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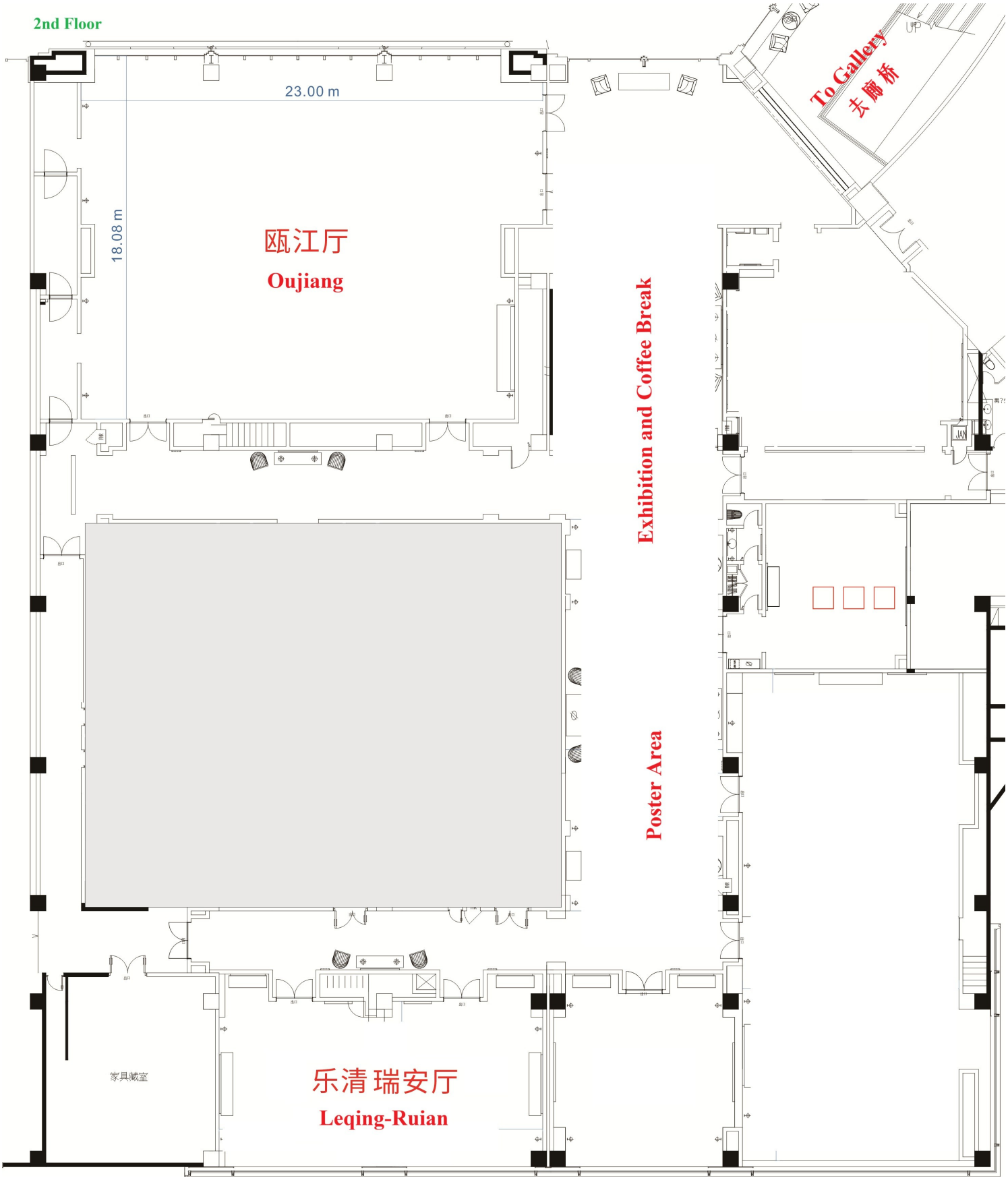

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Plenary lecture

PL1: Bioactive Polysaccharides and Health Regulation

Shaoping Nie
State Key Laboratory of Food Science and Resources, China-Canada Joint Lab of Food Science and Technology (Nanchang), Nanchang University, Nanchang 330047, China

Bioactive polysaccharides, complex carbohydrates widely sourced from plants, fungi, algae, and bacteria, have garnered significant attention in recent years for their remarkable physiological functions and health-regulating properties. As natural macromolecules, these compounds exhibit structural diversity, which directly influences their biological activities. This abstract summarizes current research regarding the extraction, structural characterization, and health-promoting mechanisms of bioactive polysaccharides, highlighting their profound impact on human well-being. A primary area of focus is their immunomodulatory capacity. Bioactive polysaccharides, such as those derived from *Ganoderma lucidum* (reishi mushrooms), ginseng, and various marine algae, have been shown to stimulate the immune system by activating macrophages, T lymphocytes, and natural killer cells, thereby enhancing the production of cytokines. Furthermore, these macromolecules play a crucial role in metabolic regulation. Extensive studies demonstrate their efficacy in ameliorating metabolic disorders, notably type 2 diabetes and obesity, through mechanisms that improve insulin sensitivity, regulate lipid metabolism, and modulate hepatic glucose output. In addition to immunomodulation and metabolic regulation, bioactive polysaccharides exhibit potent antioxidant and anti-inflammatory activities. By scavenging free radicals and reducing oxidative stress, they protect cells from damage associated with chronic degenerative diseases. Emerging research also underscores their prebiotic potential. Being largely resistant to human digestive enzymes, polysaccharides reach the colon intact, where they are selectively fermented by gut microbiota. This fermentation process promotes the proliferation of beneficial bacteria, such as Bifidobacterium and *Lactobacillus*, leading to the production of short-chain fatty acids that reinforce intestinal barrier integrity and suppress systemic inflammation. In conclusion, bioactive polysaccharides represent a promising class of functional food components and pharmaceutical agents with multifaceted health-regulating benefits. Continued interdisciplinary research into their structure-function relationships, bioavailability, and clinical applications will pave the way for the development of novel therapeutics and functional foods aimed at disease prevention and health promotion.

PL2: The Key Role of Bioactive Compounds to Overcome Cancer-stem Cells-driven Chemoresistance and Adipocyte–Tumor Crosstalk

Maurizio Battino[1,2,3]
[1]Dept Clinical Sciences, Università Politecnica delle Marche, Ancona, Italy
[2]Universidad Europea del Atlantico Facultad de Ciencias de la Salud, Santander, Spain
[3]Jiangsu University School of Food and Biological Engineering, Zhenjiang, China

Chemoresistance is a multifactorial phenomenon driven by mechanisms including epigenetic and genomic alterations, oncogenic signaling, drug efflux, the presence of a rare subpopulation of cancer stem cells (CSCs), and tumor microenvironment–related processes. CSCs and tumor microenvironment dynamics play a key role in tumor persistence and therapeutic failure. To address these mechanisms, the potential of bioactive compounds derived from two distinct sources to target CSCs and modulate microenvironment-driven resistance was evaluated using complementary models. In colorectal cancer, Manuka honey, alone or combined with 5-fluorouracil, was evaluated in colonspheres enriched in CSC-like cells. Treatment modulated spheroid morphology, increased ROS, enhanced apoptosis, and improved chemosensitivity. These effects involved pathways related to stemness, survival, drug resistance, angiogenesis, and self-renewal, including reduced expression of drug efflux transporters and CSC-related signaling. In breast cancer, particularly in obesity, adipocyte–tumor crosstalk plays a key role in shaping the tumor microenvironment. This was investigated in breast cancer cells, using conditioned media from preadipocytes, mature adipocytes, and adipocytes treated with licorice root extract. Licorice induced remodeling of the adipocyte secretome, reducing pro-tumorigenic adipokines and altering redox-related factors. While mature adipocyte signals promoted tumor-supportive effects, including reduced oxidative stress and enhanced survival, licorice-treated conditioned media increased ROS and modulated pathways involved in tumor progression, including estrogen signaling (aromatase) and the renin–angiotensin system (RAS). This may sensitize cells to ROS-dependent chemotherapeutics. Preliminary data in CSC-enriched breast cancer mammospheres show that adipocyte-conditioned media enhance spheroid growth, compactness, and tumorigenic features, reduce doxorubicin accumulation (fluorescence-based), and attenuate ROS production, indicating a protective microenvironment. In contrast, conditioned media from licorice-treated adipocytes increased drug accumulation, oxidative stress, and apoptosis, partially reversing chemoresistance. Overall, these findings highlight the potential of bioactive compounds to target CSCs and modulate tumor microenvironment–driven resistance, providing insights into strategies to overcome chemoresistance.

PL3: The Slim Blueprint: Rewiring Obesity with Natural Compounds?

