KICLS 2025 – Track on Nutrition and Food Science
POSTERS

Exploring the Nutritional Potential of Kuwaiti Seagrasses: Fatty Acid and Mineral Profiles as Food and Feed Resources

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Abstract

Seagrasses are rich in bioactive compounds and essential minerals that can address various healthcare challenges. These plants produce bioactive molecules in response to environmental changes, including polyunsaturated fatty acids (PUFAs), which have shown therapeutic effects for microbial infections, skin diseases, diabetes, muscle aches, helminthic diseases, and wounds. Additionally, seagrasses provide minerals that support bone health, electrolyte balance, and enzyme activity. Surprisingly, no seagrass from the Arabian Gulf has been studied in this context to date. This study is aimed at analyzing the total lipid (TL) and fatty acid (FA) compositions, as well as the mineral content of the most abundantly available seagrass from Kuwaiti waters in the northern Arabian Gulf, using GC-MS and ICP-MS, and to assess the impact of water quality (using variables such as turbidity, temperature, pH, and conductivity), seasonal variations and spatial hydrographical variabilities on the FA composition of three most common seagrasses. This project will serve as a baseline for future studies on seagrass as a source of natural minerals and high-quality PUFAs, with potential for efficient use in nutraceutical and pharmaceutical industries.

Nutritional Prevention of Hyperlipidemia and Hepatic Oxidative Stress by *Globularia alypum*: Relevance to Metabolism-Related Chronic Diseases

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Abstract

This study evaluated the antioxidant and hypolipidemic effects of the lyophilized aqueous extract of *Globularia alypum* leaves (1 $g \cdot kg^{-1}$ body weight) on plasma and hepatic lipids, as well as oxidative stress induced by a cholesterol-enriched diet (1 %) in adult male Wistar rats. Animals were divided into four groups: control diet (C), high-cholesterol diet (HC), control diet with *Globularia alypum* extract (C-*Ga*), and high-cholesterol diet with extract supplementation (HC-Ga). After 4 weeks, the extract had no significant effect in control rats, but in the HC-Ga group, it significantly reduced total cholesterol (−56 %), LDL-C (−44 %), VLDL-C (−46 %), triglycerides (−55 %), phospholipids (−36 %), and increased HDL-C (+54 %) compared to the HC group. Hepatic enzyme levels (ALT and AST) decreased by 64 % and 71 %, respectively, in HC-*Ga* compared to HC. In the liver, TC, TG, and PL were reduced by 75 %, 78 %, and 53 %, respectively, with a marked reduction in TBARS (−85 %) and a 53 % increase in reduced glutathione (GSH). Additionally, the activities of antioxidant enzymes superoxide dismutase (SOD) and glutathione peroxidase (GPx) increased by 45 % and 42 %, respectively. This study highlights the protective role of *Globularia alypum* aqueous extract against hypercholesterolemia and its associated damage by improving lipid profiles and enhancing hepatic antioxidant defenses. These findings support the potential inclusion of this plant in nutritional strategies aimed at preventing chronic metabolic disorders related to lipid imbalance and oxidative stress.

Evaluating the Protein Enrichment Potentials of Sweet Potato Peels Subjected to Solid State Fermentation with Lactobacillus Acidophilus Isolated from Yoghurt

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Abstract

High costs, inadequate quantities and qualities of conventional protein sources used as animal feed ingredients have necessitated the search for local alternatives. Food waste resources, such as sweet potato peels, are thus attractive for exploration when subjected to fermentation with the right microorganisms. In the present study, the protein enrichment Potentials of Sweet Potato peels were evaluated in solid-state fermentation (SSF) with Lactobacillus acidophilus isolated from Denice Yogurt, as a starter culture. Weighed quantity of Sweet Potato peel was dried, pulverized, and mixed with a broth containing a known concentration (colony forming units (CFU)) of Lactobacillus acidophilus and fermented for seven (7) days, at 30ºC, and the observed changes were recorded, as the experimental Treatment. A control treatment was also prepared in a similar manner to the experimental one, although it was not fermented. A third treatment labeled Spontaneous fermentation comprised the same experimental setup and was fermented spontaneously at the same temperature and time interval, but without the addition of Lactobacillus acidophilus culture. At the end of the experiment, after 7 days, the result of the Fermented Sweet Potato (Spontaneous and with Lactobacillus) was compared to the control sample (Unfermented Sweet Potato Peel) via Proximate composition and amino acids profiles. The Results indicated that the percentage of crude protein contents of the fermented sample with L. acidophilus increased significantly from 5.55% to 8.71 compared with the non-fermented control sample. Similarly, the profile of limiting amino acids was higher in both the fermented Sweet Potato samples. Therefore, it is concluded based on the results of this experiment that applying solid-state fermentation to agro-waste residues, especially sweet potato peels, has the potential to enhance the protein content and serve as a good source of cheap, protein-enriched feeds for domesticated livestock, such as fish and poultry.

