were isolated from the hemolymph of healthy bivalves. They produce natural antimicrobial cationic cyclolipopeptides named alterins. The structural diversity of those compounds and their antimicrobial activity spectrum have been studied (Defer et al., 2013; Desriac et al., 2020; Offret et al., 2022). Those strains exerted a beneficial effect on marine bivalves and gastropods by improving their growth or helping the survival of those species against infections (Offret et al., 2019).

The european project PAQMAN aims to evaluate those strains as potential probiotics for marine aquaculture. To do so, the effects of *Pseudoalteromonas* strains during the sexual maturation of the flat oyster *Ostrea edulis* have been assessed. The effects on the biofilm formation in the tanks have been studied with a confocal laser microscope. The microbial communities of the seawater, the biofilm and the hemolymph have been observed via a metabarcoding analysis (ADNr 16S V3-V4 regions). The impact of the *Pseudoalteromonas* on oysters' larvae emissions was also assessed.

Significant reduction of the biofilm by some *Pseudoalteromonas* strains was demonstrated as well as an improvement of the larval emission. Analysis of the microbial communities of the hemolymph of the flat oysters and the environment are in progress.



Title: Quantification of beef in products sold in Canada declaring multiple meat species - regulatory and consumer implications related to accurate labeling

Topic: FOOD QUALITY

Author: Vatin, Gabrielle - Théolier, Jérémie - Dominguez, Silvia - Godefroy, Samuel

Summary: Unlike other jurisdictions (i.e. the European Union), Canadian regulations do not require the declaration of the percentage of each species of meat present in a pre-packaged food product. The standards of identity set minimum total meat protein levels for different categories, but declaration is only required for certain products in which phosphate salts and/or water are incorporated. In addition, the term "and/or" may be used to indicate the potential presence of a particular meat species in the formulation. The objective of this study was to determine the beef content of processed mixed meat products sold in Canada that were labelled with (i) beef and (ii) 'and/or' beef. Beef DNA in 92 products declaring beef on their label (e.g. frozen burgers, sausages, canned meatballs) and in 18 products declaring "and/or" beef (e.g. pepperoni, hot dogs, meat sauce) was determined by qPCR (SureFood® ANIMAL QUANT Beef kit, R-Biopharm; MIC thermocycler), analysed in duplicate. The beef content was expressed as a percentage of the total meat present in the food product by calculating the ratio of beef DNA copies to animal DNA copies obtained with the kit's standard curve. Among products declaring beef, 9 contained no detectable beef DNA, 7 contained only traces (0.48% +/- 0.37), 19 contained between 1% and 5%, and 55 contained more than 5%. For products declaring "and/or beef", 8 contained no detectable beef DNA, 9 contained only traces (0.12% +/- 0.17) and 1 contained between 1 and 5%. In addition to these results, a survey was carried out to find out consumers' perceptions of meat labelling (202 respondents). Concerning meat products with beef as an ingredient, 76% respondents expected a minimum of 5% beef, thus 37 products are below their expectations. Then, the term "and/or" could be misleading, as almost 9% of respondents believe that "pork and/or beef" means that both species must be present in the product. Finally, most respondents would like to see the exact content of meat species declared on pre-packaged meat products (96%), as this could improve transparency and better meet the expectations of Canadian consumers.



Title: EVALUATION OF THE ANTIVIRAL POTENTIAL OF BERRY PRODUCTS

Topic: FOOD QUALITY

Author: Zia, Saba - Jubinville, Éric - Goulet-Beaulieu, Valérie - Jean, Julie

Summary: Introduction: Foodborne viruses cause serious ailments which are considered among the foremost reason of morbidity. Globally, 7.69% of the population suffer from foodborne diseases each year. In addition to health-related problems, food contamination also impacts food industry with loss in products and potential recalls. At the global scale, food safety cost 110 billion dollars annually. Therefore, it is imperative to find means and methods to eliminate or reduce the viral contamination from the food products. Viral inactivation through safe, efficacious, and cost-effective agents of natural origin is being explored as alternative to chemical disinfectants.

Goal: Therefore, this study is aimed to investigate the antiviral potential of plant-based food products i.e., Goji berry, aronia berry, acai berry, cranberry, and blueberry extracts on hepatitis A virus (HAV), human norovirus (MNV-1) and herpes simplex virus-1 (HSV-1).

Material and methods: Goji berry, aronia berry, acai berry, cranberry, and blueberry extracts will be evaluated for their cytotoxicity using MTT assay. The anti-viral activities will be determined following plaque assay using FRhK-4, RAW 264.3, and Vero cell lines for HAV, MNV-1 and HSV-1, respectively. The most active berry product/extract will be investigated for underlying anti-viral mechanism following viral RNA and capsid integrity analysis. The extracts will also be characterized chemically using high performance liquid chromatographic (HPLC) technique to identify the bioactive constituents responsible for their antiviral activity. Additionally, the extracts will also be evaluated for gastrointestinal resistance using TNO (Toegepast Natuurwetenschappelijk Onderzoek) gastrointestinal model (TIM-1).

Expected results: The results of the present study may identify antiviral extracts/ compounds from natural origin. These extracts may be used as an alternative for disinfectants or as preventive strategies of protection against viral infections. Ultimately, the application of these strategy may reduce the economic burdens caused by foodborne viruses.



Title: Persistence of Noroviruses Alone or Attached to a Food Matrix in a Simulated Human Gastrointestinal Tract

Topic: FOOD QUALITY

Author: Beaulieu, Rosie - Jubinville, Éric - Goulet-Beaulieu, Valérie - Jean, Julie

Summary: Introduction: The human norovirus (HuNoV) is the main cause of gastroenteritis worldwide. The consumption of contaminated food such as berries, leafy greens, and bivalve mollusks is recognized as the major mode of transmission. However, the behavior of the HuNoV in the human gastrointestinal tract is unknown.

Goal: The aim of this study is to evaluate the persistence of the HuNoV through the gastrointestinal tract.

Methods: The persistence of the HuNoV was studied using a surrogate, the murine norovirus (MNV) and HuNoV. The virus alone in water and in four experimentally contaminated Food matrices: raspberries, strawberries, lettuce, and oysters were submitted to two well-recognized digestive models: the INFOGEST protocol (static digestion) and the TIM-1 (dynamic digestion). The persistence of MNV-1 was studied at five key points during the static digestion: after the chewing in the mouth, just before and after the incubation in the stomach, and finally, before and after the passage through the small intestine. In the dynamic digestion, samples were taken in the stomach, duodenum, jejunum, and ileum at different times. To quantify the virus, plaque assay and RT-qPCR were used.

Results: The virus has shown an incredible persistence through the simulated human digestion. In the static digestion, the titer reduction with MNV in fruits compared to the virus alone is significantly different only at the end of the digestion for raspberries, strawberries, and oysters. The maximum titer reduction is 1.4 logs. Those results were also confirmed using real time quantitative polymerase chain reaction (RT-qPCR) after a pretreatment with PMAxx to eliminate non-infectious virus RNA. In the dynamic digestive model TIM-1, the same trend was observed for the virus alone. Very low viral reduction was observed.

Conclusions: This study will offer a better understanding of the resistance of HuNoV during in the gastrointestinal tract. This also contribute to the low number present in food might not be affected during digestion and can easily reach the targeted host cell in the intestine.



Title: Identification and Characterization of Microorganisms Isolated from Non-Compliant and/or Atypical Dairy Products Following Shelf-Life Tests

Topic: FOOD QUALITY

Author: Richter, Mariam - Jubinville, Éric - Goulet-Beaulieu, Valérie - Jean, Julie

Summary: The Quebec dairy sector is one of the most important sectors in the food industry of Canada. Because of the nutritional richness and the nature of dairy products, they might be contaminated by different microorganisms that could make the final products atypical and/or non-compliant. These problems can cause large economic losses while accentuating food waste. Different microbial persistence strategies like the production of biofilms by bacteria are known to be an important enemy for the food industry.

The lack of available information associated with spoilage microorganisms has led to the construction of a collection unique to the Quebec dairy industry. The goal of this project is to do shelf-life tests on marketed dairy products in order to isolate, identify and characterize problematic microorganisms.

To do this, Moseley keeping quality test with minor modifications, Virginia Tech shelf-life procedure and Paenibacillus test were performed on different commercialized liquid dairy products (milk, cream, etc.). Of a total of 89 products tested, 36% (32) were non-conform for at least one test, 36% (32) were non-conform after the Paenibacillus test, 17% (15) were non-conform or atypical after the Virginia Tech shelf-life procedure and 19% (17) for the Moseley test. After isolation of the strains, identification was done using MALDI-TOF analysis or sequencing. The characterization of each isolate will include a heat sensibility by a protocol of pasteurization. The capacity to form a biofilm will be determined by microplate and by MBEC (minimal biofilm eradication concentration). The sensibility to disinfectants used in industry will also be evaluated on MBEC microplates.

The creation of such a collection of spoilage microorganisms from the dairy industry in Quebec will serve as a tool for the development of future projects. For instance, the isolated and characterized could offer a base for the development of new and more efficient control strategies to enhance shelf life of product while reducing economic losses and food waste.



Title: Mimicking Inflammatory Osteoarthritis In Vitro: A Co-Culture Model for Assessing Bioactive Compounds with Anti-inflammatory and Chondroprotective Potential

Topic: NUTRITION AND SOCIETY

Author: Shan, Sirui - Iskandar, Michèle - Larder, Christina - Kubow, Stan

Summary: Osteoarthritis (OA) is an age-related degenerative disease with increasing prevalence among elderly Canadians, imposing a growing societal burden. OA patients often turn to nutritional supplements for pain management due to limitations of pharmacological treatments. In that regard, a validated, easily manipulable, reproducible in vitro OA model is lacking, which could be applied towards preclinical screening of bioactive nutritional compounds.

This study aimed to establish an in vitro co-culture model mimicking inflammatory conditions of OA for identifying bioactives with anti-inflammatory and chondroprotective potential. Macrophage-mediated inflammation and chondrocyte-driven cartilage breakdown synergistically advance OA onset and progression.

Therefore, the co-culture involved two immortalized human cell lines, C28/I2 chondrocytes and THP-1 monocytes. Assays were conducted to determine the optimal culture medium ratio for supporting both cell lines. The THP-1 monocytic cell line was activated and differentiated into pro-inflammatory M1 macrophages through a three-stage process: 1) phorbol 12-myristate 13-acetate (PMA) stimulation; 2) resting period; and 3) lipopolysaccharide and interferon (IFN)- γ stimulation. The dosages of the stimulants were optimized to prevent over-stimulation, and the activation at each stage was confirmed by assessing macrophage morphology and phenotype-specific cell surface marker expression. The C28/I2 chondrocytes were stimulated with interleukin (IL)-1 β to induce inflammation or were untreated. Three co-culture combinations were assessed for pro-inflammatory cytokine production: 1) M0 macrophages and unstimulated chondrocytes; 2) M1 macrophages and unstimulated chondrocytes; and 3) M1 macrophages and IL-1 β stimulated chondrocytes.

Trypan blue cell counting and the MTT cell viability assay were performed to determine the choice of co-culture medium involving different DMEM:RPMI ratios (0-100%). The varying DMEM: RPMI medium ratios showed no effect on cell proliferation and viability, except for 100% DMEM, which significantly ($p < 0.05$) increased viability of THP-1 monocytes. PMA dosages (5-100 ng/mL) significantly ($p < 0.05$) increased expression of the M0 macrophage CD11b surface marker after 48-h incubation, which also altered macrophage morphology. The lower PMA dosage (5 ng/mL), however, resulted in higher macrophage detachment and significant ($p < 0.05$) cell loss during the resting period. These preliminary findings describe cell culture conditions that can support the development of a validated high-throughput in-vitro model of inflammatory OA towards testing of nutritional agents for OA.



Title: Cellulose nanocrystals recycled from maple leaves as Pickering emulsion stabilizers for shrimp preservation

Topic: FOOD QUALITY

Author: Ji, Chuye - Wei, Jiachen - Wang, Yixiang

Summary: Canada is known as the land of maple leaf, but the utilization of dead leaves is limited. Considering the promising applications of nanocellulose as sustainable emulsifiers/stabilizers in food-related Pickering emulsions, in this study, cellulose nanocrystals with different crystalline allomorph (CNC I and CNC II) were obtained from maple leaves and modified by octenyl succinic anhydride (OSA) to stabilize oil-in-water Pickering emulsions. Both CNC I (length: 220.5 nm, diameter: 13.0 nm) and CNC II (length: 66.7 nm, diameter: 6.5 nm) exhibited rod-like shapes. CNC I modified with OSA at a mass ratio of 1.0/0.5 (CNC/OSA) exhibited the excellent emulsifying capacity and stability, and the potential use of emulsions stabilized by CNC/OSA was evaluated for the encapsulation and protection of cinnamaldehyde during storage. Cinnamaldehyde-loaded emulsions showed long-term antibacterial efficacy against Gram-positive and Gram-negative bacteria. The spray coating of cinnamaldehyde-loaded emulsions improved the inhibitory effect against the growth of bacteria, potentially inactivated psychrophilic bacteria responsible for shrimp spoilage, and inhibited the formation of melanosis during refrigerated storage to maximize the shelf life of shrimp. Therefore, this work demonstrates the feasibility to recycle the abundant biomass waste - maple leaves as a new source of nanocellulose and the potential applications in seafood preservation to ensure food safety.



Title: Optimization of the conditions for extraction and purification of marine secondary metabolites preventing the biological colonization of surfaces

Topic: FOOD QUALITY

Author: Heinen, Elise - Tremblay, Réjean - Lemarchand, Karine - Deschênes, Jean-Sébastien - Cardinal, Sébastien

Summary: Bacteria can attach to surfaces and secrete a matrix of exopolysaccharides, DNA, and proteins, to form a colony called a biofilm. This form of resistance gives them protection against desiccation, predation, biocidal substances, or other potentially unfavorable environmental conditions.