Milen I. Georgiev[1,2]
[1]Department of Plant Cell Biotechnology, Center of Plant Systems Biology and Biotechnology, 4000 Plovdiv, Bulgaria
[2]Laboratory of Metabolomics, Institute of Microbiology, Bulgarian Academy of Sciences, 139 Ruski Blvd., 4000 Plovdiv, Bulgaria

The prevalence of metabolic disorders, including obesity, is increasing worldwide. If current trends continue, an estimated 3.8 billion adults (more than half of the projected global adult population) will be living with overweight or obesity by 2050 [1]. Despite recent advances in obesity treatment, particularly the development of incretin-mimetic therapies, further research is needed to establish their long-term efficacy and safety [1,2]. Accordingly, identifying interventions that effectively prevent or treat obesity and reduce the risk of obesity-related complications has become a major objective of contemporary biomedical research.

Obesity is a multifactorial chronic disease defined by excessive adipose tissue accumulation and impaired regulation of energy balance, resulting in metabolic dysfunction and an increased risk of obesity-related disorders. Its development is driven by interconnected genetic, behavioural, and environmental factors that influence appetite regulation, nutrient sensing, inflammation, and insulin sensitivity [1]. Modulation of these pathways has been shown to affect body weight and metabolic health in both experimental models and clinical studies, highlighting their potential as targets for the prevention and treatment of obesity [2]. Natural products represent a rich source of bioactive molecules capable of modulating conserved metabolic pathways involved in energy homeostasis and obesity. Increasing evidence indicates that plant-derived compounds can influence lipid metabolism, nutrient sensing, mitochondrial function, and metabolic flexibility thereby improving metabolic health and reducing obesity-associated dysfunction. These features make natural products promising candidates for the prevention and treatment of obesity and related metabolic disorders [2-4]. Utilizing the model organism *Caenorhabditis elegans*, including modelling obesity through glucose-induced lipid accumulation, together with molecular pharmacology approaches, our research aims to identify and characterize natural products that improve metabolic health. By elucidating the molecular mechanisms through which natural compounds modulate conserved pathways involved in metabolic turnover, metabolic plasticity, nutrient sensing, and energy metabolism, we seek to provide mechanistic insights into the regulation of metabolic homeostasis and identify novel natural leads for the prevention and treatment of obesity and related metabolic disorders.

Acknowledgements
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PL4: Betaine for Healthy Aging: Mitochondrial Resilience and Redox Balance as Targets for Next-Generation Nutraceuticals

Cristina Sánchez-González[1], Tamara Y. Forbes-Hernández[2], Lorenzo Rivas-García[1], Andrea Sánchez-Pino[1], Suzette L Pereira[3], José M López-Pedrosa[4], Ricardo Rueda[4], José L. Quiles[1]*
[1]Department of Physiology, Institute of Nutrition and Food Technology "José Mataix Verdú", Biomedical Research Centre, Universidad de Granada, 18016 Armilla, Spain
[2]Department of Biomedical Sciences. University of Cagliari, 09042 Cagliari, Italy
[3]Abbott Nutrition R&D, Abbott Laboratories, Columbus, OH, United States
[4]Abbott Nutrition R&D, Abbott Laboratories, Granada, Spain

Population aging is reshaping food technology, creating a growing demand for dietary ingredients that help preserve functional capacity and cellular resilience in later life. Betaine, a naturally occurring methylated derivative of glycine found in several foods, is gaining attention as a promising ingredient for nutraceutical and dietary strategies aimed at healthy aging. In this study, we evaluated the effects of betaine in aged *Caenorhabditis elegans* using an integrated phenotypic and mechanistic approach. Betaine showed a favorable safety profile at the tested concentrations, with no relevant acute lethality and only mild effects on growth or fertility at higher doses. In aged worms, betaine markedly improved swimming performance, indicating preservation of neuromuscular function. This functional benefit was accompanied by lower age-associated proteotoxicity, lipofuscin accumulation, and intracellular ROS levels. At the mechanistic level, betaine attenuated the overactivation of stress-response markers, including HSP-16.2, SKN-1/NRF2, SOD-3, PINK-1, and DAF-16/FOXO-related readouts, suggesting a shift from chronic stress signaling toward improved cellular homeostasis. Importantly, betaine preserved several mitochondrial parameters altered with aging, including mitochondrial number, area, and size, supporting a role in the maintenance of mitochondrial quality and bioenergetic competence. Overall, these findings identify betaine as a potential functional ingredient for the development of nutraceuticals and dietary products for older adults, with a mechanism of action closely linked to mitochondrial health, redox biology, and the preservation of organismal performance during aging.

PL5: From Citrus Peel to Bioactive Powerhouse: The Therapeutic Journey of Auraptene in Medicine and Food

Francesco Epifano
Department of Pharmacy, University "Gabriele d'Annunzio" of Chieti-Pescara, Via dei Vestini 31, 66100 Chieti Scalo (CH), Italy

Auraptene (7-geranyloxycoumarin) (Figure 1), a naturally occurring oxyprenylated coumarin abundantly present in citrus peels and other edible plants of the Rutaceae and Apiaceae families, has emerged as a highly promising multifunctional phytochemical with broad applications in medicine and food science.

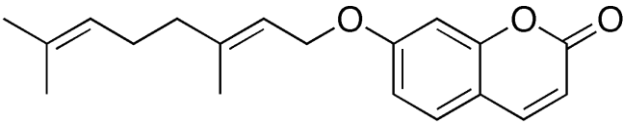

Figure 1. Structure of auraptene

Recent investigations, particularly those conducted over the last five years, have substantially expanded the understanding of auraptene's pharmacological profile, highlighting its remarkable pleiotropic activity and therapeutic versatility. Particular emphasis will be placed on the mechanisms underlying auraptene's antioxidant, anti-inflammatory, anticancer, neuroprotective, cardioprotective, metabolic regulatory, antimicrobial, antiviral, and immunomodulatory activities. Experimental evidence demonstrates that auraptene modulates several molecular pathways associated with oxidative stress, inflammation, apoptosis, and cellular proliferation, including NF-κB, PI3Kγ, AMPK/mTOR, PPARα, and ROS-mediated signaling cascades. In oncology research, auraptene has shown chemopreventive and antiproliferative effects against colorectal, prostate, glioblastoma, melanoma, hepatocellular, ovarian, breast, and gastric cancers, often enhancing apoptosis, inhibiting metastasis, and improving the efficacy of radiotherapy or chemotherapy. In neurological models, auraptene exhibited antidepressant and neuroprotective properties by reducing nitric oxide production, suppressing neuroinflammation, and improving oxidative balance, while preliminary clinical studies using auraptene-containing citrus phytocomplexes suggested beneficial effects on subjective cognitive decline. Beyond pharmaceutical applications, auraptene is gaining increasing relevance in functional foods and nutraceutical formulations due to its natural origin, safety profile, and potential contribution to sustainable citrus waste valorization. Recent advances in nanotechnology-based delivery systems, including liposomes, niosomes, and nanoparticle formulations, further support the translational potential of auraptene by improving its bioavailability, stability, and tissue targeting. Collectively, the evidence positions auraptene as a bioactive powerhouse at the interface of nutrition and medicine, offering promising opportunities for the development of innovative therapeutic agents and health-promoting food products. Nevertheless, further mechanistic studies, toxicological evaluations, and large-scale clinical trials remain essential to fully establish its efficacy and facilitate clinical and industrial applications.

PL6: Biomimetic M1 Macrophage Hybrid Nanoparticles Enable Curcumin-Mediated Breast Cancer Immunotherapy

Chanmey Kong, Jinhee Park, Donghyeon Kim, Haneul Kang, Yun Suk Huh*
Department of Biological Sciences and Bioengineering, Inha University, 100 Inha-ro, Michuhol-gu, Incheon 22212, Republic of Korea

In this work, curcumin-loaded biomimetic hybrid nanoparticles (Cur@Lip-M1NPs) were developed by integrating M1 macrophage-derived nanovesicles with synthetic liposomes for breast cancer immunotherapy. This strategy improved curcumin loading and tumor-targeted delivery while preserving M1 macrophage immunophenotypes. Cur@Lip-M1NPs increased pro-inflammatory and antigen-presenting markers, including TNF-α, IL-6, IL-1β, iNOS, and CD86, indicating sustained M1 polarization and immune activation. In 4T1 and MDA-MB-231 breast cancer models, treatment induced mitochondria-mediated apoptosis through Bax upregulation, BCL-2 downregulation, and caspase-3 activation. Interestingly, Cur@Lip-M1NPs remodeled the immunosuppressive tumor microenvironment by promoting cytotoxic T-cell infiltration and suppressing M2 polarization of tumor-associated macrophages. These effects resulted in tumor growth inhibition with minimal systemic toxicity. It would appear that Cur@Lip-M1NPs could be developed as a next-generation biomimetic platform for precision breast cancer immunotherapy.