Ginger Extract Downregulates the Expression of HSP22 in the Retina of Diabetic Retinopathy Rats

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Abstract

Diabetic retinopathy (DR) is a common complication of diabetes that damages retinal neurons and blood vessels eventually causing blindness. In Kuwait, 30.7% of diabetic patients have been diagnosed with DR. Ginger (Zingiber officinale) is an affordable and natural herbal with antioxidant and anti-inflammatory properties. Ginger attenuates DR-related inflammation, oxidation, and apoptosis. Heat shock protein 22 (HSP22) is one of the small HSPs that are overexpressed in the diabetic retina. HSP22 induces mitophagy in neurons and mediates the degradation of misfolded proteins via chaperone-assisted selective autophagy (CASA). This study aims to investigate the effect of ginger extract on the expression of HSP22 in the retina diabetic rats. Sprague Dawley male rats were divided into normal control (NC), diabetic control (DC) and diabetic rats treated daily with Indian ginger extract (DG) (500 mg/Kg). Type 1 diabetes was induced via injection with streptozotocin (STZ) (60 mg/Kg). Histological examination of the retina was done using Hematoxylin and eosin (H&E) staining. Gene expression of HSP22 in the retina was analyzed using Real-time polymerase chain reaction (RT-PCR) (n=6/group) and protein expression was analyzed using Western blot (n=3/group). Data were pooled from three repeated rat cycles and analyzed using GraphPad Prism ($P<0.05$).Our results showed that daily administration of ginger extract significantly reduced the fasting blood glucose and increased the body weight. Histological examination revealed an overall improvement in the retinal integrity of DG rats. HSP22 protein level was upregulated in DC compared to NC rats ($P<0.0001$). After eight weeks of ginger extract treatment, HSP22 was significantly reduced in DG compared to the DC group, at both gene ($p=0.045$) and protein ($p=0.0045$) levels. Our results indicate that ginger extract significantly downregulates the HSP22 expression in the diabetic retina. Previous studies have shown that inhibiting HSP22 reduces the autophagy process and contributes to retinal dysfunction. Further research is needed to determine whether the downregulation of HSP22 following ginger treatment affects autophagy in the diabetic retina.

An Evaluation of the Quality and Impact of a School Duathlon Event: Insights from Parental Perceptions

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Abstract

School-based sports events are increasingly used to promote children's physical activity and health awareness. In Kuwait, where childhood obesity is a major concern, understanding parental perspectives on such initiatives is critical. Guided by Social Cognitive Theory (SCT), this study evaluated parents' perceptions, motivations, and satisfaction with a school-organized duathlon. The mixed-methods design included 260 parents of elementary school children who participated in the duathlon. Pre- and post-event questionnaires assessed caregivers' motivations, health perceptions, weight, diet, fitness, knowledge, and satisfaction. Quantitative data were analyzed descriptively, while open-ended responses provided qualitative insights. Mothers made up most respondents (57%), reflecting their central role in supporting child participation. Most parents perceived themselves and their children as having normal weight, moderate-to-high fitness, and healthy diets. Knowledge about children's nutrition and physical activity was high, consistent with SCT's emphasis on self-efficacy and behavioral capability. The duathlon fostered reflection on family health behaviors and strengthened parental awareness of active living. These findings underscore the importance of parental engagement, particularly maternal modeling, in shaping children's participation in health-promoting events. Duathlon participation enhanced parental awareness and motivation to support healthy lifestyles. This illustrates how SCT constructs of self-efficacy, observational learning, and environmental support can inform effective program design. Integrating family-oriented components may enhance the sustainability and impact of similar school-based health initiatives in Kuwait and beyond.

An Association Study of Type 2 Diabetes Mellitus Genetic Risk Factors in the Kuwaiti Population

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Abstract

Background: The heritability of type 2 diabetes mellitus (T2DM) is estimated to be 25–80% based on family and twin studies. To date, over 200 T2DM genetic risk variants have been reported in various populations. Despite Kuwait's high T2DM prevalence, replication studies of T2DM genetic risk factors remain limited.

Objectives: To determine the association of the 10 commonly reported T2DM genetic risk factors in a T2DM population sample from Kuwait and design a genetic risk score (GRS) model specific to Kuwait.