In food industry, the formation of bacterial biofilms is a major challenge for maintaining the equipment hygiene and food safety. Indeed, in 2012, the number of deaths related to food poisoning in the United States was estimated at nearly 3000, with an associated cost of over 50 billion dollars.

Standard biofilm control strategies used in the food industry like material selection, cleaning and disinfection or surface preconditioning, are effective to a certain point, but are not sufficient to control the bacterial biofilm formation. Thus, it is necessary to find new strategies to inhibit biofilm formation and remove mature biofilms. To be relevant, those new strategies must also be aligned with current food industry and environmental norms.

In this perspective, it is relevant to investigate natural secondary metabolites found in nature for new anti-adhesive molecules. Microalgae represent a class of organisms that has attracted attention in the search for such bioactive natural products. In addition to being easily cultivable in bioreactors, these organisms have great potential to produce numerous bioactive secondary metabolites.

This main goal of this project is to investigate the secondary metabolites of microalgae endemic to the St. Lawrence ecosystem to find new natural molecules with anti-adhesive but non-toxic properties. The first objective is to optimize the extraction method to maximize yields. To date, ultrasound assisted extraction methods are very promising. When coupling this method with bead milling, a maximum extraction yield of $35\% \pm 2,3\%$ was attained. The second objective of this project is to study the biological activity of the extracts. Biological tests are conducted to determine the potential anti-adhesive and/or antibacterial effect on different strains of bacteria. Once those tests are completed, fractionation and purification of the most promising extracts will be performed in an attempt to identify the molecule or the synergistic mechanism responsible for biological activity.



Title: Impact of the Incorporation of the Edible Seaweeds *Saccharina latissima* and *Alaria esculenta* on the Physicochemical, Functional and Sensory Properties of Yogurt

Topic: FOOD QUALITY

Author: Tremblay, Ariane - Rivera Rodríguez, Martha Paola - Passo Tsamo, Claudine Valérie - Berger, Karine - Labrie, Steve - Beaulieu, Lucie

Summary: The consumption of seaweed as a food has long been popular in East Asian countries such as China, Japan, and Korea where seaweeds are part of the traditional diet. Conversely, in Western countries, there is little tradition in seaweed consumption, seaweed being mostly consumed as sushi or other imported products from Asia. Its high protein content, low-fat level, the presence of several vitamins, minerals, and bioactive compounds are reasons why seaweed is considered a food with high nutritional value. However, the lack of familiarity and the fear of trying something new are barriers to seaweed consumption in Western countries. Incorporating algae in products having already a high consumer acceptance could popularize their health benefits among consumers. Yogurt is a highly popular and widely consumed fermented dairy food and perceived as healthy. Therefore, supplementation of yogurt with seaweed is viewed as a promising approach for the development of healthy foods that benefit consumers. The impact of the addition of seaweed to yogurt was evaluated on its physicochemical, functional, and sensory properties. Two different species of brown macroalgae, *Saccharina latissima* (blanched and not blanched) and *Alaria esculenta*, were added in four different concentrations (0.25, 0.50, 0.75 and 1.00% w/w) and under two different forms (flakes and powder). The titrable acidity of all yogurts with blanched *Saccharina* was similar to the control. However, formulations with blanched *Saccharina* exhibited higher syneresis than the control. All yogurts exhibited a lower firmness than the control, especially those containing *A. esculenta* at higher concentrations. Seaweed addition had a significant impact on the color of yogurts. Quantitative descriptive analysis and hedonic evaluation performed by a trained panel showed that changes in physicochemical properties influenced the organoleptic characteristics of yogurts. Yogurts with 0.25% *S. latissima* and 0.50% *A. esculenta* in flakes were the best overall formulations and were selected for further shelf-life characterization.



Title: Faba bean (*Vicia faba* L.) flour as a health-promoting functional food ingredient with antioxidant and antihypertensive properties after in vitro gastrointestinal digestion

Topic: FOOD QUALITY

Author: Martineau-Côté, Delphine - Achouri, Allaoua - Pitre, Mélanie - Karboune, Salwa - L'Hocine, Lamia

Summary: As there is a growing interest for new sustainable and high quality protein sources with health-promoting properties, this study aimed to assess the potential bioactive properties of faba bean protein after in vitro human gastrointestinal digestion. Flours from three faba bean varieties, namely Fabelle, Malik and Snowbird were digested in comparison to two control legumes (pea and soy). Faba bean variety Fabelle stood out for its antioxidant and antihypertensive activity, and the peptides present in its digestate were further fractionated by size-exclusion chromatography, sequenced by mass spectrometry and synthesized to confirm their activities and to gain a deeper understanding of their mechanism of action using a combination of in vitro, cellular and computational studies. Nine potent antioxidant peptides were identified, namely NYDEGSEPR (NR-9), TETWNPNHPL (TL-11), TETWNPNHPE (TE-10), TETWNPNHPE (TP-9), TWNPNHPE (TE-8), VIPTPEPPH (VH-8), VIPTPEPPHA (VA-9), VVIPTPEPPHA (VA-10) and VVIPTPEPPH (VH-9). These peptides revealed to be free radical scavengers through a dual mechanism of hydrogen atom transfer (HAT) and single electron transfer (SET). Synergistic and/or additive effects were found when selected peptides were combined (TL-11, NR-9 and VA-10). None of the antioxidant peptides were potent iron chelators nor were they modulators of the Nuclear Erythroid 2-Related Factor 2/Antioxidant Response Element (Nrf2/ARE). Four peptides (VH-8, VA-9, VA-10 and VH-9) revealed to be potent ACE inhibitors, making them multifunctional. A kinetic study demonstrated that these peptides were non-competitive inhibitors and a docking investigation showed that the most probable binding sites were located at the entrance of the ACE active site cavity. This study identified and unveiled for the first time the mechanism of action of multifunctional bioactive peptides generated after the gastrointestinal digestion of faba bean, demonstrating its promising potential in the management of hypertension and non-communicable diseases.



Title: How is the texture of pound cake affected by the substitution of the wheat flour by yellow pea and black Beluga lentils purees?

Topic: FOOD QUALITY

Author: Morin, Guillaume - Perreault, Véronique - Savoir, Justine - Feroussier, Auriane - Turgeon, Sylvie L.

Summary: To meet the growing interest in plant-based and local food, this study uses black Beluga lentils and whole yellow peas - two different pulses cultivated in Quebec province - in an innovative way to modulate pound cakes characteristics. The pulses were separately cooked and grounded in their cooking water to produce purees ingredients. A formulation of pound cake was used as a model to study the impact of 20, 40, 60 and 80% substitution of the wheat flour by pulses puree on the physical characteristics of the cakes. To isolate the effect coming from the dry matters' composition of the purees, formulation without purees were produced to match the amount of humidity of those containing pulses puree. Flow behaviour of cake batters was measured to determine their consistency index (CI) using the Power law model, the specific volume of the

cakes(SV) was measured by seed displacement (AACC 10-05.01) and texture characterization was performed by texture profile analysis. The substitution of the flour by pulses puree significantly increases the CI of the batter. This could be explained by the higher amount of protein and fibres and the presence of gelatinized starch coming from the purees in the batters. As the substitution level of the flour by pulses puree increases, the SV of the cakes decreases. Addition of purees resulted in cakes with higher SV as compared to controls made of wheat flour and water. A positive correlation was found between CI of the batters and the SV of the cakes ($r=0,90$) meaning that batters with a higher consistency produce less dense cakes. Moreover, the substitution of the flour by pulses purees generally decreases the hardness of the cakes. This study highlights the interest to use pulses puree as an innovative ingredient to expand the sensorial diversity of pastry products.



Title: Development of a photo-crosslinked gelatin-based antimicrobial film by UVC-riboflavin treatment for the preservation of fresh meat

Topic: FOOD QUALITY

Author: Mahmud, Jumana

Summary: This study introduces a novel crosslinking technique to enhance the physicochemical properties of gelatin (GT) films by exposing them to UV-C irradiation in the presence of riboflavin (RF, natural photosensitizer). Then, GT-RF-antimicrobial films were also prepared by incorporating an essential oil (EO)-based antimicrobial formulation (AF) at three concentrations (0.5, 0.75, 1 % v/v) in order to use as an active packaging film for prolonging the shelf life of meat. The physicochemical properties of the crosslinked films were investigated, and results showed that UV-C crosslinking for up to 13 minutes significantly improved the film's strength, permeability, and solubility. However, the film's elongation decreased, indicating a more compact and stiff structure due to crosslinking process. Based on FTIR analysis, UV-C crosslinking caused an observable shift of absorption to a higher wavenumber of the Amide A, B, ' , and ' bands indicating a significant crosslinking effect on the conformational change of the GT. The solubility and WVP were significantly ($p \leq 0.05$) reduced by 11% and 67 % respectively, for all UVC-treated films compared to the control film (without exposure to UV-C light). The films' tensile modulus (TM) and tensile strength (TS) were also enhanced significantly, thus showing excellent mechanical properties. The release studies revealed that the GT-RF-1% AF film had the highest controlling effect on the diffusion and release rate of EO, indicating Fickian diffusion behavior. The crosslinked films showed excellent antibacterial activity against spoilage bacteria in the vapor diffusion assay. Finally, the application of the crosslinked antimicrobial films on meat extended the shelf-life from 12 to 20 days, demonstrating their potential application in meat preservation.



Title: Potential of 3D fluorescence and infrared spectroscopies coupled to chemometrics to monitor the aging and sensory quality of cheese products.

Topic: FOOD QUALITY

Author: Abi Rizk, Hala - Chamberland, Julien - Bouveresse, Delphine Jouan-Rimbaud - Cordella, Christophe

Summary: The analysis of the cheese matrix remains a major challenge given its intrinsic complexity. Hereby, the aim of our study focuses on the development of non-invasive, fast and simple methods to overcome this obstacle. Cheese was selected as a model of study as it is widely consumed around the world, and has a myriad of types, flavors, aromas, and consistencies. Recognized with its important dietary contribution, it derives from the ripening process within the interaction of dairy constituents and a variety of microorganisms that strongly affects its chemical composition and internal physical structure. Hence, the concerted biochemical changes are responsible of the development of characteristic flavors and textures. To model these aspects, 3D fluorescence and infrared spectroscopies, coupled with chemometric tools, were used to model the impact of internal changes related to aging, targeting cheddar and comté cheeses at various degrees of maturation. The fluorescence Excitation-Emission matrices were analyzed using a multi-table technique (ComDim), and the mid-infrared data were processed using Independent Component Analysis (ICA). The signals extracted by ComDim correspond to a shift in the wavelengths of a fluorophore present in dairy products, specifically tryptophan, showing distinctions between the aging stages of the studied cheeses. Variations in the normal modes of vibration of the mid-infrared bands extracted by ICA were related to functional groups associated with triglycerides, peptides, fatty acids, and amino acids, allowing the modelisation of cheese ripening progress. Thus, the coupling of these unsupervised methods with FDA and PLS-R has enabled the establishment of predictive models for cheese age with satisfactory performances. These observations are consistent with the seen changes in the microstructure of cheese during ripening, as revealed by scanning electron microscopy (SEM) images. Consequently, these results highlight the potential of front face fluorescence and infrared spectroscopies for an efficient and simple characterization of cheese products at a very low cost. These approaches offer solutions to address the challenges posed by complex sample preparation and labor-intensive techniques, all while maintaining the sample's integrity. Furthermore, they hold interest in their potential to create predictive models for sensory properties that enclose even greater industrial relevance, such as flavors, odors, and texture.



Title: Valorization of seaweed polysaccharides for the preparation of bioactive extracts with prebiotic potential

Topic: FOOD QUALITY

Author: Becker, Nicolas

Summary: Macroalgae are increasingly being described as the food of the future, which is a source of great curiosity by the researchers and industrials to promote and enhance the consumption of algae-based products. Areas such as nutrition, health and cosmetics are clients of this resource. This doctoral project brings together the Université Laval/INAF and the Merinov research teams that collaborate with Kemitek, TransBIOTech and the Marine Biotechnology Research Centre. Its main objective will be to exploit biomolecules of interest present in three species of seaweeds (*Saccharina latissima*, *Alaria esculenta* and *Agarum cribosum*) such as polysaccharides (alginate, laminaran, fucoïdan) and polyphenols. It will be necessary to determine the optimal culture depth of the 3 species at the Paspébiac site (Quebec). Then identify the optimal period and the optimal stabilization conditions to produce enriched polysaccharidic extracts. The protocols of Enzyme-assisted extraction, fractionation, determination of polysaccharides and first tangential filtration extracts will be developed in the first year. The enzymes used in the extractions, after 1 μm clarification, will produce hydrolysates of polysaccharides, polyphenols and oligosaccharides. These will be characterized to highlight the formation of mono and oligosaccharides and to better target their prebiotic potential. In the second year, micro-fermentation tests will be carried out to identify prebiotic effects on the gut microbiota. In the second year, micro-fermentation tests will be carried out to identify prebiotic effects on the gut microbiota. Indeed, it is known that some plant polysaccharides have prebiotic effects. Yet, it has been reported that algae polysaccharides can modulate the gut microbiota, but more studies are needed.



Title: The role of co-cultures in enhancing salt stress resilience in lactic acid bacteria

Topic: FOOD QUALITY

Author: Ndiaye, Amadou - Fliss, Ismail - Filteau, Marie

Summary: Salt, i.e. sodium chloride (NaCl) is associated with a risk of hypertension and development of coronary heart disease, so its consumption should be limited. However, salt plays a key role in the quality and safety of food by controlling undesirable microorganisms. Since studies have primarily focused on the effect of salts on the overall counts of the lactic acid bacteria (LAB) group, we have not yet understood how salt individually affects the strains as well as the interactions between them. In this study we characterized the effect of NaCl and a potential substitute, potassium chloride (KCl), on the growth and acidification of 31 LAB strains. In addition, we evaluated the effect of salts on a total of 93 random pairwise strain combinations. Strains and co-cultures were tested at 3% NaCl, 5% NaCl, and 3% KCl on solid medium using an automated approach and image analysis. The results showed that on average the growth of LAB was reduced by up to 68% at 5% NaCl ($p < 0.0001$). For the co-cultures, a reduction of up to 57% was observed at 5% NaCl ($p < 0.0001$). However, acidification was less affected by salt, whether for monocultures or co-cultures. Furthermore, KCl had a lesser impact on both growth and acidification compared to NaCl. More importantly, co-cultures appeared to be more resilient and had more varied responses to salt stress than the monocultures, as several cases of suppression of the significant effect of salts on acidification and growth were detected. In fact, the buffering effect of co-cultures was proportional to the ionic strength. Our results also show that salts can modulate around half of the microbial interactions detected. Altogether, our results highlight that the impact of salt on LAB growth and metabolism is strain-specific and dependent on the biotic context.