PL7: Curcumin Suppresses Growth and Progression of Human Colon Cancer Cells: SIRT1 as a Potential Target

Young-Joon Surh
College of Pharmacy, Seoul National University, Seoul 08826, South Korea

Curcumin (diferuloymethane), a major component of the spice turmeric derived from the plant *Curcuma longa* L. (Zingiberaceae), has been reported to exert chemopreventive and anti-carcinogenic effects on colon carcinogenesis. Our previous studies revealed that oral administration of curcumin significantly attenuated the severity of experimentally induced colitis in mice. In contrast to curcumin, its non-electrophilic analogue, tetrahydrocurcumin has much weaker inhibitory effects. SIRT1, an NAD+-dependent histone/protein deacetylase, is overexpressed in colorectal cancer, and exerts oncogenic effects on the development and progression of colon cancer. In the present study, we found that curcumin reduced the expression of SIRT1 protein without influencing its mRNA expression in human colon cancer cells, suggesting posttranslational regulation of SIRT1 by this phytochemical. Notably, ubiquitination and subsequent proteasomal degradation of SIRT1 were induced by curcumin treatment. Results of nano-LC-ESI-MS/MS revealed the direct binding of curcumin to cysteine 67 of SIRT1. In line with this result, the protein stability and clonogenicity of a mutant SIRT1 in which cysteine 67 was substituted by alanine were unaffected by curcumin. Taken together, these observations suggest that curcumin facilitates the proteasomal degradation of oncogenic SIRT1 through covalent modification of SIRT1 at the cysteine 67 residue.

PL8: Ginsenoside Metabolites with Anti-cancer, Anti-inflammatory and Gastroprotective Effects

Jae Youl Cho
Department of Integrative Biotechnology, Sungkyunkwan University, Suwon 16419, Republic of Korea

Ginseng (Panax ginseng), long revered as a "root of life" in traditional medicine, derives its potent therapeutic efficacy from bioactive saponins, specifically the metabolites protopanaxatriol (PPT) and protopanaxadiol (PPD), which act as master regulators of cellular signaling to offer broad applications across oncology, immunology, and dermatology. PPT combats colon cancer by directly inhibiting the AKT pathway to suppress proliferation and migration, while PPD exerts strong anti-melanoma effects by binding to the MLK3 kinase to trigger the MLK3-JNK apoptotic cascade[1,2]. Beyond oncology, PPT serves as a robust anti-inflammatory agent by suppressing oxidative stress and proinflammatory cytokines such as IL-6 and TNF-α through the inhibition of major cascades like NF-κB and JAK-STAT3[3]. Furthermore, PPT bolsters epithelial health by upregulating mucin expression and acts as an advanced cosmetic ingredient by targeting EGFR and HER2 to increase moisturizing factors like HAS-2, thereby strengthening the skin barrier[4,5]. Collectively, the synergy between ginseng's traditional heritage and modern molecular science reveals PPT and PPD as versatile, precision-targeting therapeutic candidates capable of addressing complex health challenges ranging from malignant tumors to chronic inflammation and tissue degeneration.

Acknowledgments
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PL9: Plant-Based Diets for Prevention of Cognitive Decline

Giuseppe Grosso
University of Catania, Italy

Cognitive decline and dementia represent major global public health challenges, particularly in aging populations. Emerging evidence suggests that nutrition plays a central role in brain health through its influence on inflammation, oxidative stress, metabolic dysfunction, gut microbiota composition, and neurodegenerative processes. Epidemiological studies consistently indicate that adherence to healthy dietary patterns, especially the Mediterranean diet, is associated with reduced risk of cognitive decline, dementia, and Alzheimer's disease. Experimental and intervention studies further support the potential cognitive benefits of compounds such as anthocyanins, curcumin, flavan-3-ols, and resveratrol. Plant-derived foods rich in vitamins, fiber, and phytochemicals such as (poly)phenols appear to exert neuroprotective effects through antioxidant and anti-inflammatory mechanisms. Specific (poly)phenols have been demonstrated to modulate neuronal signaling, synaptic plasticity, neuroinflammation, and oxidative damage. The presentation also highlights the emerging role of the gut–brain axis, emphasizing how fiber-rich and (poly)phenol-rich foods may influence cognitive health through microbiota-derived metabolites and immune modulation. Although current findings are promising, further long-term studies are needed to clarify causal mechanisms and optimize nutritional strategies for cognitive preservation. Given the increasing burden of cognitive impairment and the absence of effective curative therapies, nutrition-based preventive approaches may represent a sustainable strategy to promote healthy brain aging.

PL10: Improvement of Cognitive Function in Adults with Mild Cognitive Impairment Through *Kluyveromyces fragilis* and *Saccharomyces cerevisiae* Yeast Extracts, as Dietary Sources of Nucleotides: Single-Center, Randomized, Placebo-Controlled, Parallel-Arm, Double-Blind Clinical Trial

Hammad Ullah[1], Marcello Cordara[2], Maria Vittoria Morone[3], Roberto Piccinocchi[4], Lorenza Francesca De Lellis[3], Angela Cerqua[3], Alessandra Baldi[3], Gaetano Piccinocchi[6], Alessandro Di Minno[3,7], Gaia Spadarella[8], Maria Daglia[3,9]*

[1]School of Pharmacy, University of Management and Technology, 54000 Lahore, Pakistan

[2]School of Medicine, University of Milano-Bicocca, 20126 Milan, Italy

[3]Department of Pharmacy, University of Napoli Federico II, 80131 Naples, Italy

[4]Anaesthesia and Resuscitation A. U. O. Luigi Vanvitelli, 80138 Naples, Italy

[5]Applied Statistic Unit, Department of Earth and Environmental Sciences, University of Pavia, 27100 Pavia, Italy

[6]Comegen S.C.S., Società Cooperativa Sociale, 80125 Naples, Italy

[7]CEINGE-Biotecnologie Avanzate, 80145 Naples, Italy

[8]International Research Center for Food Nutrition and Safety, Jiangsu University, Zhenjiang 212013, China

Mild cognitive impairment (MCI) is a clinical condition characterized by measurable cognitive decline that exceeds normal age-related changes while largely preserving independence in daily activities. MCI is frequently regarded as an intermediate stage between healthy aging and dementia, and is associated with an increased risk of progression to neurodegenerative disorders. Given the absence of definitive pharmacological treatments, there is growing interest in safe nutritional approaches that may help maintain or improve cognitive function in affected individuals. Dietary nucleotides may support membrane phospholipid synthesis, synaptic activity, and neuroprotective processes; however, clinical evidence in older adults with MCI remains limited. This randomized, placebo-controlled trial evaluated the efficacy and tolerability of nucleotide-rich yeast extracts derived from *Kluyveromyces fragilis* and *Saccharomyces cerevisiae*. Methods: Seventy-two participants (mean age 73.5 ± 7.7 years; range 60–85) were randomly assigned in a 1:1:1 ratio to receive *K. fragilis* extract, *S. cerevisiae* extract, or placebo once daily for 180 days. Cognitive outcomes were assessed using the Montreal Cognitive Assessment (MoCA) and Mini-Mental State Examination (MMSE) at baseline (T0), 90 days (T1), and 180 days (T2). Quality of life was evaluated using the SF-12 questionnaire at T0 and T2. Treatment effects were analyzed using linear mixed-effects models adjusted for age and sex. Results: After 180 days, MoCA scores increased by 4.42 points in the *K. fragilis* group and 3.92 points in the *S. cerevisiae* group, compared with 0.58 points in the placebo group. MMSE scores improved by 1.62 and 3.11 points in the *K. fragilis* and *S. cerevisiae* groups, respectively, compared with 0.25 points in the placebo group. The SF-12 mental component score increased by 7.50 and 9.16 points in the two active treatment groups, while physical quality-of-life scores did not change significantly. No adverse events were reported. Conclusions: Nucleotide-rich extracts from *K. fragilis* and *S. cerevisiae* were well tolerated and associated with improved cognitive performance in older adults with MCI. Larger multicenter trials are needed to confirm these findings and clarify the long-term clinical relevance of nucleotide supplementation in cognitive aging.