Methods: Genotyping of *ADRB2* rs1042714, *CCND2* rs76895963, *CDKAL1* rs7754840, *CDKN2A/B* rs10811661, *FTO* rs1421085, *IGF2BP2* rs7633675, *KCNQ1* rs2237897, *PPARG* rs1801282 *TCF7L2* rs7903146, and *VDR* rs731236 was performed using Taqman assays in 200 Kuwaiti T2DM patients and 160 Kuwaiti healthy controls. Unweighted and weighted GRSs were computed.

Results: Three variants associated with T2DM risk in Kuwaitis (*TCF7L2* rs7903146T: β=0.133, 95%CI: 0.066–0.199, $p<0.001$; *VDR* rs731236G: β=0.102, 95%CI: 0.033–0.17, $p=0.004$; and *IGF2BP2* rs7633675G: β=0.075, 95%CI: 0.008–0.142, $p=0.028$). Some variants associated with risk of diabetes comorbidities (Retinopathy: *CDKAL1* rs7754840C β=0.123, 95%CI: 0.034–0.213, $p=0.007$ and *ADRB2* rs1042714G β=0.125, 95%CI: 0.024–0.226, $p=0.016$; Neuropathy: *TCF7L2* rs7903146T β=0.284, 95%CI: 0.195–0.373, $p<0.001$ and *VDR* β=0.288, 95%CI: 0.194–0.382, $p<0.001$; Myocardial infarction: *TCF7L2* rs7903146T β=0.065, 95%CI: 0.002–0.128, $p=0.034$. The best model performance was observed for the weighted GRS including the three variants significantly associated with T2DM risk together with age and BMI (82.6% Accuracy; 92.2% Sensitivity; 63.2% Specificity; β=86.885, 95%CI: 8.813-856.573, $p<0.001$).

Conclusion: Reported T2DM genetic risk factors do not consistently associate with T2DM risk among Kuwaitis, but including those variants in a T2DM prediction GRS model may refine its performance. Including established T2DM risk factors like age and BMI further enhances models' performance. A T2DM early screening GRS for Kuwaitis could enhance early interventions, curbing the T2DM burden on Kuwait's healthcare system.

Characterization of Microtubule Dysfunction Associated with Alzheimer's-like Pathology in Mouse Models of Impaired Glucose Metabolism

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Abstract

Microtubules are critical components of the neuronal cytoskeleton, essential for maintaining neuronal architecture and the transportation system. These structures, composed of tubulin proteins and supported by microtubule-associated proteins like Tau, are susceptible to dysfunction in neurodegenerative diseases, including Alzheimer's disease (AD). Emerging evidence indicates that disrupted glucose metabolism may contribute to similar microtubule-related pathology. This study aims to investigate the effects of glucose metabolism impairment on microtubule integrity, highlighting its potential role in diabetes-induced neurodegeneration. We utilized multiple mouse models to study glucose metabolism-related pathology, including 5XFAD/+ mice as a model of Alzheimer's-like amyloidosis, C57BL/6J-db/db mice as a model of type 2 diabetes and insulin resistance, and C57BL/6J-db/m mice as a normoglycemic control. Immunohistochemistry was conducted to detect tau hyperphosphorylation using the phospho-tau S396 antibody. Western blotting assessed total alpha-tubulin protein levels, while forebrain transcriptomes from high-fat diet (HFD) and normal chow diet (NCD) groups were analyzed via high-throughput sequencing for differential gene expression. In the db/db mouse model, tau hyperphosphorylation was more pronounced compared to controls. Alpha-tubulin protein levels were significantly reduced ($p < 0.05$). Transcriptomic analysis of HFD-fed mice revealed significant upregulation of kif3c and Tubgcp6 genes compared to the NCD group, suggesting altered microtubule-related gene expression in response to dietary metabolic stress. Our findings suggest that impaired glucose metabolism leads to microtubule instability by causing tau hyperphosphorylation and lowering tubulin protein levels, disrupting microtubule integrity and normal neuronal structure. These results highlight a mechanistic link between diabetes-induced cognitive decline and neurodegenerative conditions like Alzheimer's disease.