Title: Compositional Profiling for the Quality Assessment of Canadian Honey

Topic: FOOD QUALITY

Author: Shao, Mile - Tian, Lei - Liu, Lan - Mdimagh, Asma - Bayen, Stéphane - Karboune, Salwa

Summary: Honey is a natural sweetener with a long history of human consumption. Its nutraceutical value has attracted again a lot of attention in the last decades, driving a growing demand of consumers for higher quality honey, notably monofloral honeys (i.e. honeys from a predominant botanical source). Honey quality is tightly associated with enzyme activities during the maturation process and during storage. Enzymes in particular contribute to the antimicrobial property of honey. Enzyme activity profiles and the carbohydrate composition in honey are affected by a wide range of factors such as the geographic locations, the botanical sources, the climate conditions, the status of the honeybees, the treatments from the beekeepers, the extraction methods, and the storage conditions. So far, there has not been any published studies reporting the carbohydrate content and enzymatic activities of any Canadian monofloral honeys. In this study, the composition of 160 monofloral honeys, notably four of key honey types relevant to the Canadian market (buckwheat, clover, goldenrod and blueberry), mainly from British Columbia, Ontario, and Quebec beekeepers, were studied. High-performance anion-exchange chromatography with pulsed amperometric detection (HPAEC-PAD) and LC-MS are used for the quantification of fructose, glucose, 11 disaccharides, and 7 trisaccharides in honey. The enzyme activity profile was characterized and included the quantification of the catalytic activity for diastase, invertase, acid phosphatase, glucose oxidase, and catalase. In current study, higher diastase activity coupled with higher invertase activity has been found in clover and goldenrod honeys at 12.8 DN/ 4.48 U and 13.77 DN/ 4.68 U, respectively, compared to blueberry (9.05 DN/ 3.12 U) and buckwheat (9.92 DN/ 1.86 U) honeys. The highest acid phosphatase activity was detected in buckwheat honey with 683.20 mg phosphorus dephosphorated by 100g of honey per 24 hr. The correlation coefficients reflecting the relationships between the physicochemical parameters of honeys (e.g. pH, HMF concentration, color, and moisture content) or carbohydrate content and the enzyme activity profile will be presented with the aim to establish honey authentication criteria.



Title: Effect of a cranberry proanthocyanidins extract on an in vitro simplified intestinal microbiota

Topic: NUTRITION AND SOCIETY

Author: Lupien-Meilleur, Joseph - Lessard-Lord, Jacob - Desjardins, Yves - Roy, Denis

Summary: The beneficial effects of proanthocyanidins (PACs) on human health are partly attributed to their conversion by the gut microbiota into beneficial metabolites. Conversely, PACs can impact the microbial composition through a duplibiotic effect – a dual antimicrobial and prebiotic mechanism. The extent to which PACs influence bacterial metabolite production and the complex trophic and symbiotic bacterial relationships observed within the gut microbiota are not fully understood and require further clarification. However, models based on the complete intestinal microbiota are not well-suited to elucidate these phenomena due to their high bacterial complexity and significant inter-individual variations.

To address these challenges, we have developed a reproducible and simplified intestinal microbiota model known as the SiIMi. This model comprises eight bacterial strains immobilized in polymer beads and maintained within a PolyfermS-type fermenter mimicking colon conditions. A PACs extract from cranberry was introduced into this system to assess its impact on bacterial populations (using qPCR) and metabolite production (measured through GC, LC/Q-TOF).

This strategy has enabled the establishment of consistent approaches for assembling and analyzing a stable and replicable SiIMi. Initial runs of the system demonstrated PACs' ability to influence the composition and behavior of our bacterial consortium, confirming its capability to metabolize PACs. The addition of PACs to the system resulted in an increase in bifidobacteria population and a decrease in lactobacilli. It also enhanced acetate production while reducing butyrate synthesis. Furthermore, it generated metabolites from the bacterial breakdown of PACs, including epicatechins and phenolic acids.

Thus, the SiIMi model serves as a robust tool to explore microbial ecology and the intricate trophic interactions established within the microbiota in the presence of PACs and provides valuable insights into the prebiotic potential of these compounds.



Title: Haskap (*Lonicera caerulea* L.): Characterization during preharvest and postharvest stages insights into the quality and bioactive features of Aurora cultivar

Topic: FOOD QUALITY

Author: Lagarda, Ernesto - Duarte-Sierra, Arturo

Summary: Abstract: Haskap (*Lonicera caerulea* L.) is considered a relatively new crop for Canadian growers (Rupasinghe et al., 2012). Initially domesticated in The Soviet Union during the last half of the 20th century, various cultivars were released. Its ease of breeding and unique flavour caught the attention of North American growers (Thompson & Barney, 2007).

As consumer demand for high-quality fresh products increases, organoleptic conditions, defined as the perception of the fruit through human senses, have become essential selection criteria. Additionally, recent nutritional trends have raised concerns about bioactive component consumption. Despite being recognized for its high antioxidant properties through anthocyanins, phenolics content, and chemical composition, specific parameters like maturity index, ideal storage conditions, and ripening profile remain insufficiently explored (Zehfus et al., 2020; Rupasinghe et al., 2012; Jia et al., 2008). This study aims to enhance our understanding of Haskap by investigating its characteristics during early preharvest stages and late postharvest stages. Experiments were conducted using the primary cultivar for Canadian growers (Aurora), with samples provided by the company "Petits Fruits L'islet" in L'islet, Quebec, Canada. The collection stages were spread over four periods, from the preharvest early stages to the harvesting date (May 25th, June 1st, June 12th, June 20th, and July 20th). Subsequently, the samples were subjected to storage conditions of 0°C, 4°C, and 8°C at RH 90%, and were monitored for one month, with five different storage stages. During Haskap growth and storage (conducted at various stages), we monitored parameters such as respiration rate (CO₂ production), ethylene production, color, size, firmness, total soluble solids, total acidity, and weight. Additionally, we employed X-ray scanning through Bruker SkyScan 1272 Micro-CT to monitor epicarp porosity. Further samples were dried under liquid NO₂ and stored at -80°C for phytochemical characterization, which included analyses of antioxidant capacity, anthocyanins, and phenolic content. The results presented an observational description of the Aurora Haskap cultivar and assessed the quality from the early stages to the final shelf life.



Title: Investigation of water absorption by agropolymers derived from food waste in the presence of sugar and salt as co-solutes

Topic: FOOD QUALITY

Author: Sanou, Ibrahima - Gilbert, Audrey - Ahasanul, Karim - Turgeon, Sylvie L. - Khalloufi, Seddik

Summary: Given the enormous quantities generated, food waste is responsible for socio-economic and environmental problems, including the waste of resources such as water, land, energy, and labor. Indeed, the problem of food waste has stimulated research interest for its valorization by producing high value-added products, notably agropolymers. The majority of agropolymers derived from plant food waste are mainly composed from cell walls. One of the major advantage of cell walls is that they can be used and labeled as clean label, which make them very attractive in comparison to some conventional or purified fibers such cellulose, pectin, guar gum and xanthan. Indeed, recent FDA regulations requires that conventional fibers (e.g. inulin, acacia gum and xanthan) can no longer be labeled on food products as dietary fibers. This latest change in regulation concerning the use of conventional fibers such as inulin, acacia gum and xanthan are pushing manufacturers towards the direct use of unpurified fibers in response to consumer demand (clean label). In addition, the agropolymers have numerous applications in the food industry. For example, agropolymers can be used to improve texture, stability, viscosity, and water retention of food products. On the other hand, the functionalities of agropolymers depends on the ingredients included in the composition of the final food matrices such as sugars and salts. However, understanding the mechanisms responsible for the functionalities of agropolymers in presence of other ingredients remains limited. The aim of this study was to investigate the effect of sugars and salts at different concentrations on the functionalities of agropolymers suspensions. The results showed that the order of sugar addition had a significant impact on suspension stability. For example, adding sugar before processing increased stability. Furthermore, the addition of sugars such as maltose revealed better stability than adding sucrose. In general, viscosity, texture and water retention were enhanced by the addition of sugars. With respect to NaCl or CaCl₂, we observed negative interaction with agropolymers, which reduced the stability of the suspensions. The results of this study will help designing final food matrices with targeted functionalities.



Title: Application of a commercial probiotic as a supplement in the diet of fattening pigs to improve meat microbiological quality

Topic: FOOD QUALITY

Author: Touahri, Amal

Summary: Meat is a nutrient dense food, and its perishable nature is due notably to its high-water content and pH near to neutrality. The objective of this study was to evaluate whether a commercial probiotic (BioPlus 2B, Chr Hansen, Hoersholm, Denmark; *Bacillus licheniformis* and *subtilis*), added to pig feed during the entire fattening period, improves the shelf life of vacuum-packaged chilled pork loins. This project was conducted under commercial conditions for two groups of pigs (1 000 each) with and without probiotics repeated twice (4 000 pigs in total). Vacuum-packed loins from those pigs were randomly selected and stored at 0 °C for microbiological analysis; 25 loins were analyzed within hours of cut-out (day 0) and then after 27, 48, 62 and 76 days according to a three-class sampling plan. Metataxonomic analysis (sequencing of 16S rDNA amplicon) was also carried out on loins samples. The results of the microbiological analyses (Enterobacteriaceae, presumptive lactic acid bacteria and *Pseudomonas*) indicate a significant positive impact of the treatment ($P < 0.01$) at D0, but all log differences were below 1 log unit. Metataxonomic results indicate that α -diversity and β -diversity both showed a significant effect of the treatment ($P \leq 0.003$) at D0. In fact, all α -diversity indices indicated that species diversity is lower for the supplemented compared to the control group ($P < 0.01$). Also, β -diversity confirmed that microbial populations are significantly different between the two groups. At D0, the microbial population is diversified containing multiple bacteria including *Bacillus*. *Bacillus* is present on loins, but in a similar abundance for the two groups ($P > 0.05$). After 27 days, *Carnobacterium* became the prevailing genera. However, for the first repetition, *Lactobacillus* and *Hafnia-Obesumbacterium* outgrew *Carnobacterium* and became prevalent after 48 days. For the second band of pigs, those two were still under control on the loins from the probiotic supplemented group at D62. This difference between the two repetitions was most likely due to a better control of refrigeration for the second one where a more performant refrigeration unit was acquired. The probiotic treatment allowed *Carnobacterium* to remain the prevailing genera up to the end of shelf life provided that refrigeration was optimal.



Title: Predicting Pore Formation within Dried Foods using Extreme Learning Machine

Topic: FOOD QUALITY

Author: Thibault, Bruno - Zeynoddin, Mohammad - Ebtehaj, Isa - Bonakdari, Hossein - Ratti, Cristina - Khalloufi, Seddik

Summary: Pore formation is a critical phenomenon during food dehydration, which significantly impacts the volume, appearance, texture, and functional properties of dried products. Controlling pore formation is crucial for producing high-quality dried foods and enhancing the efficiency of the drying processes. Porosity and bulk density are two properties directly linked to pore formation within food matrices. Conventional mathematical models for predicting pore formation, such as theoretical and empirical models, have practical limitations. This paper investigates the application of Extreme Learning Machine (ELM) to model the porosity and bulk density of dried foods using eight input variables: product type, initial moisture content, initial porosity or bulk density, pretreatment, technology, temperature, pressure, and microwave power. A dataset comprising more than 400 dehydration cases was gathered for the analysis, and the models were evaluated using statistical indices, including the correlation coefficient (R), root mean square error (RMSE), root mean square relative error (RMSRE), mean absolute error (MAE), and mean absolute relative error (MARE). The results demonstrate that the most accurate models for predicting bulk density or porosity involved the combination of product, technology, temperature, and pressure as input variables. For bulk density predictions, these four input variables yielded to the highest R index (0.88) and the lowest indices of RMSE (0.09), RMSRE (0.30), MAE (0.07), and MARE (0.22). On the other hand, for porosity predictions, adding the input variable of pretreatment to the four inputs resulted in the most accurate model, with an R index of 0.89, RMSE of 0.10, RMSRE of 0.41, MAE of 0.08, and MARE of 0.23. The obtained ELM models provide valuable tools for estimating porosity or bulk density. These tools will allow food engineers designing drying processes in order to enhance pore formation and therefore, to tailor the desired food products with targeted functionalities.



Title: Effects of UV-C irradiation on the proximate composition, protein profile and structure of whole and skim milk

Topic: FOOD QUALITY

Author: Abed, Hanane - Perreault, Véronique - Doyen, Alain

Summary: Ultraviolet irradiation (UV-C) has various benefits for the pasteurization of milk and dairy fluids due to its low energy requirement, minimal impact on protein structures and ability to extend shelf life. However, the low penetration of UV light in milk represents the major barrier to its implementation in dairy industries. To address this challenge, the Lyras company has recently designed a UV-C system with turbulent flow to enhance UV penetration. However, little data is available regarding the efficiency of this technology, called Raslysatation, on milk and dairy fluids.

Consequently, this work aimed to compare the impact of HTST and UV-C treatments on the proximate composition (total solids, ash, protein, lipid, and lactose) of whole and skim milk. To characterize the effect of both technologies on the serum protein and lipid fractions, whole milk was separated by centrifugation and the cream and skim milk fractions were recovered. HTST and UV-C treated dairy fluids were analyzed for their protein profiles (gel electrophoresis) and sulfhydryl group content.