PL11: Food-Derived Modulators of Dopaminergic Signaling in Cancer Prevention

Hye-Kyung Na
Department of Food Science and Biotechnology, College of Engineering, Sungshin Women's University, Seoul 01133, Republic of Korea

Dopamine has traditionally been recognized as a neurotransmitter that regulates movement, cognition, reward, and emotion. Beyond its well-established role in the central nervous system, accumulating evidence indicates that dopamine receptors are also expressed in a wide range of human cancers, where they regulate tumor cell proliferation, survival, angiogenesis, metastasis, and antitumor immunity. Consistent with these observations, several dopamine receptor agonists and antagonists originally developed for neurological and psychiatric disorders have demonstrated promising anticancer activities in preclinical and clinical studies, highlighting dopaminergic signaling as a promising therapeutic target in oncology. In contrast, remarkably little attention has been paid to naturally occurring dopaminergic molecules in foods. Dopamine, L-DOPA, salsolinol, and other dopaminergic metabolites are found in various edible plants and fermented foods, yet their biological significance in cancer prevention remains largely unexplored. We hypothesized that these dietary dopaminergic molecules represent an overlooked class of food-derived bioactive compounds that can modulate cancer-associated signaling pathways. To test this hypothesis, we investigated the biological activity of salsolinol, a naturally occurring tetrahydroisoquinoline derived from dopamine. Our studies demonstrate that salsolinol suppresses hepatocellular carcinoma growth by reprogramming dopamine receptor-mediated STAT signaling. Mechanistically, salsolinol suppresses mitochondrial and canonical STAT3 signaling, promotes reactive oxygen species-dependent STAT1 activation, and induces mitochondrial dysfunction, apoptosis, and pyroptosis. These molecular changes significantly inhibit tumor growth in vivo while simultaneously alleviating anxiety-like behavior associated with hepatocarcinogenesis, suggesting a functional link between dopaminergic signaling in cancer and the brain. Collectively, these findings highlight the potential of food-derived dopaminergic molecules as bioactive compounds for cancer prevention.

PL12: Dietary Phytochemicals for Chemoprevention of Colorectal Carcinogenesis

Min-Hsiung Pan
Institute of Food Science and Technology, National Taiwan University, Taipei, Taiwan, China

Colorectal cancer (CRC) is one of the leading causes of cancer-related morbidity and mortality worldwide. Exposure to dietary and environmental xenobiotics, including food-borne carcinogens, environmental pollutants, and pesticides, is recognized as an important risk factor contributing to colorectal carcinogenesis. Xenobiotic metabolism plays a pivotal role in determining the biological fate of these compounds and involves coordinated phase I and phase II detoxification pathways. Phase I enzymes, primarily cytochrome P450 (CYP) enzymes, catalyze oxidation reactions that may convert pro-carcinogens into highly reactive intermediates capable of inducing DNA damage and mutagenesis. In contrast, phase II detoxification enzymes promote conjugation reactions that facilitate the elimination of these reactive metabolites and protect cells from carcinogenic insults. Accumulating evidence indicates that dietary phytochemicals can modulate xenobiotic metabolism and thereby suppress colorectal carcinogenesis. Numerous phytochemicals regulate the expression and activity of CYP enzymes while simultaneously activating phase II detoxification enzymes through the Nrf2 signaling pathway. For example, citrus polymethoxyflavones (PMFs) inhibit the expression and catalytic activity of carcinogen-activating CYP enzymes, whereas stilbenoids suppress the metabolic activation of pro-carcinogens and attenuate DNA damage. In addition, S-allylcysteine (SAC), a major bioactive compound in aged black garlic, enhances Nrf2-mediated antioxidant and detoxification responses while suppressing CYP450 expression, thereby reducing colorectal tumor development induced by dietary carcinogens. Recent studies further suggest that the chemopreventive efficacy of phytochemicals extends beyond xenobiotic metabolism through the modulation of inflammatory signaling, oxidative stress, gut microbiota, and host–microbiome interactions. These integrated mechanisms provide new opportunities for precision chemoprevention of CRC. This presentation will summarize current advances in the molecular mechanisms by which dietary phytochemicals regulate xenobiotic metabolism and related signaling pathways, highlighting their translational potential for the prevention of colorectal carcinogenesis.

PL13: Bee Products as Functional Ingredients: Bioactive Compounds, Their Bioaccessibility, and Bioavailability

Ilayda Sanli, Elif Sena Ugur, Gulay Ozkan, Esra Capanoglu*
Department of Food Engineering, Faculty of Chemical and Metallurgical Engineering, Istanbul Technical University, 34469 Maslak, Istanbul, Türkiye

Bee products, including honey, propolis, bee pollen, bee bread, and royal jelly, have attracted increasing attention as natural functional ingredients due to their rich composition of phenolic compounds, flavonoids, peptides, vitamins, minerals, and other bioactive constituents. These compounds contribute to various biological activities, including antioxidant, antimicrobial, anti-inflammatory, immunomodulatory, and metabolic regulatory effects. However, their functional potential is not determined only by their initial bioactive composition. Their botanical and geographical origin, production conditions, processing, food matrix interactions, and gastrointestinal stability strongly influence their bioaccessibility and bioavailability. Despite their promising health-related properties, many bee-derived bioactives suffer from poor water solubility, limited gastrointestinal stability, degradation under digestive conditions, and restricted intestinal transport. Therefore, encapsulation strategies such as liposomes, chitosan-coated liposomes, β-cyclodextrin inclusion complexes, and supercritical antisolvent processing have emerged as effective approaches to improve the stability, controlled release, bioaccessibility, and bioavailability of bee product bioactives. In addition, these strategies support their incorporation into real food matrices such as bread, kefir and juices. To conclude, bee products represent promising functional ingredients, but their successful application requires an integrated understanding of composition, standardization, gastrointestinal behavior, delivery systems, and food matrix compatibility.

Invited lecture

IL1: Metabolomics and Natural Products in Overcoming Drug Resistance in *Mycobacterium Tuberculosis*

Elwira Sieniawska
Department of Natural Products Chemistry, Medical University of Lublin, Lublin, Poland

Metabolomics has become an integral component of modern medicinal chemistry and multi-omics strategies, providing systems-level insight into pathogen physiology and drug response. In tuberculosis (TB) research, metabolomics delivers essential contributions to both the discovery of novel therapeutics and the optimization of existing regimens. By enabling comprehensive profiling of small-molecule dynamics, this approach advances the understanding of *Mycobacterium tuberculosis* (Mtb) biology, infection processes, and adaptive mechanisms that underpin antimicrobial resistance. Recent metabolomics-based investigations have elucidated host metabolic responses to Mtb virulence, enabled differentiation of *Mycobacterium* strains, and uncovered cellular networks critical for survival under stress. Importantly, metabolomic analyses have identified metabolites and pathways involved in early adaptive responses, characterized metabolic signatures associated with drug resistance, and supported profiling of antibiotic modes of action. These insights are particularly relevant in the context of natural products, which increasingly emerge as modulators of mycobacterial metabolism and as adjuvants capable of restoring antibiotic efficacy against drug-resistant strains. By perturbing central carbon metabolism, lipid remodelling, redox balance, and energy homeostasis, natural compounds can sensitize Mtb to frontline drugs and counteract resistance mechanisms.

Acknowledgements
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IL2: Beneficial Effects of Enoki Mushroom Extract on Male Menopausal Symptoms in Japanese Subjects: A Randomized, Double-Blind, Placebo-Controlled Study

Shizuo Yamada
Center for Pharma and Food Research, School of Pharmaceutical Sciences, University of Shizuoka, Shizuoka, Japan

With the increase in average life expectancy, age-related male menopause has become a cause of decreased quality of life in men. The enoki mushroom (*Flammulina velutipes*), a major edible mushroom, has long been recognized for its nutritional value and delicious taste, with proven biological and pharmacological properties, becoming a prevalent health food in Japan. In our previous study, the administration of enoki mushroom extract increased testosterone production in a cisplatin-impaired mouse model, with the involvement of adenosine suggested as the active component. We also investigated efficacy and safety of powdered enoki mushroom extract containing adenosine (test food) for menopausal symptoms in middle-aged and elderly men based on evaluation test such as Heinemann's Aging Males' Symptoms (AMS) scores. Test food and placebo were administered to healthy men with AMS scores of 27-49 for 12 weeks. AMS score and testosterone level were evaluated before and 12 weeks after the intake of test food and placebo. The intake of test food for 12 weeks significantly improved sexual dysfunction of AMS. The number of subjects with increased total testosterone levels of $\geq$ 0.5 ng/mL was significantly higher in test food group than in placebo group. Furthermore, in the Pittsburgh Sleep Quality Index (PSQI), enoki mushroom extract provided beneficial effects on age-related symptoms such as sleep disturbance in middle-aged and older men. These results suggest beneficial effects of enoki mushroom extract on symptoms of male menopause.