The Prevalence and Burden of Avoidant/Restrictive Food Intake Disorder (ARFID) in a Clinical Sample in Kuwait

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Abstract

Avoidant/Restrictive Food Intake Disorder (ARFID) is a newly recognized eating disorder characterized by persistent food avoidance that leads to inadequate nutritional or energy intake. It differs from other eating disorders as it is not associated with body image concerns but rather aversions to sensory properties of food, fear of negative consequences, or lack of interest in eating. Despite increasing global recognition, there is limited data on ARFID prevalence in Arab countries, including Kuwait and studies involving clinical samples are non-existent. This cross-sectional study aims to estimate the prevalence of ARFID in Kuwait and assess its associated comorbidities and demographic correlates. The study will also validate and assess the reliability of the questionnaires used, ensuring their suitability for the Kuwaiti context. Data will be collected from 332 participants aged 14 and above in AL-Ahmadi governmental primary health centers using validated tools. Findings will contribute to understanding ARFID in Kuwait, aiding in awareness and culturally tailored interventions.

A Moderate Amount of Quinoa Consumption Improves Cardiovascular Risk Factors in Kuwaiti Adults with Obesity: A Pilot Study

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Abstract

As obesity and cardiovascular diseases (CVDs) continue to escalate worldwide, there is growing interest in whole grain alternatives for their potential health benefits. Quinoa (*Chenopodium quinoa Willd.*), a pseudo-cereal recognized for its high-quality protein, dietary fiber, and low starch content, has emerged as a promising substitute for refined grains such as wheat, corn, and rice. Clinical risk factors for CVDs include overweight, elevated blood pressure (BP), triglycerides, total cholesterol, and low-density lipoprotein (LDL) cholesterol. Kuwait is among the countries with the highest obesity and hypertension rates globally. Quinoa's resilience and adaptability to extreme climates, including arid and saline conditions, further supports its potential for local cultivation in regions like Kuwait [1]. This study aimed to evaluate the effects of quinoa consumption on cardiovascular health markers in obese Kuwaiti adults. A total of 24 participants with obesity were randomized into a quinoa (Q) group or a control (C) group. The Q group consumed 40 g of cooked quinoa daily for 12 weeks, and dietary guidelines for healthy eating, The C group followed only dietary guidelines similar to the Q group, excluding quinoa. Clinical assessments were conducted at baseline and post-intervention, including BP, lipid profile, and inflammatory markers. Analysis of covariance (ANCOVA), adjusted for body mass index, revealed significant reductions in BP among quinoa consumers: systolic BP decreased by 10.3 mm Hg ($p = 0.023$, $\eta^2_p = 0.234$) and diastolic BP by 7.6 mm Hg ($p = 0.008$, $\eta^2_p = 0.302$). Trends in reduction of total cholesterol (−0.454 mmol/L; $p = 0.390$), LDL cholesterol (−0.445 mmol/L; $p = 0.364$), and C-reactive protein (−1.82 mg/L; $p = 0.255$) were observed. In conclusion, daily quinoa intake for 12 weeks resulted in significant improvements in BP and favorable trends in lipid and inflammatory markers in obese Kuwaiti adults. These findings support the incorporation of quinoa as part of a heart-healthy diet in populations at high risk for obesity-related CVDs. A full fledge study is recommended to confirm these initial results.

Assessment of Nutritional Status of Patients with Inflammatory Bowel Disease

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Abstract

Malnutrition is a common but often underdiagnosed complication in patients with Inflammatory Bowel Disease (IBD), including Crohn's Disease (CD) and Ulcerative Colitis (UC). This study aimed to evaluate the nutritional status of IBD patients and its association with disease characteristics such as disease type, duration and severity, and medication, using multiple nutritional indicators. A cross-sectional study was conducted on 52 IBD patients. Nutritional classification was based on anthropometric measurements, laboratory parameters and dietary intake using a 24-hour recall. The Malnutrition Universal Screening Tool (MUST) was used for assessing the risk of malnutrition. Chi-square tests were used to assess associations between nutritional status and disease type, duration, severity, and medication type. 40.3% of patients were underweight, whereas, 53.8% were classified as overweight/obese. Vitamin D deficiency and low iron levels were highly prevalent (53.8% and 56%, respectively). MUST Score was significantly associated with the disease type ($p = 0.017$), indicating that UC patients were more likely to have moderate nutritional risk. Wrist circumference ($p = 0.023$), arm circumference ($p = 0.015$), and waist-to-height ratio ($p = 0.037$) were significantly associated with disease duration, Similarly, wrist circumference ($p = 0.005$), arm circumference ($p = 0.018$), and waist-to-height ratio ($p < 0.001$) showed significant associations with type of medication, particularly differentiating patients on biological versus non-biological treatment. These findings demonstrate that specific anthropometric indicators such as wrist and arm circumference and waist-to-height ratio are sensitive to disease duration and treatment type. The presence of vitamin D and iron deficiencies across both UC and CD patients underscores the need for routine nutritional screening and supplementation in IBD care.