For skim milk, similar proximate compositions (total solids, protein, fat, lactose, and ash) were obtained for HTST and UV-C-treated samples. Similarly, the protein profiles (native, non-reducing and reducing conditions) as well as free thiol and disulfide bond contents were similar for HTST and UV-C treated skim milk. Regarding the skim milk recovered from HTST and UV-C-treated whole milk, the lipid concentration was higher in HTST compared to UV-C whereas an opposite trend was noticed for protein. Protein profiles indicated formation high molecular weight protein aggregates (> 250 kDa) only for HTST samples with an increase of the free thiols compared to UV-C-treated sample. Finally, the lipid content was also higher in HTST compared to UV-C treated cream whereas protein concentrations were similar. These preliminary results indicated that UV-C and HTST had similar effect on skim milk but, when whole milk was pasteurized, HTST seemed to negatively impact the protein structure and aggregation compared to UV-C. The distribution of lipids in the skim milk and cream fraction obtained from whole milk was also impacted by both technologies. However, further research is needed to confirm these initial observations.



Title: Unveiling the antifungal potential of maple sap bacteria: an exploration of different biotic and abiotic contexts

Topic: FOOD QUALITY

Author: Gupta, Gunjan - Labrie, Steve - Filteau, Marie

Summary: Antifungal microorganisms show significant potential for effectively controlling fungal contamination in diverse food environments, as well as throughout the processes of their production and transformation. Nonetheless, the identification of strains displaying robust antifungal activity poses challenges owing to the complex and highly context-dependent responses. Both biotic (e.g., microbial interactions), and abiotic (e.g., nutrient availability, temperature, and pH) have substantial impacts on antifungal expression. Therefore, to fully harness the potential of antifungal isolates as biocontrol candidates, it is crucial to systematically evaluate them across a range of biotic and abiotic contexts. However, current experimental approaches to systematically consider microbial interaction effects are limited. To overcome this bottleneck, we present a highly adaptable and scalable method using a robotic platform to study the antifungal properties of 1097 microorganisms obtained from maple sap. We used M17+lactose (M17L), Plate count agar (PCA), and Synthetic allantoin media (SALN) culture media to isolate microorganisms and screen for their antifungal activity alone or in pairs. The antifungal activity of microorganisms was tested against *Kluyveromyces lactis*, *Candida boidinii*, and *Saccharomyces cerevisiae*. We found that microorganisms exhibited less often antifungal activity on SALN and PCA than on M17L, suggesting the latter is a better screening medium. We also analyzed the ecological interaction outcomes between pairs (cooperation or competition) and examined the influence of these interactions on the antifungal potential of the microorganisms. Microorganisms displaying consistent competitive behavior were more likely to display antifungal activity than expected by chance. However, co-culturing rarely induced antifungal production. In fact, interaction-mediated suppression was more prevalent in our dataset. These findings highlight the importance of incorporating both biotic and abiotic factors into systematic screening designs for the bioprospection of microorganisms with environmentally robust antifungal activity. In conclusion, our approach allowed the identification of promising candidates for biocontrol against fungal contamination in maple sap and other environments.



Title: Understanding the influence of pores on the properties of dehydrated food products

Topic: FOOD QUALITY

Author: Aghajanzadehsuraki, Sara - Thibault, Bruno - Sultana, Afroza - Ratti, Cristina - Khalloufi, Seddik

Summary: Dehydration is a widely used process to prolong the shelf life of food products. This process involves the removal of water from the food through evaporation or sublimation, which can lead to the formation and evolution of pores within the food's structure. The formation of pores during food dehydration is influenced by a combination of extrinsic and intrinsic factors. Extrinsic factors are directly related to the dehydration process, including the technology used, process conditions, and any pre- or post-treatments applied. The utilization of various dehydration methods, such as microwave drying, freeze-drying, and air-drying, yields different porosity levels in the final products. Process conditions, like temperature, pressure, relative humidity, and air velocity, also play significant roles in the alteration of porous structures. On the other hand, intrinsic factors are inherent properties of fresh food being dehydrated, including composition, initial porosity, density, cellular structure, and water distribution. These intrinsic attributes, combined with the dehydration process, collectively determine the porosity of the resulting dehydrated products. Generally, the pores are distributed throughout different parts of the food structure and have implications for stability, rehydration kinetics, and organoleptic properties. Moreover, the presence of pores profoundly influences the textural and mechanical attributes of foods, such as hardness, strength, crispness, and chewiness. The porous structure also facilitates mass transfer, enhancing the efficiency of the dehydration process. However, the existence of pores may present challenges as they promote moisture absorption from the environment, potentially leading to microbial growth and a loss of crispness. Foods with high porosity, like freeze-dried products, might be more susceptible to lipid oxidation. In conclusion, the porosity of dehydrated foods plays a crucial role in their properties and quality. Understanding the factors affecting pore formation enables optimization of the dehydration process, leading to improved food quality and extended shelf life. This study provides valuable insights into the relationship between pore formation and food properties, contributing to advancements in the field of food dehydration.



Title: The effect of pasteurization treatment and skimming conditions on distribution of human milk proteins

Topic: FOOD QUALITY

Author: Gharbi, Negar

Summary: Human milk banks (HMBs) utilize various processes such as pasteurization and skimming to ensure milk safety prior to its distribution and provide skimmed milk (SM) for infants who require a modified fat diet. Currently, there is no data on 1) how HM bioactive proteins are affected by skimming conditions and 2) how the pasteurization method applied before skimming affects the HM protein distribution between the cream and the SM fractions. Consequently, this project aimed to determine the effect of pasteurization methods (Holder, HTST and HHP) and skimming parameters on the protein contents and profiles of SM and cream.

The whole human milk (HM) was pasteurized by Holder Pasteurization-HoP (62.5 °C, 30 min), HTST (72 °C, 15 s), and HHP (600 MPa, 3 min, 4 °C). Then the raw and pasteurized whole HMs (HoP, HTST, HHP) were skimmed by centrifugation at different G forces (1700, 3800, and 10 000×g) and durations (5, 10, 15 min) at 4 °C. After the skimming, cream and skim milk were separated and analyzed individually. To identify the effect of pasteurization methods and centrifugal conditions on proteins, protein contents of cream and SM were determined by Dumas and Kjeldahl, respectively. Moreover, the protein profiles of cream and SM were determined using SDS-PAGEs. HHP prior to skimming resulted in lower cream protein content (46 g/kg, dry basis) compared with those for HoP and HTST (55 and 65 g/kg dry basis, respectively). Enhancing centrifugal force from 1700 to 10 000×g led to the reduction of the cream protein contents (average, from 53 to 45 g/kg, dry basis), mainly through removing casein and β -lactalbumin. However, due to the significant effect of centrifugal force on volumes and moisture contents of creams and SMs, the SM protein contents were not proportional to those of creams, and it varied from 88 to 97 g/kg (dry basis) without significantly affecting the protein content and profile. These findings provide new information on choosing the suitable pasteurization method and skimming conditions for donor HM processing in HMB to provide high quality donor HM.



Title: Enrichment of Food Matrices by Dietary Fibers and Their Effects on Fat Hydrolysis

Topic: FOOD QUALITY

Author: Mohammadi, Leila - Osse, Emmanuel-Freddy - Aider, Mohammed - Khalloufi, Seddik

Summary: Dietary fibers are commonly used in the food industry to improve different physiological and/or technological functionalities of food products. However, their inclusion in food matrices can lead to an increase in viscosity, which could affect the hydrolysis of macronutrients in the food during their digestion. The present study reviewed the impact of dietary fibers on fat hydrolysis and how their addition could impact fat enzymatic hydrolysis. Several dietary fibers such as Arabic gum, guar gum, locust bean gum, pectin, xanthan, and β -glucan were investigated and used to control the viscosity. The outcomes of these investigations revealed that, in general, the addition of dietary fibers resulted in delaying and/or inhibiting fat hydrolysis, leading to the control of blood cholesterol levels. However, very few studies have reported a positive effect of dietary fibers, such as Arabic gum, locust bean gum, xanthan, or β -glucan on fat enzymatic hydrolysis. Several mechanisms such as diffusion, active site accessibility, release, and binding surface interactions were mentioned to explain the effect of dietary fibers on fat hydrolysis. In addition, it is reported that the concentration of dietary fibers and their characteristics, such as molecular weight, have also a significant impact on fat hydrolysis. This contribution highlights some promising perspectives that can give more insights into the effect of dietary fibers on fat hydrolysis. Therefore, the food industry can use this knowledge to design targeted products with specific functionalities that respond to market trends.



Title: Application of electro-activated calcium ascorbate solution as antioxidant agent in processed meat

Topic: FOOD QUALITY

Author: Rezaee, Mahsa - Aider, Mohammed

Summary: Lipid and protein oxidation plays a significant role in determining the acceptability and overall quality of meat products, while also leading to the degradation of their flavor and taste. In processed meat products, antioxidants act as hydrogen atom donors or electron acceptors, serving the purpose of inhibiting or delaying oxidative reactions. However, due to the synthetic nature of the main antioxidants used in the food industry, there is a growing movement to reduce the reliance on artificial food additives and identify novel safe components with antioxidant properties. As an innovative and non-thermal technology, electro-activation can be used to produce highly active antioxidant aqueous solutions following specifically targeted electrochemical modifications and using food-grade components. The process involves subjecting the aqueous solution of food-grade salts to an external electric field within a reactor modulated with anion and cation exchange membranes, allowing the production of the final solutions with desired antioxidant properties. This study aimed to investigate the influence of adding electro-activated calcium ascorbate solution (EAS) to meat batter as an antioxidant agent on its total antioxidant capacity, fat and protein oxidation, physicochemical properties, stability, rheological properties, and microstructure of processed meat systems. To achieve this goal, the water content of the meat batter formulation was replaced by EAS at 25, 50, 75, and 100% levels. The results showed that increasing the EAS ratio increased total antioxidant capacity and decreased pH value of meat products. Fat oxidation showed an initial increase after two weeks, followed by a subsequent decrease after four weeks. The most significant reduction in fat oxidation was evident in samples containing 100% EAS. Additionally, samples with 75% and 100% EAS were characterized by a significant difference in firmness compared to control (100 water = 0% EAS). The color was typical of the product and a difference was observed only for samples with total water replacement.



Title: Omega-3 pharmaco-nutraceuticals: A promising avenue to enhance the therapeutic response of fibrates for the treatment of cholestatic autoimmune liver diseases

Topic: NUTRITION AND SOCIETY

Author: Lavoie, Audrey-Anne - Verreault, Mélanie - Marette, André - Barbier, Olivier

Summary: Background: The accumulation of toxic bile acids (BA) in the liver is a key factor in the pathogenesis of primary biliary and sclerosing cholangitis (PBC and PSC), two autoimmune liver diseases deprived of any curative options. While PBC and/or PSC treatment are currently limited to Ursodiol® (UDCA) and Ocaliva® (OCA), fibrates, such as fenofibrate and bezafibrate, are currently tested in off-labeled trials. Since we already reported that omega-3 polyunsaturated fatty acids, such as the eicosapentaenoic (EPA) and docosahexaenoic acids (DHA), improve the response to UDCA and OCA, we sought to test the possibility that similar improvement also occurs with fenofibrate and bezafibrate.

Methods: Human HepG2 cells were treated for 24H with vehicle (DMSO-ethanol 0.01%/0.01% v/v), 100µM fenofibrate and 100µM bezafibrate, in the presence or absence of EPA/DHA (50:50µM). Total RNA was purified, and the expression of essential genes related to BA transport, synthesis and detoxification was quantified by qRT-PCR.

Results: When used alone, fenofibrate and bezafibrate caused respectively a 37% and 34% reduction in the CYP7A1 transcript levels. However, in the presence of EPA/DHA, mRNA levels of this rate-limiting enzyme for BA synthesis were reduced by 58% and 52% with the same dosage of fenofibrate and bezafibrate. Similarly, the addition of EPA/DHA to fenofibrate reinforced the overexpression of the export gene MRP2 from 1.5 to 29-fold over control. Interestingly, the combinations EPA/DHA +fenofibrate ($p<0.001$) and +bezafibrate ($p<0.01$) caused a 58% and 47% reduction of the CYP27A1 transcripts, a BA-synthesizing enzyme. When used alone the 2 drugs failed to modulate this gene expression. A similar inhibition was also observed for the NTCP transcripts but only with the EPA/DHA +bezafibrate combination.

Conclusion: The addition of EPA/DHA to fibrates seems to be a promising way to reduce the hepatic BA concentration. Further analysis are, however, required to validate this hypothesis.



Title: Development of antifungal formulations using silver nanoparticles and natural antimicrobials for preservation of strawberries and cruciferous vegetables

Topic: FOOD QUALITY

Author: Moosavi, Seyedeh Elmira

Summary: New demands for natural antimicrobials instead of synthetic fungicides for food safety and environmental protection have created a need for new and safe plant spoilage microorganisms control strategies. It is estimated that about 30% of total fruits and vegetables are lost each year due to fungal spoilage. Therefore, this study aimed to find natural antifungals that can be used for the control of devastating fungal spoilage in strawberries and cruciferous vegetables such as *Botrytis cinerea*, *Rhizopus stolonifer*, and *Alternaria brassicae*. Here, the antifungal activities of 22 plant-derived essential oils (EOs), fruit extracts (FEs), and commercial silver nanoparticles (AGPPH, AGC 0.5) were tested and chemical composition of the selected EOs was identified. Twenty-two components, representing more than 93 % of the EOs, were identified by high performance liquid chromatography (HPLC) method. The main components included trans-cinnamaldehyde, p-methoxy cinnamaldehyde, thymol, carvacrol, p-cymene, γ -terpinene, borneol, α -terpineol, linalool, β -caryophyllene, camphene and trans- β -ocimene. Four active formulations (AFs) (AF1: Mediterranean formulation/ Cinnamon EO/ AGPPH, AF2: Cinnamon EO/ Oregano EOs/ AGPPH, AF3: Cinnamon EO/ Mediterranean formulation/ AGC 0.5, AF4: Oregano EOs/ Thyme EOs/ Cinnamon EO/ AGC 0.5) were developed using a checkerboard method. An agar diffusion assay was carried out to confirm the fungal activity of selected 4 AFs. They exhibited the highest antifungal activities with inhibitory capacity (IC, %) values from 100% to 77.87% against *Rhizopus stolonifer*, from 100 % to 86.5% against *Botrytis cinerea* and from 100 % to 86.37% against *Alternaria brassicae*. The obtained formulations at acceptable concentrations could be applied as promising and green agents in the preservation of strawberries and cruciferous vegetables.