IL3: Anatolian Flora: Biodiversity Inspiring Therapeutic Innovation

İpek Süntar
Gazi University, Faculty of Pharmacy, Department of Pharmacognosy, Ankara, Türkiye

Anatolia is recognized as one of the world's major biodiversity hotspots, harboring an exceptionally rich flora with a high degree of endemism and a long-standing history of medicinal plant use. This remarkable botanical diversity continues to provide valuable opportunities for the discovery of bioactive natural products with therapeutic potential. This study will present recent research highlighting the contribution of selected Anatolian medicinal plants to contemporary drug discovery. Emphasis will be placed on the integration of phytochemical characterization with pharmacological evaluation using both in vitro and in vivo models. Representative studies will demonstrate the therapeutic potential of plant-derived extracts and secondary metabolites in inflammation, wound healing, cancer, and other disease models. Particular attention will be given to investigations exploring molecular biomarkers and signaling pathways associated with the observed biological activities, providing mechanistic insights into their pharmacological effects. The study will also discuss the importance of combining biodiversity-driven natural product research with multidisciplinary approaches, including pharmacognosy, phytochemistry, molecular pharmacology, and translational research, to accelerate the identification of promising therapeutic candidates. By illustrating how the unique botanical wealth of Anatolia can inspire innovative therapeutic strategies, this presentation aims to highlight the continuing relevance of medicinal plants as an invaluable resource for future drug discovery and evidence-based phytotherapy.

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IL4: From Floral Pollen to Bee Pollen: Unveiling the Phytochemistry and Pharmacological Activities

Etil Guzelmeric[1]*, Nisa Beril Sen[1], Elif Begüm Yıldırım[1], Ecesu Sezen[1], Hande Sipahi[2], Irena Vovk[3], Hasan Kırmızıbekmez[1]
[1]Department of Pharmacognosy, Faculty of Pharmacy, Yeditepe University, Atasehir, 34755 Istanbul, Türkiye
[2]Department of Toxicology, Faculty of Pharmacy, Yeditepe University, Atasehir, 34755 Istanbul, Türkiye
[3]Laboratory for Food Chemistry, National Institute of Chemistry, Hajdrihova 19, SI-1000 Ljubljana, Slovenia

Bee pollen is produced by honeybees through the collection of floral pollen grains and their subsequent mixing with nectar and salivary secretions. Consequently, the chemical composition of bee pollen is strongly influenced by its botanical origin[1,2]. Although biochemical alterations occur during the conversion of floral pollen into bee pollen, several common constituents are retained and can serve as key markers for identification and standardization. The development of standardized bee pollen extracts based on these marker compounds is crucial to ensure consistent composition and reproducible biological activities, thereby facilitating their use in scientific research and potential therapeutic applications.
This presentation focuses on the comparative evaluation of flower pollen grains from *Hedera helix*, *Castanea sativa*, *Salix alba*, *Quercus spp*, *Papaver somniferum*, *P. rhoeas*, *Cistus creticus*, *C. salviifolius*, and *C. laurifolius*, as well as related bee pollen samples[1,2]. The evaluation was based on the chemical composition of the pollen grains, with particular emphasis on the main marker compounds, including spermine and spermidine derivatives and flavonoids. These compounds were isolated and structurally characterized by NMR and HRMS analyses. The chemical profiles of the pollen extracts were further investigated using HPTLC and (U)HPLC. Furthermore, the following bioactivity assays were evaluated using standardized extracts to support their biological relevance: xanthine oxidase (XO) inhibition (HPTLC-XO inhibitory activity); antioxidant activities using HPTLC-DPPH together with in vitro assays such as DPPH, CUPRAC, and FRAP; and anti-inflammatory activities, including nitric oxide inhibition.

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IL5: Chamuangone from *Garcinia cowa*: From Traditional Thai Edible Plant to a Multi-Target Chemotherapeutic and Functional Food Candidate

Pharkphoom Panichayupakaranant
Phytomedicine and Pharmaceutical Biotechnology Excellence Center, Faculty of Pharmaceutical Sciences, Prince of Songkla University, Hat-Yai 90110, Thailand

Chamuangone, a naturally occurring polyisoprenylated benzophenone derivative isolated from the leaves of *Garcinia cowa* Roxb., a traditional Thai edible and medicinal plant, has emerged as a promising bioactive compound with broad therapeutic potential[1,2]. Initially identified for its antibacterial activity, chamuangone has been systematically investigated for its antiparasitic, anticancer, and anti-inflammatory properties through integrated in silico, in vitro, and in vivo studies, together with advances in analytical standardization, green extraction technologies, and safety evaluation. Chamuangone exhibited potent leishmanicidal activity against *Leishmania major* promastigotes (IC_{50}=10.7 μM) and strong cytotoxic effects against a broad range of human cancer cell lines, including lung, leukemia, colorectal, breast, and cervical cancers[3]. Notably, it demonstrated superior efficacy against multidrug-resistant leukemia cells (K562/ADM, IC_{50}=2.2 μM), outperforming doxorubicin. Mechanistic investigations revealed that chamuangone induces dose- and time-dependent apoptosis via caspase-3/7 activation, suppresses cancer cell proliferation and migration, and functions as a highly potent epidermal growth factor receptor tyrosine kinase (EGFR-TK) inhibitor (IC_{50}=2.85 nM), surpassing gefitinib in cervical cancer models[4]. For quality control and sustainable development, a validated HPLC method was established, and a green microwave-assisted extraction using rice bran oil was developed to yield a chamuangone-enriched oil with selective cytotoxicity toward cancer cells and minimal toxicity to normal cells[3,5]. In vivo studies further demonstrated that oral administration of chamuangone or a chamuangone-enriched extract (73.0% w/w chamuangone) significantly suppressed tumor growth and lung metastasis in breast cancer mouse models, with efficacy comparable to doxorubicin, through modulation of key biomarkers associated with apoptosis, inflammation, angiogenesis, epithelial-mesenchymal transition, and metastasis[6-8]. Toxicological evaluations confirmed its safety at therapeutic doses[9]. Despite pharmacokinetic limitations predicted for pure chamuangone, its potent bioactivity supports further development. Overall, chamuangone and its enriched extracts represent promising candidates for multi-target drug development and chemopreventive nutraceutical applications.

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IL6: Pilot Study of a Herbal Formulation Composed of *Bidens pilosa* for Constipation in Humans

Wen-Chin Yang[1,2,3]*, Greta Yang[1,] Tien-Fen Kuo[1,] and Yi-San Lee[1,3]
[1]Agricultural Biotechnology Research Center, Academia Sinica, Taipei, Taiwan, China
[2]Pharmasaga Co. Ltd
[3]Institute of Biotechnology, National Taiwan University, Taipei, Taiwan, China

The gut microbiota and their metabolites are associated with constipation and other gastrointestinal diseases. Dietary phytochemicals are crucial factors shaping gut microbiota. Here, we conducted a first-in-human trial of the herbal formulation BP, composed of a *Bidens pilosa* extract (BP) and excipient, in volunteers with constipation. Data from the Bristol Stool Form Scale, Cleveland Clinic Constipation Score, and the Quality of Life Scale for Patients with Constipation indicated that BP improved constipation and quality of life in patients with constipation. Metagenomic data showed that BP increased the abundance of bacterial

genera with beneficial potential and decreased the abundance of those with harmful potential in the stools of most volunteers. To dissect the clinical mechanism of BP, loperamide-treated mice were used to tease out its anti-constipation mechanism. Mouse data demonstrated that BP improved loperamide-induced constipation and modulated the gut microbiota. Mechanistic studies showed that BP at ≥ 0.5 μg/mL promoted probiotics, including *Bifidobacterium* and *Lactobacillus*, and at 800 μg/ml or higher, it inhibited pathogens, such as *Escherichia coli*, *Salmonella enterica*, and *Clostridium difficile*. Inter-bacterial antagonism data revealed that probiotics could inhibit pathogens. Taken together, BP promoted relief of constipation and modulated the gut microbiota, involving increased levels of probiotics and their metabolites that antagonized pathogenic bacteria.

IL7: AI Agent-Based Discovery of Bioactive Natural Products Modulating the Gut-Organ Axis

Kyungsu Kang
Korea Institute of Science and Technology, South Korea

Recent advances in artificial intelligence (AI) and data technologies have been widely adopted across diverse industries, dramatically improving productivity. AI has also become an indispensable tool in natural product research. The KIST Gangneung Institute of Natural Products is the only government research institute in Korea dedicated exclusively to natural product research. Last year, we introduced NPI-Finder, a natural product-specialized AI platform developed by KIST. Building upon this platform, we have recently integrated AI agent technology to further enhance the efficiency and intelligence of our research workflow. In this seminar, I would like to introduce KIST's AI agent-based natural product research platform and present representative case studies highlighting the discovery and development of bioactive natural products that promote intestinal health, modulate the gut–organ axis, and ultimately contribute to the prevention and treatment of human diseases. By integrating AI-driven discovery with experimental validation systems, we have successfully identified bioactive natural products that improve the gut–organ axis, demonstrating the potential of AI agents to accelerate natural product-based drug discovery.