Food Quality Assurance in Nutrition Science: Detecting Honey Adulteration Using UV-Vis Spectroscopy and Chemometric Methods

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Abstract

Honey is not only a natural sweetener but also a nutrient-rich food containing bioactive compounds such as polyphenols, enzymes, vitamins, and minerals, which provide numerous health benefits including antioxidant, anti-inflammatory, antimicrobial, and prebiotic effects, thereby enhancing overall health and nutritional resilience. Traditional laboratory methods for detecting honey adulteration are often labor-intensive, expensive, and time-consuming. To overcome these challenges, UV-Visible (UV-Vis) spectroscopy combined with chemometric analysis offers a rapid and cost-effective alternative. This approach can identify subtle spectral differences in honey's composition, enabling effective discrimination between authentic and adulterated samples. In this study, 1,100 samples of Kuwaiti Sidr honey including pure and syrup-adulterated specimens were analyzed using UV-Vis spectroscopy alongside advanced statistical methods. The findings demonstrated high accuracy in detecting adulteration and determining the samples' geographical origin, underscoring the potential of these techniques for routine honey authentication. Ultimately, this research aims to protect consumers, promote transparency within the local honey market, and strengthen trust in high-quality natural products. Given the global issue of food adulteration particularly in valuable items like honey deploying rapid, reliable, and non-destructive testing methods is vital for public health. Coupling UV-Vis spectroscopy with chemometrics not only ensures product authenticity and supports nutritional resilience but also boosts consumer confidence. Specifically, orthogonal partial least squares-discriminant analysis (OPLS-DA) achieved 94% accuracy in distinguishing genuine honey from adulterated samples, while OPLS regression effectively quantified adulteration levels ($R^2 = 0.96$). Overall, UV-Vis spectroscopy proves to be a dependable, cost-effective tool for verifying honey's origin and purity.

Cold tolerance of Woodland Strawberry (*Fragaria vesca*) is Linked to Cold Box Factor 4 and the Dehydrin Xero2

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Abstract

Domesticated strawberry is susceptible to sudden frost episodes, limiting the productivity of this cash crop in regions where they are grown during early spring. In contrast, the ancestral woodland strawberry (*Fragaria vesca*) has successfully colonized many habitats of the Northern Hemisphere. This suggests that *F. vesca* harbors genetic determinants that confer cold tolerance. From a germplasm collection of 70 wild *F. vesca* accessions, we identified a pair with contrasting cold tolerance based on phenotypic survival under controlled frost exposure. To investigate the basis of this natural variation, we compared the physiological, biochemical, and metabolic responses of the tolerant and sensitive genotypes under controlled cold stress. We identified the transcription factor Cold Box Factor 4 and the dehydrin *Xero2* as molecular markers associated with superior tolerance to cold stress. Overexpression of *Xero2* fused to green fluorescent protein (GFP) in tobacco BY-2 cells conferred cold tolerance to these recipient cells. A detailed analysis of the metabolome for the two contrasting genotypes allows the definition of metabolic signatures correlated with cold tolerance versus cold stress. This study demonstrates the value of wild *F. vesca* accessions for uncovering genetic elements involved in abiotic stress tolerance, offering concrete molecular targets, such as *Xero2* and Cold Box Factor 4, for future breeding or genetic engineering strategies aimed at improving cold resilience in commercial strawberries and other frost-sensitive crops.

Visualizing Sha-1: Enhancing the Educational Understanding of Cryptographic Algorithms

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Abstract

This paper presents EduSHA, a web-based interactive learning tool designed to enhance comprehension of the SHA-1 hashing algorithm, with a primary focus on advanced undergraduate computer science students studying cryptographic functions. EduSHA addresses limitations observed in conventional cryptography education, where complex algorithms are often taught through text-heavy lectures or static diagrams that fail to support deeper conceptual understanding. EduSHA is built upon the Hypermedia Algorithm Visualization (HalVis) architecture and integrates SVG-based diagrams with step-by-step animations to demonstrate key components of SHA-1, including message padding, preprocessing, and compression. The platform incorporates interactive exercises, problem-based learning tasks, and user-driven input to create a highly engaging and accessible learning experience. A mixed-method evaluation was conducted with advanced undergraduate students (n=small sample) to assess EduSHA's effectiveness. Quantitative results indicated that participants using EduSHA achieved higher post-test scores compared to pre-tests, suggesting improved understanding of SHA-1 concepts. However, the statistical reliability of the findings was limited by a small participant pool, uneven distribution, and varying learning environments. Qualitative feedback, on the other hand, strongly supported EduSHA's effectiveness, with students consistently reporting that the tool was educational, engaging, and highly accessible EduSHA meets its design objectives of fostering active learning, improving accessibility, and increasing engagement in cryptographic education. While further large-scale studies are needed to strengthen the quantitative evidence, the qualitative findings suggest that EduSHA has significant potential as a supplementary laboratory resource in computer science curricula. By combining interactivity, visualization, and problem-based learning, EduSHA addresses known shortcomings in cryptographic education and provides a robust foundation for future interactive tools targeting other complex security algorithms.