Title: Sensory, physicochemical and phytochemical optimization of wild blueberry juice

Topic: FOOD QUALITY

Author: Zarate Carbajal, Alberto - Duarte-Sierra, Arturo

Summary: Wild blueberry is one of the most popular fresh fruits produced in Canada, as well as one of the most nutritious. However, it is only produced for two months in the year, which limits its consumption. Therefore, processing it into juice warrants its consumption throughout the year. The main goal of this work was to enhance the process by identifying the key factors that have the greatest impact on the juice production. Two experimental designs utilizing screening methods were formulated to optimize the juice extraction process. These designs relied on the physicochemical and sensory analysis of 10 juice batches produced under different operating conditions (such as thawing time, extraction method, centrifugation speed, enzymation, and pasteurization) in comparison to a commercially available juice.

The process conditions that most affected the juice were the type of extraction, as well as the use of an enzyme in the production process, which significantly reduces the turbidity and viscosity of the juice. Furthermore, through a penalty analysis (i.e., Just About Right (JAR) vs Hedonic scores), flavor enhancement factors were identified in samples pasteurized at 90 °C/45 s, as well as in commercial juice. Through the application of correspondence analysis (CA), significant descriptive attributes were identified. Floral, citrus, and sweet were determined to be positive attributes, while fermented, earthy, and tongue picoment were identified as negative attributes.

By a Quantity Descriptive Analysis (QDA) the whole profile of wild blueberry juice was found. In anthocyanin values a fast thawing (oven 40°C 8 min) can help to obtain a juice with a higher value.

By analyzing the QDA, physicochemical and anthocyanins values and appropriately adjusting the most influential operating factors, such as the thawing method (oven), use of pectinase, and pasteurization conditions (1 minute at 90 °C), it becomes feasible to produce a juice that is sensorially appealing.



Title: Characterization of wild yeasts as biocontrol agent in brewing

Topic: FOOD QUALITY

Author: Unterberg-Piché, Édouard

Summary: The ever-rising demand for new and innovative beers has been motivating brewers around the world to provide products with distinct flavors and properties. However, craft production often lacks the resources to properly control the quality of their beers and faces more contamination problems than the industrial alternative. Likewise, some beer styles such as non-alcoholic beers and spontaneously fermented beers are more prone to contamination regardless of commercial or artisanal origin. Since the addition of chemical agents to improve the conservation of beer is widely unpopular, an acceptable alternative would be the use of bioprotective cultures, as they meet the consumer's demand for natural products. As some yeasts are known to have antagonistic activity against beer spoilage microorganisms, this study aims to develop a method to identify suitable candidates from a wild yeast collection using high-throughput screening and validation testing to determine their potential as bioprotective agents for brewing applications. From an initial pool of 640 isolates, 307 isolates showed antagonistic activity towards different brewery contaminants (*Lactobacillus brevis*, *Lactobacillus plantarum*, *Pediococcus damnosus*, *Brettanomyces clausenii*, *Brettanomyces bruxellensis*, *Pichia membranifaciens*, *Pichia fermentans*, *Pichia kluyveri*, *Pichia kudriavzevii* and *Gluconobacter oxydans*). However, 97 also showed antagonistic activity against two common *Saccharomyces* brewing strains. Three compatible yeast strains candidates were retained. Confirmatory tests were carried out on these strains using supernatant test and another test using a variable concentration of each strain mixed with *S. cerevisiae*. None of the candidates showed significant antagonistic activity reduction while being mixed with *S. cerevisiae* and only one candidate's supernatant had antagonistic activity. Further tests were carried out to determine the candidate's impact on fermentation performances in a coculture context. Final testing will be conducted to assess the candidate's ability to prevent the growth of a contaminant without altering the fermentation performance of *S. cerevisiae*. These results could then show that this method can be applied to identify new innovative strains for brewers.



Title: Characterization of the variability of minor compounds in cow's milk and its impact on the cheese-making process

Topic: FOOD QUALITY

Author: Gravel, Catherine - Gentès, Marie-Claude - Chamberland, Julien

Summary: Variability remains a major problem in the cheese industry, despite the standardization of milk protein and fat on an industrial scale. This variability could be due to variations in the minor constituents of cow's milk, which could affect the acidification rate of the lactic bacteria and the curd permeability during the cheese-making process. Therefore, this research project aims at determining if there is a relationship between the variability of minor constituents in cow milk and the growth of lactic acid bacteria. Milk samples will be collected every two weeks for one year at the Centre de recherche en sciences animales de Deschambault (CRSAD, QC, Canada). Environmental and herd data will be collected. The first objective is to characterize milk composition throughout the year. Minor compounds targeted in this study are amino acids and B vitamins. They will be analyzed using UPLC-UV/MS and UPC2, respectively. Fourier-transform infrared spectroscopy (FTIR) will be used to measure the contents of major constituents (protein, fat, lactose). The second objective is to determine how milk composition variations affect lactic bacteria growth and their acidification rate using high-throughput methodology. Data science and chemometrics tools will establish the link between all the information on milk composition, environmental data, and the acidification rate of lactic bacteria. This work will improve our understanding of factors contributing to cheese variability and pave the way for new milk standardization strategies considering the nutritional requirements of the lactic bacteria used in cheese production.



Title: Bacteriocins as alternatives to antibiotics in poultry production

Topic: FOOD QUALITY

Author: Mamjoud, Amal - Fliss, Ismail - Zirah, Séverine

Summary: Bacteriocins are antimicrobial peptides produced by bacteria and involved in bacterial competition to colonize an ecological niche. They display a remarkable structural diversity associated with varied mechanisms of action. They are being exploited in food preservation and are emerging as a promising alternative to antibiotics (Soltani et al., 2021).

The prolonged and unregulated use of antibiotic growth promoters has led to the emergence of antibiotic-resistant commensal and pathogenic strains that can subsequently be transmitted to humans via the environment and food, causing serious health problems (He et al., 2020). In Canada, since 2017, the use of antibiotics belonging to categories I and II has been banned in the poultry industry. These two categories are considered of high importance in human medicine (Canada, 2017). Following these restrictions, there is an urgent need to develop alternatives to conventional antibiotics for animal production.

The aim of this project is to study the impact of bacteriocins produced by Gram-positive and Gram-negative bacteria on the composition and metabolic activities of avian colonic microbiota using an in vitro model of colonic fermentation (Asare et al., 2021). Initially, two different concentrations of antibiotic and bacteriocin treatments were tested, using penicillin bottle microfermentations to cultivate microbial communities from fresh fecal samples under static conditions over a short period of time (24h). Collected samples are analyzed by 16S RNA metabarcoding and targeted metabolomic analysis (acetate, butyrate and propionate). The results show that the impact on the microbiota is different between antibiotics and bacteriocins, even for those sharing the same molecular target. This step will enable us to select a suitable concentration of treatments for continuous fermentation by the PoyFermS model.



Title: Biochemical characterization of *Nannochloropsis oculata* and antibacterial activity of organic extracts

Topic: FOOD QUALITY

Author: Kefil, Sarah - Cardinal, Sébastien - Deschênes, Jean-Sébastien - Tremblay, Réjean - Lemarchand, Karine

Summary: Bacterial biofilms are complex biological systems that are difficult to eradicate, as they confer bacteria effective protection against external factors and antimicrobial agents.

In agri-food sector, this phenomenon causes important problems. The safety of food is a critical worldwide public health and economic issue, as numerous individuals suffer from short and long-term illnesses resulting from the consumption of unsafe food.

Consequently, guaranteeing the safety of food represents a paramount concern within the food industry, which requires consideration during not only food composition formulation but also in their handling and storage. For safety purpose, the food industry has historically employed various chemical antimicrobial agents. However, there is currently a resurgence of interest in replacing chemically derived food safety additives with natural alternatives that can also act as antimicrobial agents. One potential source of such metabolites is microalgae: these microorganisms have developed various means of defense against bacteria.

Antimicrobial metabolites produced by microalgae are highly affected by environmental conditions or stimuli. This project thus aims at enhancing the production of molecule(s) that would avert the development of biofilms for a wide spectrum of bacterial species through process optimization and stress induction strategies. The biochemical characterization of the microalgae will be determined after each production and the extracts will be tested on biofilm forming bacteria.



Title: Study of the nutritional profile, safety and organoleptic properties of Nunavik marine resources.

Topic: AUTONOMY, PROSPERITY AND FOOD ACCESSIBILITY

Author: Côté, Samuel - Lemire, Mélanie - Beaulieu, Lucie

Summary: The study of the nutritional profile, safety, and organoleptic properties of certain coastal marine resources (known as tininnimuitait) consumed by the Inuit communities of Nunavik (the Nunavimmiuts) aims to support food security. These resources, which can be easily harvested from the coastline of this northern region of Quebec, are still relatively undocumented and are already part of the traditional Inuit diet. The project will focus specifically on sculpin (a fish from the Cottidae family), the soft-shell clam (*Mya truncata*), and various species of algae (*Palmaria palmata*, *Fucus* sp., *Saccharina* sp., *Alaria esculenta*, *Mytilus* sp.). Analyses will be conducted near different communities and during various periods of the year to assess the spatiotemporal variations in the chemical composition, organoleptic qualities, and safety of these marine resources. The analyses will cover chemical composition, fibres, polyphenols, carotenoids, minerals, metals, and, if necessary, their speciation, volatile organic compounds, free amino acids, nucleotides, and microbiological safety. The measured concentrations will be combined with the Inuit knowledge regarding these species, documented through community workshops, to better understand which characteristics may have the most influence on taste and odour. The results of this study will provide the Inuit communities of Nunavik with data on the different harvesting sites of these marine resources and will help promote their consumption.



Title: Exploring the texture of a diversity of Quebec forest mushrooms

Topic: AUTONOMY, PROSPERITY AND FOOD ACCESSIBILITY

Author: Raharimanana, Fanilo Tsiory - Boumail, Afia - Turgeon, Sylvie L. - Frøst, Michael Bom - Perreault, Véronique

Summary: The enthusiasm for Quebec forest mushrooms has increased among consumers in recent years although these products were once considered as niche products not very accessible for the vast majority of Quebecers. Professional chefs and cooks are one step ahead of this craze. Sensory description is identified as a judicious tool to support the promotion of a wider diversity of species, which is in line with a perspective of sustainable development. The main purpose of our initiative is to document some sensory characteristics (aromas, texture) and some related physicochemical properties specific to each species of a selection of edible forest mushrooms from Quebec. This first study focuses on texture properties. Ten (10) species harvested by professional pickers in Mauricie (Quebec) during summer and fall (2022) were selected aiming for a wide diversity of textures and a good representation of various forest mushrooms available. Upon reception, the fresh mushrooms were cleaned and sliced into 5 mm thick slices. Mushrooms' texture was measured for each species at fresh and cooked/stir-fried states with a texturometer (TA.XTplus, Stable Micro Systems), by uniaxial compression using a knife probe, which allowed to obtain various texture parameters including firmness, hardness, resilience, and elasticity (Young's modulus).

According to the results, three texture groups can be identified among the selected mushrooms: firm and tough mushrooms (*Hypomyces lactifluorum*, *Laetiporus sulfureus*, and *Tricholoma magnivelare*), medium firm mushrooms (*Boletus chippewaensis*, *Cantharellus cibarius*, and *Chlorophyllum rhacodes*), and less firm- crumbly mushrooms (*Lactarius lignyotus*, *Pleurotus ostreatus*, *Sarcomyxa serotina*, and *Suillus cavipes*).

These first results will feed an upcoming sensory study involving chefs, professional cooks and mycology experts to generate sensory descriptors for the different mushrooms species. All this, hoping to support the sector in promoting a diversity of species and to better guide consumers and chefs in their selection for culinary uses and innovation.



Title: Impact of pre-concentration on the extraction of protein from tofu whey by a combination of electro-dialytic processes

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Deschênes Gagnon, Rosie - Lutin, Florence - Langevin, Marie-Ève - Bazinet, Laurent

Summary: Tofu whey is a by-product of tofu production which represents a major challenge in the industry, considering treatments that must be applied before its disposal to reduce its environmental impact. Rich in nutrients, such as protein and minerals, tofu whey valorization represents an interesting alternative. In this study, the impact of a pre-concentration step by nanofiltration prior to the electro-dialysis and electro-dialysis with bipolar membrane (ED+EDBM) treatment on protein recovery was investigated for the first time. Three conditions were tested: tofu whey without concentration (1X) and volume concentration factors of 2X and 3X. Results showed that the 3X condition allowed a protein recovery about 20% higher than the 1X. Also, protein purity of the recovered fraction was similar for these three conditions, with an average value of 44.8 % on dry powder basis. Regarding energy consumption, the lowest relative energy consumption (REC) of 2.7 Wh per g of protein recovered was achieved with the 3X VCF ; as the VCF increased, up to 3.5 times less energy was required to isolate the same amount of protein. Finally, for the first time, the proteins recovered from tofu whey were identified. The NF+ED+EDBM was particularly efficient to recover the proteins with the highest molecular weights. Although the pre-concentration step improved protein recovery, recovery yields are still low and should be increased by an additional optimization step.