IL8: Novel Tea Biscuits with Lyophilized Medlar (*Mespilus germanica L.*) Fruit: A Strategy for Functional Food Product

Nenad Mićanović[1], Aleksandar Ž. Kostić[1], Jelena Ladjarević[2], Svjetlana Janković-Šoja[1], Nemanja Krgović[3], Jelena Popović-Djordjević[1]*
[1]University of Belgrade, Faculty of Agriculture, Belgrade, Serbia
[2]University of Belgrade, Faculty of Technology and Metallurgy, Belgrade, Serbia
[3]Institute for Medicinal Plants Research "Dr Josif Pančić", Belgrade, Serbia

Functional food is a food that, in addition to its basic nutritional value, contains bioactive compounds capable of modulating physiological functions and contributing to the prevention of chronic diseases[1]. Medlar (*M. germanica L.*) fruits are a good source of nutrients and biologically active compounds. Despite these facts, there is no significant industrial application of the fruit[2]. Biscuits are the most popular cereal snacks worldwide, especially among children[3]. These baked products are mostly made from wheat flour and can be easily enriched with bioactive ingredients. Hence, they are suitable for the development of functional foods. For this purpose, three biscuit formulations were developed; control (TBC) with no medlar lyophilized fruit powder (LM), with 5% and 10% of LM (TB5 and TB10, respectively). All samples, including LM, were characterized by FTIR and examined for their phytochemical (total phenolic content-TPC, total flavonoid content-TFC, total carotenoid content-TCC, proanthocyanidins-PANC), and functional characteristics. The FTIR spectra of LM reflect their main chemical constituents, including polysaccharides, phenolic compounds, lipids, and pectin, as evidenced by their characteristic functional groups.Chemical characterization revealed that samples were significantly different in regard to all studied parameters (Tukey test, $p<0.05$), with the highest values of TPC (350.52±3.55 mg GAE/100 g), TFC (77.70±2.29 CE/100 g) and PANC (1.7±0.07 μg/g) in LM, and TCC (612.04±1.00 μg/100 g) in TB10. The highest antioxidant activity in TAC (13.05±0.15 mg/g AAE) and CUPRAC (5.36±0.32 mg/g AAE) assays showed TB10. On the other hand, LM was the most active in DPPH· (24.59±1.29 μmol/g Trolox), FRP (2.45±0.01 mg/g AAE) and ABTS·+ (99.31±0.95 μmol/g Trolox) assays. Additionally, α-glucosidase inhibitory activity of biscuits increased in a concentration-dependent manner, indicating improved hypoglycemic potential of samples TB5 and TB10.
The enrichment of tea biscuits with lyophilized medlar fruits resulted in enhanced values for all studied parameters compared to the control ($p<0.05$), and it was especially pronounced for TB10. Based on the obtained results lyophilized medlar fruits could be useful adds-on for the development of novel functional tea biscuits.

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IL9: Gut Microbiota Protects against Liver Injury and Fibrosis via Activation of the CYP Eicosanoid Pathway

Quancai Sun
Macau University of Science and Technology, Macao, China

Gut microbiota has been shown to play an important role in the progression of liver injury and fibrosis, but the specific microbial factors or pathways involved remain poorly defined. Eicosanoids are endogenous lipid signaling molecules that exert potent effects to regulate inflammation, immune responses, and tissue homeostasis. We hypothesize that the gut microbiota modulates the biosynthesis of tissue-protective eicosanoids in the liver, thereby mitigating liver injury and fibrosis. Using LC-MS/MS-based lipidomics to compare hepatic profiles of eicosanoids of conventionally raised mice with germ-free or antibiotic-treated mice, we show that the gut microbiota induces the cytochrome P450 (CYP) eicosanoid pathway in the liver. Furthermore, by administering exogenous indole or mono-colonizing germ-free mice with indole-producing *Bacteroides thetaiotaomicron* or a mutant strain lacking indole production, we demonstrate that gut microbial metabolites, notably indole, contribute to the microbiota's inducing effects on the liver's CYP eicosanoid pathway. Finally, we find that disruption of the microbiota-liver-CYP axis, through inhibition or genetic ablation of CYP monooxygenases, or antibiotic suppression of gut microbiota, exacerbates chemically or surgically induced liver injury or fibrosis. Conversely, activation of this axis attenuates liver injury and fibrosis. These findings support that the gut microbiota confers protection against liver injury and fibrosis through activation of the hepatic CYP eicosanoid pathway. This microbiota–liver–CYP axis represents a critical mechanism by which the gut microbiota modulates host liver metabolism and disease progression.

IL10: From Medicinal Fungi to RNA Nanomedicine: Harnessing Extracellular Vesicles for Precision Oncology

Hui-Min David Wang
Graduate Institute of Biomedical Engineering, National Chung Hsing University, Taiwan, China

Extracellular vesicles (EVs) have emerged as promising natural nanocarriers for the delivery of therapeutic biomolecules. In this presentation, I will discuss our recent studies on extracellular vesicles derived from *Antrodia cinnamomea*, a medicinal fungus widely recognized for its bioactive properties. These nanosized vesicles exhibit selective antitumor activity against hepatocellular carcinoma while maintaining excellent biocompatibility toward normal hepatocytes. Mechanistic investigations identified a novel vesicle-associated microRNA that suppresses tumor progression through modulation of RAD and inhibition of the PI3K/AKT signaling pathway. Furthermore, fungal-derived EVs regulate oxidative stress and induce mitochondrial apoptosis in cancer cells. This work highlights the potential of natural extracellular vesicles as next-generation RNA nanomedicines for precision cancer therapy and translational biomedical applications.

IL11: Integrating Untargeted Metabolomics and Bioactivity Profiling to Reveal Bioactive Constituents of Malaysian Plants

Pei Lou Wong, S.Jasrey Max Suil, Faridah Abas*
Department of Food Science, Faculty of Food Science and Technology, Universiti Putra Malaysia, 43400 Serdang, Selangor, Malaysia

Metabolomics is a holistic, system-level approach that reflects the biochemical state of biological systems and provides direct insight into plant metabolic composition. Conventional standardization of herbal materials often relies on a limited number of chemical markers determined by chromatographic techniques, which may not adequately represent the complex and synergistic nature of bioactive constituents. In contrast, metabolomics enables comprehensive profiling of plant metabolites and offers a more reliable strategy for understanding bioactivity and ensuring quality consistency. In this study, nuclear magnetic resonance (NMR)–based metabolomics was employed as the primary analytical platform due to its high reproducibility, quantitative capability, minimal sample preparation, and suitability for metabolic fingerprinting. NMR analysis was complemented by liquid chromatography–mass spectrometry (LC–MS) to enhance metabolite coverage and facilitate the detection of low-abundance compounds with high sensitivity. The integrated approach provides a robust framework for metabolite annotation, sample differentiation, and bioactivity correlation. This work highlights the application of NMR metabolomics and LC–MS/MS profiling to investigate the bioactive potential of selected Malaysian medicinal plants, namely *Ardisia elliptica* and *Ficus racemosa*. Multivariate data analysis coupled with bioactivity assays was used to correlate metabolite profiles with biological effects, enabling the identification of key metabolite signatures linked to functional properties. The findings demonstrate the value of metabolomics-driven strategies in supporting evidence-based utilization, quality control, and future development of Malaysian medicinal plants.

IL12: 3D-Bioprinting Sustainable Encapsulation of Bioactive Compounds for Enhanced Bioavailability and Bioaccessibility

Ribeiro M.H
Research Institute for Medicines (iMed.ULisboa), Faculdade de Farmácia, Universidade de Lisboa, Av. Prof. Gama Pinto, 1649-003 Lisboa, Portugal
University College London (UCL), London, England

Some bioactive compounds, such as *curcumin*, exhibit beneficial properties for human health, including antioxidant and anti-inflammatory activities. However, their poor aqueous solubility and low bioavailability limit their applications in medicine, pharmaceuticals, and nutraceuticals. Curcuminoids have been approved by the U.S. Food and Drug Administration (FDA) due to their safety, tolerability, and therapeutic potential. The aim of this study was to investigate improvements in the physicochemical properties and bioavailability of bioactive compounds, using *curcumin* as a model compound, through complexation or encapsulation using 3D bioprinting technology. Phase-solubility studies demonstrated a positive correlation between cyclodextrin concentration and *curcumin* solubility. The resulting complexes were further evaluated for antioxidant activity using the DPPH assay and for anti-inflammatory activity through inhibition of albumin denaturation.
The results showed that both encapsulation and complexation enhanced *curcumin* bioavailability. In particular, β-cyclodextrin and its derivatives, especially hydroxypropyl-β-cyclodextrin, significantly improved the solubility and functional properties of curcumin. Phase-solubility studies provided valuable information regarding the complexation process, including stability constants and complex stoichiometry, highlighting the role of cyclodextrins in enhancing *curcumin* solubilization and, consequently, its bioavailability. Since solubility is a key determinant of bioavailability, improved solubility was associated with enhanced antioxidant and anti-inflammatory activities.
In vitro solubility studies further demonstrated that the polymer matrices protected *curcumin* from the acidic and alkaline conditions of the gastrointestinal tract, resulting in greater stability compared with free *curcumin*. Finally, bioaccessibility was assessed using both an in vitro digestion model and an in vivo inflammatory model. Overall, the complexation and encapsulation using 3D-bioprinting represent promising strategies for improving the bioavailability and biological efficacy of this bioactive compound.