Genetically Modified Foods in Kuwait: Public Perception, Awareness, and Attitudes

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Abstract

Genetic modification -also referred to as genetic engineering or transgenic technology- involves altering an organism's genetic machinery to introduce new traits. Advances in biotechnology now allow for the genetic editing of organisms, leading to the commercial production of transgenic crops with desirable traits such as herbicide and insect resistance. In Kuwait, GMOs, also referred to as bioengineered foods, are present in certain supermarket products. However, labelling is limited, and regulatory measures are still underdeveloped. A 2024 study in Kuwait analysed food products containing GMOs using PCR testing. The findings revealed the presence of GMO sequences in 8 of 31 product studied. Public awareness of GMOs in Kuwait is generally low, and to our knowledge, there are no known public surveys or peer-reviewed studies specifically measuring public awareness towards GMOs in the country. Therefore, the purpose of this study is to investigate consumer awareness and perceptions of genetically modified (GM) food in Kuwait. Using the Microsoft Forms questionnaire, we assessed participants' understanding of GM foods, their ability to distinguish GM foods from processed and organic products, and their trust in GM foods. The questionnaire remains open to collect additional data. The current sample included 1047 participants of various ages, genders, and educational backgrounds (80% females and 20% males). Preliminary findings reveal varying levels of awareness and several misconceptions about the characteristics and safety of GM foods. 64.76% of participants reported having heard of GM foods, this included 52.44% of females and only 12.32% of males. Most participants who heard of GM products confirmed reading food labels, suggesting a basic awareness of food product contents. However, label-reading does not necessarily imply comprehension. Although 79% of the same respondents reported knowing the difference between GM and organic foods, only 40.9% claimed to understand the distinction between GM and processed foods. At the end of survey, participants who heard of GM products were asked: If given two options, one genetically modified and one non-GM, which would you choose? The results showed that 85.4% preferred non-GM foods, 11.2% had no preference, and only 3.4% chose GM foods. In conclusion, while most participants in Kuwait are aware of GMOs, their understanding remains limited and often shaped by misconceptions. The strong preference for non-GM options reflects widespread caution and uncertainty, highlighting the need for improved public education, clearer food labelling, and more transparent regulatory practices to help consumers make informed choices.

Impact of Milk-Derived Metal Ions on Structural and Functional Stability of β-Galactosidase Bound to Native and Polyaniline–Chitosan–Silver Nanocomposites: A Multi-spectroscopic Study

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Abstract

Sustainable food processing demands innovative strategies to enhance enzyme activity, stability, and reusability in complex biological environments. β-galactosidase is vital to dairy industries, as it is utilized in dairy industries for lactose hydrolysis in dairy products, thus contributing to lactose-free formulations and value-added processing with minimal wastage. The present study demonstrates the effect of metal ions predominantly found in milk, such as Zn^{2+}, K^{+}, Ca^{2+}, and Mn^{2+}, on the structural and functional integrity of native polyaniline chitosan nanocomposite (PANI-CS NC) and polyaniline chitosan silver (PANI-CS-Ag NC)-bound *Aspergillus oryzae* β-galactosidase. Using a multi-spectroscopic approach, including UV-vis, fluorescence, 3D fluorescence, FTIR and circular dichroism (CD), conformational changes and activity measurements were recorded and compared for native enzyme, PANI-CS-bound enzyme, and PANI-CS-Ag-bound enzyme. Our findings revealed a multifold enhancement in the catalytic performance of the bound enzyme in the presence of the cocktail of all the ions. These findings were supported by 3D fluorescence, CD and FTIR studies that established significant conformational changes in the secondary structure, thereby providing a protective microenvironment that mitigated activity loss and preserved enzyme structure more effectively in the case of the PANI-CS-Ag matrix. This improved resilience in the presence of metal ions suggests potential for repeated enzyme use in dairy processing, aligning with the principles of green chemistry and resource optimization. This study underscores the importance of a robust immobilization system with enhanced catalytic efficiency and stability contributing to the development of enzyme-based technologies in the dairy industry, supporting cleaner production and enhanced nutritional value in line with global sustainability goals.