Title: Effect of buttermilk concentration by reverse osmosis and ultrafiltration on the rennet gel formation and rheological characteristics of cheese milk

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Krebs, Louise - Larouche, Jules - Remondetto, Gabriel - Chamberland, Julien - Venema, Koen - Brisson, Guillaume

Summary: During cream churning in butter making, the milk fat globule membrane (MFGM) surrounding the fat globules is disrupted and released in the aqueous phase, the buttermilk (BM). As a result, the BM composition is similar to skim milk (SM) and contains valuable compounds, such as MFGM proteins and phospholipids (PL), possessing several health benefits. However, BM is still undervalued due to its poor techno-functional properties when added to dairy products. For example, in cheese, the presence of PL and lipoprotein complexes result in a high moisture content and soft texture curd. The concentration of BM by membrane filtration could be used to improve BM use in cheese manufacture. In this study, the impact of BM concentration by reverse osmosis (RO) and ultrafiltration (UF) on the coagulation properties and rheological characteristics of cheese milk was studied. Two-fold concentrated BM samples were renneted alone or in a mixture with the corresponding SM concentrate at a ratio of 1:4 or 1:1 and compared to unconcentrated BM and SM. Oscillatory rheology was used to determine the rennet gel coagulation properties (rennet coagulation time [RCT], storage modulus [G'] at 2' RCT, maximal firming rate [MFR]). The rheological data was used for calculating the fractal dimension and determining the gel regime and structural characteristics. The gel microstructure was studied by confocal laser scanning microscopy (CLSM) and scanning electron microscopy (SEM). RO and UF of BM significantly increased the retentate's protein content and, consequently, the G' at 2' RCT and the MFR ($p < 0.05$). Conversely, both values significantly decreased ($p < 0.05$) when increasing the ratio of BM added for both the non-concentrated and concentrated samples. According to the calculated fractal dimension and microstructural images, all gels were in the transition gel regime, with non-concentrated samples tending towards a strong-link (inter-particles linked) gel, and concentrated samples tending towards a weak-link gel regime (intra-particles linked). This study provided new insights into BM rennet gel characteristics based on the concentration process (RO, UF), and the BM-SM ratio used. Especially UF improved BM rennet gel coagulation which could facilitate its use in cheese manufacture.



Title: Evaluation of the antimicrobial and prebiotic effects of macroalgae sulfated polysaccharide hydrolysates (*Porphyra* sp.)

Topic: NUTRITION AND SOCIETY

Author: Généreux, Pamela - Tremblay, Ariane - Malenfant, Nicolas - Lemay, Jean-François - Desjardins, Yves - Beaulieu, Lucie

Summary: *Porphyra* (Nori) is a red macroalga belonging to the *Bagiaceae* family. Mainly grown and consumed in Asian countries, it is also established to be the most economically important alga in the world. Nonetheless, many of these countries are struggling with water pollution problems. Québec's marine environment, on the other hand, is not very polluted, which makes it a favorable place for the development of seaweed products intended for human consumption. Nori, mainly composed of porphyran: a sulfated polysaccharide, has several potential biological activities such as antitumor, anticancer, antioxidant and immunogenerating properties. However, the antimicrobial properties and their effects on gastrointestinal health as a prebiotic remains very poorly documented. Although, it is known that polysaccharides similar to porphyran can be substrates selectively used by microorganisms conferring health benefits. Furthermore, studies on mono- and oligosaccharides derived from porphyran hydrolysis have demonstrated that their beneficial properties and, more particularly, their antioxidant capacities could be improved. This present study focuses on the production of hydrolysates from porphyran extracted in Atlantic Nori (Océan de Saveurs) with potential biological activities for health (antimicrobial and prebiotic effects and influence on the intestinal microbiota) thanks to specific enzymes discovered by Roscoff Biological Station (RBS), agarase β and porphyranase β . To do this, characterization of the hydrolysates will be studied by various quantitative and qualitative chemical methods such as the concentrations of reducing sugars (DNS) and total sugars (Dubois), anhydrosaccharides (resorcinol), sulphates (rhodizonate) as well as by HPLC and HPAEC-PAD. First, the biological characterization will be carried out by antimicrobial and antifungal tests on a variety of strains related to the intestinal microbiota as well as food safety by t well diffusion method. Then, prebiotic effects and impact on the intestinal microbiota will be conducted by micro-fermentation and the use of a multi-compartmental dynamic Simulator of the Human Intestinal Microbial Ecosystem (SHIME). The knowledge acquired with this research will thus lead to benefits for Québec, industries, end users and for the advancement of knowledge in marine biotechnologies.



Title: Production of polyphenols-enriched cranberry juice through electro dialysis with filtration membrane: How physicochemical properties of filtration membranes impact anthocyanins

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Revellat, Eva - Bazinet, Laurent

Summary: Health-promoting effects credited to anthocyanins have been extensively studied and recent discoveries have suggested their impacts on the modulation of the gut microbiota. Cranberry juice - a goldmine of anthocyanins - could be enriched to enhance its health benefit. In previous studies, electro dialysis with filtration membrane (EDFM) could selectively enrich juice in anthocyanins. The present study focused on this green and promising technology especially on understanding how physicochemical properties of filtration membranes impact global and selective anthocyanin migration during their separation by EDFM. Thus, six polyether sulfone (PES) and polyvinylidene fluoride (PVDF) membranes with molecular weight cut-offs (MWCO) of 150kDa, 200kDa, 250kDa, 300kDa and 500kDa were characterized and used during EDFM treatment. Membranes were characterized in terms of thickness, conductivity, contact angle, % of hydrophilic pores, porosity, zeta-potential, roughness. Juices were analysed using HPLC to assess the individual and global anthocyanins, proanthocyanidins and organic acids migration. Results have shown an impact of MWCO, membrane material and initial anthocyanins abundance on anthocyanin's enrichment. Results have also displayed an influence of MWCO, membrane material and initial organic acid abundance on acid organic's impoverishment. With a global anthocyanin migration rate of 3.5 ± 0.4 g/m².h, the highest migration of total anthocyanin was obtained with PVDF 250 kDa. To understand the correlation between membrane physicochemical properties and global and individual anthocyanins migration during EDFM, statistical approaches (RDA and multivariate regression analysis) were used. Two FM properties (mesopore porosity and hydrophilic porosity) were significantly correlated to the anthocyanin's migration. They explained 67.4 % of total variation in individual anthocyanins migration. Thus, such an innovative technology will allow the production of cranberry juices with a selective content of anthocyanins and organic acids and will help to determine the synergistic effect of anthocyanins and organic acids on the modulation of the composition of the intestinal microbiota and on the intestinal inflammation in future study.



Title: How selective peptide migration is induced by electrical current modes during electrodialysis with ultrafiltration: A comprehensive machine learning-based peptidomic

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Cournoyer, Aurore - Bazinet, Mathieu - Clément, Jean-Pierre - Plante, Pier-Luc - Bazinet, Laurent

Summary: Porcine blood is a major coproduct from slaughterhouses. Its precipitated part after centrifugation, cruor, is mainly composed of hemoglobin. After its enzymatic hydrolysis, a wide variety of peptides is obtained, especially antimicrobials. To produce fractions of peptides with increased bioactivities and higher purity, electrodialysis with ultrafiltration membrane (EDUF) was proposed. Indeed, this technology is a promising ecoefficient strategy to recover bioactive peptides. EDUF is a hybrid ED process with a selectivity based on both charge (ED process) and molecular mass (UF membrane). Although a continuous electrical current (CC) is commonly applied, alternative electrical current modes can be employed to enhance or modify selectivity, minimize fouling, or optimize energy consumption. However, demonstrations were conducted on the global migration of peptides and/or amino acids, but it was impossible to link specific peptide migration with electrical current conditions. Hence, five electrical current conditions were tested: continuous current (CC), PEF ratio 1 and 10, and PR ratio 1 and 10 on a well-characterized porcine cruor hydrolysate. From UPLC-MS/MS results, migration rates were calculated for each peptide, under each condition of electric current. A total of 41 physicochemical characteristics of peptides were calculated using bioinformatic tools. A machine learning peptidomic-based approach using a regression decision tree procedure was carried out to deepen the understanding of these data. The goal was to link the migration rates of peptides in the different electrical current conditions to their physicochemical characteristics and to identify current condition associated phenomena inducing this selective migration of peptides. First results highlighted that the most important variable (root node) to predict migration is different for condition PR 1 (molecular mass) compared to CC, PEF 10, and PR 10 (pI). Furthermore, PEF 1 would have an intermediate regression tree. Similarities between trees were estimated to compare electrical current conditions and to predict the main physicochemical parameters inducing migration of different peptides. It was the first time that such an approach was used in the membrane processes field to explain selective separation of peptides from a complex solution. The next step is to evaluate the antimicrobial activities of the EDUF fractions produced.



Title: Structure, composition, and functionality of water lentils protein extracts produced by electrodialysis with bipolar membrane and chemical extraction

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Muller, Tristan - Bazinet, Laurent

Summary: Water lentils are free-floating aquatic plants which can grow almost anywhere on Earth. They have a great agronomic potential since they can double their biomass in less than 24h and are very rich in RubisCO. RubisCO is a protein that has promising properties for human consumption since it is tasteless, odourless, and white coloured as well as having a high nutritive value and excellent functional properties. However, the use of water lentils for human nutrition and foods is limited due to the protein extraction step. In a previous work from our team, a water lentil protein concentrate containing 57% protein with an extraction yield of 60% was obtained : the highest ever reported in litterature for leaf protein extraction. However, this protocol required the use of a large volume of sodium hydroxide and hydrogen chloride, which is not environmentally friendly. Therefore, in this study, water lentil proteins were purified for the first time using electrodialysis with bipolar membrane (EDBM), a technology that has been developed as an ecofriendly alternative to chemical acidification. The obtained products were compared in terms of proximal composition, protein yields, structure (FTIR, circular dichroism and DSC), composition by proteomics, and functionality (solubility, foaming, gelling and emulsifying properties). Their fonctionnal properties were also compared to egg, soy, and whey protein isolates as references. Water lentils extracts produced by EDBM had similar protein extraction yields, content, structure, and composition as extracts produced by chemical extraction. However, the protein content of one the EDMB by-products, compared to chemical extraction, was greatly increased due to EDBM demineralization effect. An increase from 20% to 40% protein on dry matter basis was observed and resulted in better fonctionnal properties of this by-product. Moreover, water lentils protein extracts had excellent fonctionnal properties, such as better foaming capacity (700%) compared to egg white (450%) for the same foaming stability. Therefore, this study demonstrated the possibility of using water lentils as a well-suited protein source for human nutrition and foods.



Title: Is the application of a hexane defatting step during the production of pea protein isolate by membrane filtration necessary in a context of sustainable processing?

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Gravel, Alexia - Dubois-Laurin, Florence - Turgeon, Sylvie L. - Doyen, Alain

Summary: The use of pea protein isolates (PPI) in the formulation of plant-based products has surged with the increasing demand for sustainable proteins. The PPI process typically includes a defatting step with hexane, followed by alkaline extraction and isoelectric precipitation (IEP) of proteins. However, these steps generate large amount of non-eco-friendly organic and acidic/alkaline wastewaters. Consequently, eco-friendly approaches, such as elimination of the defatting step or replacement of IEP by ultrafiltration/diafiltration (UF/DF), were developed but there is a lack of information about their impact on PPI composition and properties are not well discussed. Consequently, this work aimed 1) to study the effect of the hexane-defatting step on PPI protein profiles and techno-functionalities and 2) to evaluate the impact of different UF membrane molecular weight cut-offs (MWCO of 30, 100 and 300 kDa) on PPI composition. Thus, PPI were produced by UF/DF with and without a hexane defatting step, and protein profiles and techno-functionalities were compared. Firstly, we showed that the hexane-defatting step had no impact on protein electrophoretic profiles and surface hydrophobicity. Only a slight difference was obtained between defatted and non-defatted PPI for protein net surface charge (-20.68 and -17.83 mV, respectively) and particle size (monomodal (~0.2 μm) for defatted PPI and bimodal (~0.3 and 1.9 μm) populations for non-defatted PPI). Techno-functionality (solubility and emulsifying properties) was not affected by the defatting step, except for foaming stability, which reached up to 97% for defatted PPI. Consequently, the defatting step is not crucial for PPI production. Secondly, results showed that UF/DF performances as well as composition and protein profiles of non-defatted PPI were similar, regardless the UF MWCO. However, some differences were observed in terms of protein species and molecular weights. Our findings can be used to improve the sustainability of PPI production with limited impact on the ingredient techno-functionalities.



Title: Impact of the blanching treatment on the techno-functionalities of yellow mealworm protein isolate produced by ultrafiltration-diafiltration

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Barrot, Juliette - Pinel, Gwenn - Berthelot, Ugo - Brisson, Guillaume - Doyen, Alain

Summary: Currently, the low acceptability for whole and visible insects integrated in diet remains a great challenge in product development, particularly in Western countries. Nevertheless, consumer acceptability can be enhanced by using of insect protein-rich ingredients such as protein isolate. Currently, this ingredient is mainly produced by isoelectric precipitation. However, the use of ultrafiltration/diafiltration (UF/DF), not already applied on insect matrix, is of a great interest due to its ability to preserve the native protein structure and potentially improve techno-functional properties. Consequently, the objective of this work was to evaluate the techno-functional properties of a mealworm protein isolate produced by UF/DF.

Two blanching conditions, 90°C for 3 min (90/3) and 75°C for 20 min (75/20), were applied on mealworms before protein extraction by alkaline solubilization and concentration by UF/DF. Isolate were evaluated for their solubility and techno-functional properties at pH 7 and 9. Results showed that the solubility of the isolates at both pH were similar, regardless of the blanching treatment. Isolate 75/20 (I75/20) exhibited higher foaming capacity (FC) than isolate 90/3 (I90/3) for both pH with respective values of 83.3 and 14.8 % for FC at pH 7 and 69.0 and 16.2 % for FC at pH 9. Additionally, foaming stability (FS) was also higher for I75/20 compared to I90/3 for both pH. Emulsifying properties were lower for I75/20 than I90/3 at pH 7 with respective values of 12.9 and 18.6 m²/g for the emulsion activity index and 14.9 and 17.2 min for the emulsion stability index. No differences were observed at pH 9.