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IL13: Chinese Sweet Tea as a "Sweet" Remedy for Metabolic Disorder Management

Zhao Danyue
Department of Food Science and Nutrition, The Hong Kong Polytechnic University, Hong Kong, China

The escalating global burden of obesity, diabetes, and related metabolic disorders underscores the urgent need for safe, effective, and sustainable therapeutic strategies. While current single-target pharmacotherapies are often hampered by low response rates and adverse effects, multi-target, orally administered, and cost-effective Chinese herbal medicines may provide a promising alternative. Chinese sweet tea (*Rubus suavissimus* Lee), a traditional remedy used by minority nationalities in southwestern China, has documented benefits for metabolic health, yet its mechanisms of action remain poorly understood. This study comprehensively investigated the metabolic benefits of *R. suavissimus* leaf extract (RSE) and its probiotic-fermented product (fRSE) in vitro and in vivo and pinpointed the major active phytochemicals. Employing established genetic and diet-induced mouse models of obesity and type 2 diabetes, gut microbiota manipulation in germ-free mice, alongside integrated multi-omics analyses, we demonstrate that both RSE and fRSE effectively prevent excessive weight gain, improve systemic glucose homeostasis, and ameliorate dyslipidemia, with pronounced efficacy against hepatic steatosis and pancreatic dysfunction. Mechanistic exploration reveals that the lipid-lowering properties are mediated through a gut microbiota-dependent pathway. By contract, the anti-diabetic effects primarily involve direct actions targeting pancreatic β-cell functions independent of the gut microbiota. Further phytochemical fractionation and screening identified multiple RSE-derived ellagitannins as the most potent agents for reducing hepatic lipid accumulation. Collectively, this work provides the first evidence for the dual therapeutic efficacy of RSE against hyperlipidemia and hyperglycemia via distinct mechanistic pathways. It highlights the substantial potential of RSE preparations and their bioactive constituents to serve as cost-effective, natural herbal remedies for the management of metabolic disorders, offering valuable translational insights for future clinical applications.

IL14: Chromatographic and Effect-Directed Analyses of Phytochemicals in Plant and Food Samples - Solving Analytical Challenges

Irena Vovk[1]*, Vesna Glavnik[1], Maja Bensa[2], Breda Simonovska[1], Živa Vipotnik[1], Etil Guzelmeric[3], Ágnes M. Móricz[4], Uroš Gašić[5]
[1]Laboratory for Food Chemistry, National Institute of Chemistry, Ljubljana, Slovenia
[2]Research Institute of Faculty of Health Sciences, Faculty of Health Sciences, University of Ljubljana, Ljubljana, Slovenia
[3]Department of Pharmacognosy, Faculty of Pharmacy, Yeditepe University, Istanbul, Türkiye
[4]Plant Protection Institute, HUN-REN Centre for Agricultural Research, Budapest, Hungary
[5]University of Belgrade, Department of Plant Physiology, Institute for Biological Research "Siniša Stanković", National Institute of Republic of Serbia, Belgrade, Serbia

The discovery of new sources of phytochemicals in plant materials, development of new food supplements and functional food products as well as control of food quality and safety, require methods based on complementary chromatographic techniques and effect-directed analysis (EDA). This presentation will address challenges in the development of methods based on chromatographic and hyphenated techniques—such as high-performance thin-layer chromatography (HPTLC-densitometry, HPTLC-image analysis, HPTLC-MS/(MS)), and high-performance liquid chromatography ((U)HPLC-UV/Vis, (U)HPLC-MS/(MS))—for targeted and non-targeted analyses of phytochemicals in plant and food matrices. Among the challenges discussed will be stability of the analytes, lack of commercial standards and standard reference materials, lack of chromophores, and isomeric structures. Examples will cover analyses of phytochemicals from different groups in plant samples (medicinal plants, invasive alien plant species (tree of heaven[1,2], Russian vine, Chinese knotweed, Japanese knotweed, Bohemian knotweed and giant knotweed), flower pollen[3,4], etc.) and food samples (e.g., food supplements[5], bee pollen[3,4,6], food waste). Furthermore, the presentation will include challenges in non-targeted (HP)TLC–EDA analyses of antimicrobial compounds, antioxidants and enzyme inhibitors in crude extracts (from different parts of invasive alien plant species, flower pollen and bee pollen) which are mostly be related to the stationary phase, detection reagents and detection modes.

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IL15: Dietary Galacto-Oligosaccharides Alleviate Respiratory Syncytial Virus-Induced Pulmonary Inflammation by Modulating the Gut–Lung Axis

Miao Guo[1], Jiabao Liu[2], Daishun Liu[3]*, Shengpeng Wang[1]*
[1]State Key Laboratory of Mechanism and Quality of Chinese Medicine, Institute of Chinese Medical Sciences, University of Macau, Macao, China
[2]Donnelly Centre for Cellular and Biomolecular Research, University of Toronto, Toronto,
[3]Department of Respiratory and Critical Care Medicine, Guizhou Provincial People's Hospital, Guiyang, China

Respiratory syncytial virus (RSV) remains a leading viral cause of pediatric and geriatric hospitalization worldwide[1], yet effective dietary interventions targeting RSV-induced lung inflammation are lacking. Given that dietary polysaccharides have been widely recognized for their antiviral potential [2], we screened over ten dietary polysaccharides to identify promising prebiotic candidates capable of mitigating RSV infection. Among them, galacto-oligosaccharides (GOS) emerged as the most potent candidate, significantly promoting the proliferation of the key gut commensal *Clostridium scindens* and alleviating RSV-induced pulmonary immunopathology in vivo. To elucidate the underlying immunometabolic mechanism, fecal metabolomics and single-cell RNA sequencing were performed. We found that GOS-mediated enrichment of *C. scindens* restored the level of its secondary bile acid precursor, deoxycholic acid (DCA), in the gut. Stable isotope tracing further demonstrated that microbiota-derived DCA undergoes host taurine conjugation into taurodeoxycholic acid (TDCA), which preferentially accumulates in lung tissue. At the cellular level, TDCA suppressed the pathogenic metabolic and inflammatory activation of pulmonary dendritic cells, thereby dampening excessive lung inflammation. Collectively, our findings establish a novel dietary strategy where GOS targets the *C. scindens*–TDCA axis to confer tissue-specific pulmonary immune protection, highlighting the potential of specific prebiotic polysaccharides as functional food ingredients for controlling respiratory viral infections.

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IL16: Marine Bioresources as Natural Factories of High-Value Compounds: From Environmental Drivers to Sustainable Valorization

Sónia A.O. Santos
CICECO-Aveiro Institute of Materials, Department of Chemistry, University of Aveiro, Portugal

Marine organisms are continuously exposed to fluctuating abiotic factors, such as temperature, salinity, light, and nutrient availability, as well as biotic interactions including competition, predation, and symbiosis. These environmental cues shape their metabolism and drive the production of a remarkable diversity of specialized metabolites, making marine bioresources true natural factories of high-value compounds. Blue biorefinery provides a sustainable framework to harness this metabolic plasticity and convert marine biomass and side streams into bioactive ingredients and advanced materials, thereby contributing to a circular and low-carbon bioeconomy.

This work highlights the role of green separation processes in unlocking the full potential of marine resources. In particular, eutectic solvents and biosolvents are presented as versatile and environmentally benign media for the selective extraction and purification of marine-derived compounds, such as lipophilic and phenolic compounds [1,2], offering enhanced process efficiency and reduced environmental impact. Integrated strategies for the recovery and valorization of these biomolecules will be discussed, together with their translation into nutraceutical, cosmetic, and pharmaceutical applications.

Special emphasis will be placed on the exploration of extremophilic microorganisms within the framework of the XTREAM project, which seeks to elucidate how extreme environmental conditions drive the biosynthesis of unique enzymes and metabolites, thereby expanding the chemical space available for the discovery of novel drugs and other value-added products. By linking environmental drivers of marine metabolism with sustainable extraction and biorefinery approaches, this work illustrates new pathways for the responsible valorization of marine bioresources.