Dissecting the Molecular Mechanism Underlining the Interactions With the Autoimmune Regulator Protein

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Abstract

Autoimmune Polyendocrine Syndrome Type 1(APS-1) is a progressive autosomal autoimmunedisease triggered by loss-of-function mutations in the autoimmune regulator (AIRE) gene. AIRE protein is primarily expressed in the medullary thymic epithelial cells and peripheral dendritic cells. It is a transcription factor that regulates over a thousand genes and is critical to the function of the thymus, particularly the negative selection of T-cells. AIRE acts in a protein complex by interacting with numerous proteins such as the transcriptional coactivators: cyclic AMP response element-binding protein and DNA-dependent protein kinase. To further understand how AIRE is operating, it is crucial to determine the full set of AIRE binding partners. The aim of this study is to detect novel protein-protein interactions using yeast-two-hybrid(Y2H) system. Since most APS-1 mutations are found in the PHD1 domain, this region was chosen for screening. AIRE-PHD1 domain was cloned into the bait pGBKT7 plasmid then transformed into Y2H Gold yeast cells. The domain was screened by mating the respective transformed yeast with the Universal Normalized Human Mate & Plate™ Library and grown on selective medium. Surviving colonies were isolated, prey plasmid was extracted and sequenced. The PHD1 domain exhibited no autoactivation in the Y2H system and was subsequently screened for novel interactions. Three proteins were identified including the proliferating nuclear antigen (PCNA) which was previously reported to interact with AIRE-PHD1. Hence, validated our screening system. Among the set of proteins identified is Syntaxin 8(STX8), a family member of SNARE which is expressed in lytic granules and is co-localized with the T cell receptor upon formation of immunological synapse. In conclusion, by understanding how AIRE operates, we will be able to further appreciate the relationship between AIRE gene malfunction and the breakdown of self tolerance, which promises to help unravel the pathogenesis not only of APS-1 but also of other types of autoimmune disease.

Health Risk Assessment of Heavy Metals in Coffee: Quantifying Exposure for Coffee Consumers in Qatar

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Abstract

The presence of heavy metals in coffee products has raised significant concerns regarding food safety and human health. This study assessed the concentration variation of key heavy metals, which include arsenic (As), cadmium (Cd), copper (Cu), cobalt (Co), chromium (Cr), lead (Pb), nickel (Ni), manganese (Mn), and zinc (Zn), in dry coffee samples from Ethiopia, Papa New Guinea, South America, and Yemen, further categorised by their degree of roasting (light, medium, and dark). Results showed that manganese (Mn) was the predominant heavy metal across all samples, with the highest concentration observed in dark roasted coffee from South America at 30.312 µg/kg, followed by Papa New Guinea at 23.714 µg/kg and Ethiopia at 14.170 µg/kg. Copper (Cu) concentrations were also significant in all roasting degrees, with levels reaching 11.817 µg/kg in light roasted coffee from South America and zinc (Zn) levels averaging 4.252 µg/kg in Ethiopia. Cadmium (Cd) was detected at concentrations of 0.177 µg/kg in light roasted coffee from Ethiopia, which raises concerns given its toxicity. Lead (Pb) levels were found to reach 3.829 µg/kg in Ethiopian dark roasts, highlighting the ongoing risks associated with lead exposure. The results underscore the need for continuous monitoring of heavy metal concentrations in coffee and the implementation of strategies to minimize contamination, ensuring safety for consumers. This study provides crucial insights for consumers, food industries, and regulatory agencies targeting coffee origins with lower heavy metal content to enhance food safety and mitigate potential health effects.

Compartmentalization of Rosmarinic Acid Improves Tolerance in White Desiree Potato exposed to Oxidative Stress

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Abstract

Global food security programs prioritize crops based on their contribution to caloric intake, nutritional value, and agroecological adaptability. Crops like potatoes (*Solanum tuberosum* L.) occupy a second-tier position but play a critical strategic role in food system programs. This study investigates the role of rosmarinic acid in enhancing potato seedling growth under varying salinity conditions, with a focus on the subcellular responses of mitochondria and peroxisomes. These organelles serve as key indicators of oxidative stress and energy metabolism, making them critical physiological traits for identifying the mechanisms underlying sodium tolerance (Na^+).