The differences in the techno-functional properties of isolates could be related to the higher lipid content in I90/3 than I75/20. Indeed, after removing the residual lipids with chloroform-methanol, similar techno-functional properties were observed for isolates at both blanching conditions. Moreover, foaming properties were largely improved with a firm and fluffy foam. Consequently, controlling the residual lipid content in mealworm protein isolates becomes a crucial element in enhancing their techno-functionalities. The next step will involve a detailed characterization of the lipids profile and exploring the different mechanisms that contribute to the techno-functional properties.



Title: Deacidification of acid whey by coupling electrodialysis under pulsed electric fields and preconcentration by nanofiltration

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Poitras, Danika - Perreault, Véronique - Gaaloul, Sami - Bazinet, Laurent

Summary: Acid whey is a by-product of the dairy industry. Mainly, it is obtained from the production of Greek yogurt and certain cheeses, such as cottage cheese. A large amount of acid whey is produced every year. Considering the current Greek yogurt market growth, the amount of acid whey produced has continued to increase. Unlike sweet whey, which can easily be dried into a powder to be valorised, acid whey's drying process faces challenges due to its high calcium and lactic acid concentrations. For this reason, a demineralization and a deacidification of the acid whey prior to drying would be beneficial and allow a more ecoefficient process. Therefore, preconcentration by nanofiltration coupled with deacidification and demineralisation by electrodialysis can enhance drying process and increase the quality of the powders. In this study, nanofiltration was carried out with a tangential unit using a membrane with a 150-300Da molecular weight cut off. Acid whey was concentrated to 4.0-4.8X concentrating factor before proceeding to electrodialysis. Electrodialysis was then performed on the concentrated acid whey until 70% demineralisation rate was reached. Three different conditions of electric field were tested such as constant current (CC), pulsed electric field (PEF) 5s on/5s off and PEF 15s on/15s off. No significant difference in energy consumption was noticed between the three conditions. The Electrodialysis process resulted in a 46% reduction of lactic acid in the acid whey. An interesting inflection point has occurred in the global system resistance once 50% demineralisation rate was reached. Mineral composition analysis are currently under way for the acid whey's sample and will provide further information on this observation and the potential selective demineralization effect of PEF. 1. Bolwing et al. Valorisation of Whey: a tale of two Nordic dairies. From Waste to Value: Valorisation Pathways for organic Waste Streams in circular Bioeconomies, (2019) 162-186



Title: Discovery and characterization of selected 4,6- α -glucanotransferases

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Roshanineshat, Rana - Karboune, Salwa

Summary: 4,6- α -glucanotransferases (4,6- α GTs) are the recently discovered subfamily of glycoside hydrolase 70 family. 4,6- α GTs are able to cleave the α -(1,4) glycosidic linkages of substrates such as starch and starch hydrolysates and introduce novel α -glucan polymers with α -(1,6) or α -(1,3) glycosidic linkages. The synthesized polysaccharides with α -(1,6) are resistant or slowly digestible carbohydrates that are able to enhance intestine and overall health by reducing the rapid glycemic response in the human body. In this study, a BLAST search was conducted in a lactic acid bacteria database consisting of 27 strains for identification of potential 4,6- α GTs producing bacteria. Among the nine bacterial strains that were identified as hits, further studies for the characterization of the enzyme from strain *Pediococcus pentosaceus* was performed using amylose and soluble starch as substrates. The assessments including total activity, transglucosylation extent and FTIR analysis suggests the formation of health promoting α -(1,6) glycosidic linkages.



Title: Compositional Profiling of Quinoa and Assessment of its Potential as a Source of Quinoa-Based Ingredients

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Rodriguez, Diana - Seguin, Philippe - Karboune, Salwa

Summary: Quinoa (*Chenopodium quinoa* Willd.) stands out as a potential crop for plant-based functional ingredients due to its composition and nutritional properties. In addition, quinoa can grow in adverse climate conditions representing an advantage in facing food security. So far, there has not been any published study on the compositional profiling of quinoa grown in Quebec. Characterizing the nutritional composition of different varieties of quinoa is a key first step for the development of quinoa-based ingredients with higher added value. Indeed, the quinoa composition differs in terms of content and quality attributes depending on quinoa varieties, and growing conditions. In the present study, eight quinoa varieties cultivated in Quebec submitted to different management practices were submitted to compositional profiling with the aim to identify the best varieties for producing fiber enriched quinoa flour and for protein isolation. The compositional profiling includes protein, lipid, ash and moisture and saponin content as well as amino-acid profiling. As expected, the protein content of quinoa was dependent on the variety and the agronomic practices used and covered a range from 12.5 to 20.0% (w/w). Similar to protein content, the variation in lipid content (3.34-6.95%, w/w) and ash content (2.79-5.24% w/w) was significant. It is known that quinoa has a balanced minerals content that includes potassium, sodium, magnesium, calcium and iron. The presence of bitter saponins may have a detrimental effect on the nutritional value of quinoa and its acceptance. The 'Quinta' variety had the highest saponin content, which although varied depending on agronomic practices used. The functional capacity of quinoa related to its compositional profiling will be discussed. The potential for sustainable value development of quinoa-based ingredients is assessed for both wet and dry extraction methods based on the compositional profiling and on a review of the literature.



Title: Impact of okara on the stability of fermented soy milk during storage

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Osse, Emmanuel-Freddy - Gumiere, Thiago - Aider, Mohammed - Khalloufi, Seddik

Summary: The soy industry produces large quantities of waste each year, including hulls, defatted soy flakes and okara, which is the solid phase left after the soymilk has been extracted. Okara quantities have increased significantly in recent years because of the growing interest shown by industry and consumers in soy-derived products. However, poor management of okara, like most industrial waste, leads to economic losses and socio-environmental problems, which raises the question of its effective valorization. One way of adding value to okara is its use in food formulations as a structuring agent that simultaneously provides fibre, protein, and other nutrients. It is in this vein that the present project was carried out with a "zero waste" approach by producing fermented soy milk enriched with okara. The aim was to improve the stability of fermented products during storage. To achieve this objective, two different samples of soymilk were prepared and then fermented using lactic acid bacteria (*Streptococcus thermophilus* and *Lactobacillus delbrueckii* subsp. *bulgaricus*). The samples were soymilk (SM) and fibre-enriched soymilk (without elimination of okara) (WSM). The physicochemical parameters were then analysed. The results showed an increase in syneresis in all fermented products during storage. Syneresis reached its maximum value after 21 days and then decreased slightly. On the other hand, okara significantly reduced the syneresis of the samples. Syneresis at 21 days storages fell from $8.05 \pm 2.76\%$ for SM to $2.47 \pm 0.02\%$ for WSM. These results confirm that the use of okara in soymilk reduces the syneresis of fermented products. They also suggest that other parameters such as texture and particle size should be studied to improve the stability of this type of product.

Key words: okara, syneresis, storage, stability



Title: Comparison Between Dewatering Technologies and Their Impacts in the Preparation of Food Powders

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Sultana, Afroza - Aghajanzadeh, Sara - Thibault, Bruno - Ratti, Cristina - Khalloufi, Seddik

Summary: Food powders, such as those made from fruits or vegetables, milk, coffee, or nutraceuticals, are widely used in our daily cuisine. The dewatering methods employed have a significant impact on the functionalities of those powders, such as solubility, dispersibility, reconstitution, nutrient retention, or shelf-life. Although dewatering is an ancient and widely used method of preparing powders, some dewatering technologies encounter difficulties due to stickiness, caramelization, and foaming. Additionally, due to the diverse nature of foods (starchy, protein-rich, and fatty), their viscosities, and the focused application of powders, the production of powder from liquid feed or slurry is quite challenging. Furthermore, energy consumption and dewatering kinetics are crucial factors in selecting an effective dewatering technology. As a result, it is of the utmost importance to select appropriate technology while keeping the aforementioned factors in mind. This study presents a comparative scenario between the dewatering procedures applied to prepare food powders, which will assist the food practitioner in choosing the most appropriate technology based on their specific needs. This review also includes several cutting-edge dewatering processes that may overcome constraints in another method, which will contribute to the advancement of the drying sector.

Keywords: dewatering, food powder, stickiness, powder properties



Title: Artificial intelligence to study phage-host interactions and their impacts on metabolic health in individuals representing the general population of Quebec

Topic: NUTRITION AND SOCIETY

Author: Boulay, Alexandre - Leblanc, Benjamin - Germain, Pascal - Rousseau, Elsa

Summary: Bacteria are the most studied organisms in the gut microbiome as they are recognized to have a profound impact on human gut health. The relationship between the gut bacteria and their host is often described as symbiotic, as the bacteria enjoy a constant source of nutrients and a stable environment, while the host benefits from additional metabolic capabilities and protection against pathogens. Albeit being the most abundant biological entities on the planet, the viruses that infect them, called bacteriophages or phages, have received much less attention. Recent studies have shown that phages modulate microbiome community dynamics due to their obligate predator-prey interactions with their bacterial hosts. Thus, bacteriophages are also increasingly believed to play a role in human health. A study performed on 116 healthy adult Quebecers explored the interplay between the bacterial fraction of the gut microbiota, the endocannabinoid system and human health. Importantly, study subjects were chosen to represent the general population with different body compositions, dietary habits, and levels of daily physical activity. Individuals were recruited at the Institute of Nutrition and Functional Foods at Université Laval and the anthropometric and metabolic characteristics of all subjects were measured. In addition, whole metagenome shotgun sequencing was performed on fecal samples from these individuals. For this ongoing project, we are exploring the viral component from this sequencing data. Artificial intelligence (AI) methods will be applied to investigate the associations between phages, bacteria, and human health. Particular attention will be placed upon choosing interpretable approaches. AI models will be trained on microbial abundance data to predict variables of metabolic and anthropometric health. Then, these models will be studied to identify phages and bacteria biomarkers of those health variables. An emphasis will be put on understanding the interactions between phages and bacteria. These analyses will further our understanding of the roles that phages and phage-bacteria interactions play in nutrition and health.



Title: Influence of the processing on protein composition and profile of mung bean protein isolates produced by ultrafiltration-diafiltration and isoelectric precipitation

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Dubois-Laurin, Florence - Doyen, Alain

Summary: Currently, there is a need to generate plant-based protein isolates since it represents the main ingredient in plant-based meat analogues. Mung beans (*Vigna radiata*) are of a great interest for this application due to their high protein content. Two main process, isoelectric precipitation (IEP) and ultrafiltration-diafiltration (UF-DF) are used to produce plant-based protein isolates. However, the benefit and challenges related to these processes were never evaluated to generate mung bean protein isolate (MBPI). Consequently, as preliminary experiment, this study aimed to compare the protein content and profiles of MBPI generated by IEP or UF-DF.

Mung bean seeds were firstly ground into a flour and proteins were extracted by alkaline solubilization at pH 9 for 120 min. A liquid protein concentrate was recovered and separated into two parts. The first part was used to generate MBPI by UF-DF (30-kDa UF membrane, 3 cycles of concentration-diafiltration) whereas the second part was used to produce the MBPI isolate by IEP at pH 4.5. Performance of the UF-DF filtration process was assessed by the evolution of the permeate flux. Moreover, both isolates were compared for their protein content, measured by Dumas combustion method (nitrogen-to-protein conversion factor of 6.25) and protein profiles by gel electrophoresis under non reducing and reducing conditions.

These preliminary results showed no drastic decrease of permeation flux suggesting minor UF membrane fouling. Moreover, similar profiles were obtained in both UF-DF and IEP MBPI. The protein content was higher in the UF-DF MBPI (~87.4%) compared to the one produced by IEP (~83.0%). Indeed, no protein was detected in the UF-permeate validating a total protein retention by using the 30-kDa UF membrane. However, a loss of proteins, mainly vicilin subunits, was noticed in supernatant recovered after mung bean protein precipitation by IEP validating that all protein did not precipitate at pH 4.5. These findings showed that UF-DF seemed to be more suitable than IEP to improve the recovery and concentration of proteins. The next step will consist to and compare the techno-functional properties of both UF-DF and IEP MBPI to anticipate their use in various food formulations.



Title: Harnessing Banana Peel as an Effective Adsorbent for Heavy Metal Remediation from Wastewater

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Mpiri Maleka, Robercia Christelle - Ahasanul, Karim

Summary: The pollution of wastewater contaminated with heavy metals in our environment has been a significant challenge for scientists and a global concern for several decades. Among the surface removal techniques for heavy metals in aqueous solutions, adsorption stands out as one of the most effective, low-cost, and environmentally friendly methods. In this context, the present study focused on eliminating lead from wastewater using agro-polymers, specifically banana peels. The adsorption behavior of lead on the banana peel was studied by analyzing different parameters such as pH, porosity, and contact time, varying the initial concentration of lead. The concentration of lead was measured using an atomic adsorption spectrometer. The results showed that the banana peel efficiently adsorbs lead, providing a valuable method for heavy metal remediation and simultaneous waste valorization. By studying its capacity and potential as an adsorbent in lead removal from wastewater, we have demonstrated a promising application for this agri-food waste.