Cultures of white Desiree potato were micropropagated in MS media adjusted to pH 5.8 and were grown under zero stress (control), supplemented with rosmarinic acid (0, 20, 40, 60 mg/l) and NaCl (0, 90, 120, 180, and 250 mM) in a controlled culture room at 22-25°C. Data indicated that White Desiree Potato is well-suited for climate-resilient agriculture due to its short growing cycle and adaptability to high salt in the media. Low and moderate stresses exhibited stimulatory effects, while extreme oxidative stresses (180 and 250 mM NaCl) caused severe inhibitory damage to cell expansion. Supplementation of RA caused an increase in the frequencies of mitochondria and peroxisomes. Interestingly, TEM micrograph data showed deposition of RA in the cytoplasm of Na-stressed cells. Tissue RA contents increased significantly with increasing Na-stress levels, and this is likely to eradicate reactive oxygen species (ROS) such as superoxide radicals ($O2\cdot-$), hydroxyl radicals ($OH\cdot$), and hydrogen peroxide (H_2O_2) generated under stress.

Nutrition Impact Symptoms as Key Indicators of Malnutrition in Kuwaiti Colorectal Cancer Patients: A Cross-Sectional Study Using the PG-SGA and PG-SGA SF

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Abstract

Background/Objectives: Malnutrition is a common but frequently overlooked complication in colorectal cancer (CRC), with global prevalence estimates ranging from 20% to over 70% depending on disease stage and assessment method (Arends et al., 2017). It is associated with poor treatment tolerance, longer hospital stays, and reduced survival (Reber et al., 2021; Opanga et al., 2017). Nutrition Impact Symptoms (NIS) such as dry mouth, taste changes and early satiety are known to impair intake and contribute to nutritional decline (Shakhshir et al., 2024). Despite international guidelines recommending early screening (Arends et al., 2017), data on malnutrition and NIS in colorectal cancer patients remain limited in the Middle East and have not yet been studied in Kuwait.

Methods: This cross-sectional study included 65 CRC outpatients at Kuwait Cancer Control Center. Nutritional status was assessed using the full Patient-Generated Subjective Global Assessment (PG-SGA) and its Short Form (PG-SGA SF). NIS were evaluated by the symptom components of the PG-SGA/PG-SGA SF. Logistic regression was used to identify NIS associated with malnutrition.

Results: Malnutrition was identified in 60% of the patients. Significant NIS included anorexia, dry mouth, and nausea ($p < 0.004$), with dry mouth as an independent predictor (OR = 17.65, 95% CI: 2.02–154.19). Notably, only 23.5% of patients identified with moderate malnutrition had been referred for nutrition intervention, indicating a substantial gap in clinical practice.

Conclusion: Malnutrition is highly prevalent among CRC patients in Kuwait and is strongly linked to key nutrition impact symptoms, particularly anorexia, dry mouth, and nausea. These findings highlight the urgent need for routine screening with validated tools like the PG-SGA SF, followed by comprehensive nutritional assessment and timely, individualized interventions to enhance treatment tolerance, improve clinical outcomes, and support overall quality of life.

Impact of Hydrolyzed Wheat Protein Fractions on Antioxidant, alpha-Amylase, and Angiotensin-Converting Enzyme Inhibition

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Abstract

This study aimed to comparatively assess the composition and functional properties of white wheat flour (WF) and WF protein fractions, and the effect of hydrolysis with digestive proteases on their biological activities *in vitro*, namely antioxidant properties and inhibitory potential toward Angiotensin-I converting enzyme (ACE) and α-amylase. WF protein fractions were sequentially extracted and then characterized along with WF using established methods. The most abundant protein fractions were albumins, glutelin-1, glutelin-2, and prolamins. All were rich in cysteine, glutamic acid, and leucine, except prolamins which contained the highest concentrations of glutamic acid, histidine, lysine, serine, and aspartic acid. WF displayed superior water holding capacity, followed by prolamins. Albumins conferred superior foam stability, while albumins, glutelin-1, and WF conferred moderate emulsion stability. Biological activities varied greatly among fractions and were generally influenced by proteolysis. High antioxidant activities were found with prolamins and glutenin-1 before and after pepsinlysis. High ACE inhibitory activities were found with globulins (before and after trypsinolysis and chymotrypsinolysis, and after pepsinolysis), prolamins (after trypsinolysis and chymotrypsinolysis), and WF (before pepsinolysis). High inhibition of α-amylase was found with globulins, prolamins, and WF (before and after trypsinolysis and chymotrypsinolysis) and albumins (after pepsinolysis). Results indicate that WF and select WF protein fractions could be exploited as biofunctional ingredients in applications that require specific functionalities to improve quality, nutrition as well as physiological benefits.