Title: Valorization of dietary plant fibers as bio-sorbents: A sustainable approach to remove toxic heavy metals

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Raji, Zarifeh - Ahasanul, Karim - Karam, Antoine - Khalloufi, Seddik

Summary: Global population growth and changes in lifestyle have indeed contributed to a significant increase in agri-food waste. Nearly one-third of the food produced annually is wasted. In developed countries, this waste is produced from the food manufacturing industry (39%), household sources (42%), and remaining in agriculture, retail, and distribution. Food waste contains rich bioactive compounds such as dietary fibers, polyphenols, and protein, which, if not managed properly, can pose a serious threat to the environment, human health, and food security. In this sense, managing agri-food waste through valorization or circular economy has become an urgent global issue. Heavy metals such as arsenic, cadmium, lead, or mercury present in wastewater and polluted water pose another significant threat to human health. In this context, the aim of the study was to revise the current literature concerning the application of waste-derived plant fibers for the treatment of heavy metal-rich wastewaters. The purified water would be suitable for drinking and the preparation of food and could be reintroduced into a drinking water distribution system. These fibers, abundant in food waste, possess functional and bioactive groups, as well as a porous structure that facilitates the adsorption of heavy metal ions. The adsorption ability of dietary fibers depends on their specific structure (solubility or insolubility). The adsorption capacity and efficiency of these residues are influenced by factors such as pH, temperature, contact time, initial ion concentration, adsorbent dose, specific surface area, crystallinity, porosity, particle size, and cation exchange capacity. Moreover, this study explored the potential of physical, chemical, and/or biological treatments to improve adsorption and to identify their possible applications in a variety of food matrices. To overcome some remaining challenges posed by heavy metal contamination, further research efforts are needed to optimize adsorption efficiency, identify suitable fibers for specific metal ions, develop some functional foods that help reduce heavy metal contents, and address challenges such as hornification phenomena and regeneration capacity.



Title: Advancements in Osmotic Dehydration: Enhancing Food Quality and Enabling Functional Foods

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Asghari, Ali - Zongo, Pingdwendé Assana - Khalloufi, Seddik

Summary: Osmotic dehydration (OD) has emerged as a promising technology with wide applications in food preservation and quality enhancement. By utilizing hypertonic solutions, OD efficiently removes water from cellular food products, particularly fruits and vegetables. This comprehensive contribution consolidates current knowledge on OD, providing valuable insights for researchers, food technologists, and industry professionals engaged in food processing. The mechanisms involved in OD, including mass transfer pathways, and influencing factors, are thoroughly examined. Additionally, the kinetics of OD are investigated, focusing on crucial measurement parameters and a subsequent discussion on mathematical modeling and the Biot number. This work also explores cutting-edge technologies aimed at bolstering the effectiveness of OD, such as coating, freezing, freeze/thawing, ultrasound, pulsed electric field, high hydrostatic pressure, vacuum, centrifugal treatment, and fruit skin treatments. The mechanisms of action and corresponding results of each technology are presented and discussed. Moreover, the study delves into the potential infusion of bioactive components into food products through OD, highlighting mechanisms of action and achieve outcomes. Furthermore, this contribution discusses the synergistic combination of technologies to intensify the OD process. The review concludes by analyzing the opportunities and challenges associated with OD. Opportunities encompass its potential for food preservation, improving nutritional properties, and driving innovative product development. The challenges are addressed in terms of process optimization, maintaining product quality, and ensuring economic feasibility. The outcomes of this investigation can serve as a valuable guideline for the food industry and scientists in designing optimized products that respond to market trends.



Title: Predicting the remaining shelf life of fresh produce through hyperspectral imaging and scientific computing

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Mckinnon, Carole - Sasseville, Louis

Summary: The issue of food loss and waste concerns the entire food supply chain. Whether it occurs during transportation, storage, retail, or within households, the ability to swiftly and non-destructively assess the freshness of fruit and vegetables could greatly improve inventory management and contribute to mitigating losses and reducing food waste.

The objective of this study was to monitor the shelf life of fruit and vegetables by hyperspectral imaging within the visible and near-infrared range (400–1000 nm) and to develop a predictive model for the remaining shelf life of these produce through the use of regression algorithms.

The hyperspectral images acquisition system's parameters were optimized to extract valuable information from the captured images. A daily scan was obtained using a line-scan hyperspectral camera until the product was visually deemed inedible. Principal Component Analysis was subsequently executed to reduce the dimensionality of the data derived from the images and retain the most informative spectral details. Image preprocessing involved the selection of regions of interest, removal of background noise, segmentation, labeling, and detection through blob analysis. This process yielded an individual image for each fruit or vegetable. Multiple regression algorithms were trained concurrently to enable the selection of an appropriate model.

Encouraging results have been obtained, as the algorithm successfully determined the remaining shelf life in days for various produce including pears, bean sprouts, mushrooms, bananas, strawberries, raspberries and blueberries. The versatility of the algorithm enables its adaptation to different produce for determining their remaining shelf life.

Overall, this approach offers a non-destructive and efficient method to monitor and manage inventory, reduce food waste and improve supply chain efficiency.



Title: Effect of drying technologies on the structure and physical properties of dietary fibers derived from food waste

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Jougbou Nkala, Herman Douglas - Aghajanzadehsuraki, Sara - Turgeon, Sylvie L. - Khalloufi, Seddik

Summary: Abstract

Annually, the food production industry generates a substantial volume of waste, presenting an opportunity to utilize this waste as a valuable source of dietary fibers (DFs) to improve the quality of food products. The drying process plays a crucial role in the DFs production due to having a profound effect on their physicochemical properties, thereby influencing their functional and physiological attributes. Therefore, choosing the most appropriate drying technology is a crucial step in the processing of DFs. This study aimed to compare the effects of air-drying and freeze-drying technologies on the structure and physical properties of dehydrated DFs derived from food waste. In this study, a mixture of DFs (2%) in water was prepared and then subjected to high-shear mixing and high-pressure homogenization (HPH) treatments. The prepared samples were dried in an air dryer at $55 \pm 1^\circ\text{C}$ for 24 h. In freeze-drying, HPH-pretreated samples were spread on an aluminium tray, and freeze-dried at -55°C and 0.01 kPa (vacuum pressure) for 72 h. The obtained results revealed that the choice of drying technology influenced the physical properties of DFs. In comparison to the Freeze-dried DFs, air-dried ones showed lower porosity and specific surface area, and particle sizes, as well as higher bulk density. These observations could be attributed to the occurrence of the hornification phenomenon during the air drying of DFs. The Scanning electron microscopy evaluation further supported these findings by revealing a porous structure in freeze-dried DFs and a compact arrangement in air-dried DFs. The superiority of freeze-drying as a drying technology for preserving the physical properties of DFs highlights its potential as a preferred method in the food industry. The insights gained from this research into the underlying phenomena involved in the dehydration of DFs provide valuable knowledge for optimizing processing techniques and enhancing their utilization as ingredients in food formulations. The obtained results from this research contribute to the advancement of sustainable practices in the food industry by maximizing the utilization of food by-products and reducing waste.

Keywords: Food waste; Dietary fibers; Freeze-drying; Air drying; Physical properties



Title: Impact of high hydrostatic pressure on interactions between pea proteins and casein micelles

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Serrano León, Gabriela

Summary: Research on mixed protein systems, mainly generated by pea and dairy protein interactions, is of a great interest to generate innovative, sustainable, and techno-functional ingredients for food formulation. Currently these mixed protein systems were produced by heat treatment, but little data are available regarding the impact of non-thermal technologies on the formation of mixed protein systems. Consequently, the aim of this study was to investigate the effect of high hydrostatic pressure (HHP) on the interactions between pea protein isolate (IPP) and casein micelles (CN).

For this purpose, protein mixtures with different CN to IPP ratios (100:0, 50:50, 0:100) were prepared at a total protein content of 4% (w/v) and pH 7.2. The pressure applied was 600 MPa for 5min. All samples were compared with a positive control treated at 90°C for 60 min. Changes in protein structure and profile were assessed by measuring the turbidity, sulfhydryl content, surface hydrophobicity and protein profile.

Results revealed a significant decrease in turbidity optical density (from 0.34 to 0.13) on the 50:50 ratio (CN-IPP) after HHP treatment compared to heat treatment, indicating a major destabilization of CN by HHP. Free SH groups increased from 3.4 to 4.0 $\mu\text{mol/g}$ protein after HHP treatment compared to heat treatment, suggesting protein unfolding phenomenon in HHP-treated mixed protein whereas protein aggregation by disulfide bonds occurred after heat treatment. These results were confirmed by protein profiles since large CN-IPP protein aggregates were visualized after heating whereas HHP seemed to have slight impact on protein-protein interactions. Similarly, the difference in surface hydrophobicity index of heat-(86.2x10³) and HHP-treated (76.6x10³) mixed protein samples at ratio 50:50 was related to protein unfolding after heat treatment.

The findings showed that heat treatment had a greater effect on CN-IPP interactions compared to HHP. Moreover, it appears that HHP could induce CN-IPP through non-covalent interactions. Results of mass spectrometry, currently under analysis, will help to characterize the proteins involved in the formation of aggregates.



Title: Revealing the potential of Brewer's Spent Grains in Human Nutrition: Exploration of Protein Extraction Performance and Functional Properties

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Gagnon, Jonathan - Turgeon, Sylvie L. - Mikhaylin, Sergey

Summary: To reduce the environmental impact and waste management costs of the brewing industry it is necessary to find new ways to increase the value of brewer's spent grain (BSG), the main organic waste associated with beer production. Currently, most of this by-product is relegated to animal feed or landfills but it could have added value when used for human consumption (2). To investigate BSG proteins and identify potential food applications, native BSG, methods using simple and double alkaline extraction were compared with extracts produced by isoelectric precipitation for a wide range of functional properties at pH 2, 4, 6 and 8.

Both methods of protein extraction yielded extracts with higher protein content than native BSG. Alkaline extraction without isoelectric precipitation yielded extracts with up to 30 % protein content.

BSG showed no emulsifying or foaming properties while protein extracts demonstrated significant improvements in these functional properties, comparable with whey protein isolate. Functional properties were improved around neutral pH conditions (pH 6 and 8) and were lowest at pH 4 where isoelectric precipitation was observed. Overall low BSG proteins solubility in acid conditions is the main obstacle to food applications.

Structure of extracted proteins was further investigated by circular dichroism, FPLC, SDS-PAGE, surface hydrophobicity analysis. Free thiols content was also evaluated.

Based on results obtained, BSG protein extracts could have interesting applications in human consumption especially regarding their emulsifying and foaming properties even when using simplified extraction methods. Future food applications should focus on low-acid foods to maximize BSG protein extracts' potential.



Title: ENZYMATIC HYDROLYSIS OF INDUSTRIAL WHITE WATER FOR OPTIMAL PRODUCTION OF ANTIFUNGAL PEPTIDES

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Damen, Diala

Summary: The dairy industry produces large amounts of wastewater, including white and cleaning wastewater originating principally from rinsing and cleaning-in-place procedures. Therefore, to improve the sustainability of dairy plants and as part of a circular economy, there is an opportunity to valorize, dairy constituents present in white water such as proteins. Enzymatic hydrolysis resulting in the formation of bioactive peptides has been highlighted as a major approach to protein valorization and, more specifically in the case of these effluents, the production of antimicrobial peptides to be used on final dairy products.

In this work, the physicochemical characteristics of white water from an ultrafiltration system of skimmed (collection) milk were first evaluated. The amount of total solids was 1.38% including 1.28% protein compared to 3.2-3.5% protein in milk. Then, enzymatic hydrolysis tests were performed according to the optimal conditions of four different enzymes: pepsin, trypsin, thermolysin and pronase E. The degree of hydrolysis (DH) was quantified by the o-phthalaldehyde (OPA) spectrophotometric technique. Among the four enzymes, pronase E exhibited the highest DH reaching up to 13.79% after 240 minutes of reaction. Pepsin and trypsin led to lower DH of 3.66% and 4.65%, respectively. The hydrolysates were analyzed by HPLC-MS/MS to validate the hydrolysis mechanisms and to identify the peptide sequences present in each hydrolysis condition. The physicochemical and structural characteristics of the identified peptides were studied using bioinformatics databases in order to identify peptides with potential antibacterial and antifungal activities. These peptides were also statistically analyzed, and peptide sequence identification was performed from known milk proteins. The first analyses showed a great variability between the peptide sequences found in the hydrolysates suggesting completely different bioactivities. These results form a promising database for the selection of potential antifungal peptides whose antifungal effects are currently under study.



Title: Management and recycling of chicken eggshell wastes in the context of circular economy

Topic: SUSTAINABLE SYSTEMS FOR FOOD PROCESSING

Author: Soufan, Raghad - Karam, Antoine - Ajjane, Ahmed - Khasa, Damase

Summary: In most developing countries, commercial egg production has increased over the past few decades, resulting in a huge amount of eggshell waste generated from egg breaker factories, households and restaurants and disposed into landfills. In a context of sustainable development, disposing of food and organic waste in landfills should be avoided, for both ethical and environmental reasons. The valorization of these organic food co-products rich in calcium carbonate (CaCO_3) and containing certain important nutrients and organic compounds is an ecological way that has a significant environmental and economic impact. Meanwhile, heavy metals contamination of waterways from mine waste rock and acidic sulfide mine tailings in mining area ecosystems poses many ecological and health risks. The most common application for reducing acidity is the use of limestone- a common alkaline sedimentary rock composed primarily of the calcium carbonate mineral, calcite (CaCO_3).

The objective of the first part of this work is to summarize the literature and the current knowledge on the applications of chicken eggshell wastes. The literature has revealed that chicken eggshell/eggshell membrane wastes can be used as human nutritional supplements, bone substitutes and drug delivery carriers, antibacterial materials, animal feed additives, catalysts, cosmetics and biomaterial composite, fertilizer, and natural adsorbents for removing heavy metals and other xenobiotics from wastewater.

The second part is experimental and concerns mainly the use of chicken eggshell residues (CER) as a lime amendment to neutralize the acidity of mine water (AMW) from the former Aldermac mine near Noranda (Abitibi-Témiscamingue, Quebec). Three types of CERs were used: CER dried at 60°C and finely ground (CER1), CER1 calcined at 500°C for 24 hours (CER2) and CER1 calcined at 700°C for 6 hours (CER3). The ANOVA test showed a highly significant effect ($p \leq 0.001$) of CERs doses on pH value of AMW. After 1080h of reaction time, the pH value of AMW amended with the highest rate of CER (4.0g CER/40 ml of AMW) increased from 3.07 (without amendment) to 7.07 for CER1, 7.39 for CER2, and 11.20 for CER3. In conclusion, CERs are acid-neutralizing materials and could be used to reclaim abandoned acid mine drainage sites.

Keywords: bio-waste, bio-amendment, acid-neutralizing biomaterials, calcium carbonate, mine reclamation