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IL17: Bioactive Metabolites from *Glycyrrhiza foetida* in the Modulation of Metabolic Syndrome

Elena Serino[1], Hekmat B. Al-Hmadi[2,3], Fabio Arturo Iannotti[4], Arianna Pastore[1], Rosa Maria Vitale[4], Saoussen Hammamic[3], Mariano Stornaiuolo[1], Giuseppina Chianesea*, Orazio Taglialatela-Scafati[1]
[1]Department of Pharmacy, School of Medicine and Surgery, University of Naples Federico II, Via D. Montesano 49, 80131 Napoli, Italy
[2]Department of Chemistry, College of Medicine, AL-Muthanna University, Samawah, Iraq
[3]Laboratory of Environmental Chemistry and Clean Processes (LR21ES04), Faculty of Sciences of Monastir, Monastir University, Monastir, 5000, Tunisia
[4]Institute of Biomolecular Chemistry, National Research Council (ICB-CNR), Via Campi Flegrei 34, 80078, Pozzuoli (NA), Italy

Metabolic syndrome (MetS) is a cluster of obesity-related conditions that significantly increase the risk of cardiovascular disease and type 2 diabetes. In 2019, cardiovascular and diabetes-related complications accounted for over 20 million deaths worldwide. During the early stages of MetS, lifestyle modifications and the use of nutraceuticals, rather than pharmacological interventions, are recommended to slow disease progression. Among potential nutraceuticals, *Glycyrrhiza foetida*, a lesser-known species of licorice, has emerged as a promising candidate. Traditionally used in folk medicine, *G. foetida* has been found to contain amorfrutins, acetate-derived polyphenols with insulin-sensitizing effects through PPARγ agonism[1]. A phytochemical investigation of its aerial parts led to the isolation of 29 compounds with distinct structural features, including 11 previously undescribed amorfrutins and a novel prenylated flavanone. Their structures were fully elucidated using 2D NMR and HR-MS analyses. The amorfrutins were evaluated for their activity on PPARγ and PPARα. Among them, amorfrutin A showed potent PPARγ activation, while amorfrutins H and E acted as selective PPARα and dual PPARα/γ agonists, respectively[2]. Additionally, all isolated compounds were assessed for their effects on two other dysfunctional pathways associated with MetS. This analysis highlighted amorfrutin M and decarboxyamorfrutin A as mitochondrial stimulators, and amorfrutin 2 as a promoter of glucose uptake[3]. Computational studies further supported the observed structure–activity relationships.
Thus, *G. foetida* is a rich source of bioactive compounds that act on multiple pathways implicated in metabolic syndrome. These findings support its traditional use and highlight its promise as a functional food or nutraceutical for MetS prevention and management.

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IL18: Oxyresveratrol Ameliorates Diabetes-Associated Neuropathy through Modulation of Microglial Neuroinflammation and Autophagy

Wai San Cheang[1,2]*, Yizhen Bai[1,2], Haoran Chang[1,2], Feiyang Zheng[1,2]
[1]State Key Laboratory of Mechanism and Quality of Chinese Medicine, University of Macau, Macau SAR, China
[2]Institute of Chinese Medical Sciences, University of Macau, Macau SAR, China

Diabetic neuropathy remains a debilitating condition with no disease-modifying therapies for millions of patients. This study investigated the neuroprotective potential of oxyresveratrol, a natural flavonoid, emphasizing its coordinated regulation of microglial neuroinflammation, autophagic dysfunction, and associated oxidative stress. We employed both in vivo and in vitro approaches. Male mice fed a high-fat diet (HFD) for 3 months to model diabetic neuropathy and treatment group received oxyresveratrol (30 mg/kg/day) by oral gavage for 7 weeks. Behavioral performance was assessed via Y-maze, open field, and motor function tests, while molecular changes in brain tissue were analyzed by Western blotting and immunohistochemistry. Concurrently, LPS-stimulated BV2 microglial cells were treated with oxyresveratrol (1-20 μM), and were evaluated using MTT, Griess, ROS fluorescence, RT-qPCR, and Western blot assays. Oxyresveratrol markedly improved systemic glycemic control, glucose tolerance, and insulin sensitivity in diabetic mice, alongside reversing cognitive and motor deficits. Mechanistically, oxyresveratrol exerted multi-target effects: it quelled neuroinflammation by downregulating NLRP3, COX-2, iNOS, and ICAM-1; restored autophagic flux via modulation of LC3B-II and p62; and significantly reduced oxidative stress in both brain tissues and microglial cells. These results establish that oxyresveratrol alleviates diabetic neural injury through dual modulation of microglial autophagy and neuroinflammation, effectively breaking the pathological feedback loop between these pathways. Thus, oxyresveratrol emerges as a promising candidate as healthcare product to combat against diabetic neuropathy.

Acknowledgments
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IL19: Curcumin Differentially Regulates Ferroptosis and Oxidative Stress in Doxorubicin-Resistant Lung Cancer and Cigarette Smoke Extract-Exposed Lung Cells

Wing-Hin Lee, Ching-Yee Loo*
Faculty of Pharmacy and Health Sciences, Royal College of Medicine Perak, Universiti Kuala Lumpur (UniKL RCMP), 30450 Ipoh, Perak, Malaysia

Excessive oxidative stress and impaired antioxidant defense systems can threaten both healthy and cancer cells through the generation of reactive oxygen species (ROS). Recently, ROS-mediated lipid peroxidation driven by increased intracellular iron accumulation has been reported to play a critical role in regulating cellular metabolism. Our recent findings in the doxorubicin-resistant lung cancer cell line H69AR demonstrated that co-delivery of curcumin (CUR) effectively sensitized H69AR cells to doxorubicin (DOX). We observed that CUR promoted intracellular iron overload, which subsequently induced lipid peroxidation and ferroptosis, as confirmed using N-acetyl-L-cysteine (a ROS inhibitor) and ferrostatin-1 (a ferroptosis inhibitor). In turn, enhanced cytochrome c release and caspase-3 activation were observed, leading to DNA fragmentation and apoptosis in H69AR cells. In contrast, in cigarette smoke extract (CSE)-treated lung epithelial cells, CUR appeared to reduce ferroptosis. It was accompanied by enhanced antioxidant defenses, including glutathione and superoxide dismutase levels, as well as the activities of nuclear factor erythroid 2-related factor 2 (NRF2) and glutathione peroxidase 4 (GPX4). These protective effects were partially associated with inhibition of the inflammasome system in CSE-treated Calu-3 cells.

IL20: Food-Grade Liposome-Loaded Delivery Systems for Bioactives

Ayse Karadag
Food Eng. Department, Chemical and Metallurgical Eng Faculty, Yildiz Technical University, 34210 Istanbul, Turkiye

Liposomes are promising food-grade carriers for bioactive delivery due to their biocompatibility and ability to encapsulate both hydrophilic and lipophilic compounds. They can improve the solubility, stability, controlled release, and bioavailability of nutraceuticals. However, conventional liposomes often suffer from aggregation, leakage, and low structural stability. To overcome these limitations, recent studies have focused on hybrid systems integrating liposomes into secondary matrices such as nanofibers, hydrogels, films, particles, and emulsions[1]. Our recent studies demonstrated that combining liposomes with food-grade polymeric matrices can significantly improve the functionality of bioactive delivery systems[2–5]. For example, propolis-loaded liposomes embedded in xanthan gum-salep hydrogels exhibited preserved liposome integrity, enhanced mucoadhesiveness, and improved gastrointestinal protection of phenolics, resulting in higher bioaccessibility during simulated digestion. Moreover, these liposomal hydrogels could potentially be adapted for 3D food printing applications, enabling the development of products with tunable textures for personalized and elderly nutrition[2]. In another study, black mulberry extract-loaded liposomes were incorporated into pullulan/pectin electrospun nanofibers, resulting in enhanced mucoadhesiveness, improved anthocyanin transport across Caco-2 cells, and nearly two-fold higher anthocyanin bioaccessibility compared to non-liposomal systems[3]. Similarly, glutenin hydrolysate-loaded liposomes incorporated into uni-axial and co-axial electrospun pullulan/carboxymethylcellulose fibers provided enhanced gastrointestinal stability and sustained release of antioxidant peptides. Particularly, co-axial liposome-loaded fibers reduced premature gastric release while preserving antioxidant activity during digestion, demonstrating the advantages of combining liposomal encapsulation with advanced electrospinning strategies[4]. Beyond oral delivery applications, liposome-loaded fibers have also shown potential as bioactive biomaterials. Propolis-loaded liposomes embedded into gelatin-zein co-axial electrospun fibers exhibited improved thermal and mechanical properties, enhanced mucoadhesiveness, antimicrobial activity against Staphylococcus aureus, and improved fibroblast cell viability, suggesting potential applications for oral and wound-healing delivery systems[5]. Food-grade hybrid liposome-loaded systems provide synergistic advantages compared to conventional liposomes alone by improving structural stability, protecting sensitive bioactives during gastrointestinal digestion, enhancing mucoadhesion, and enabling controlled release profiles, and epresent a promising platform for next-generation functional foods, nutraceuticals, and oral delivery applications. Future studies should focus on large-scale production, long-term stability, food matrix interactions, and in vivo validation to accelerate their industrial translation.

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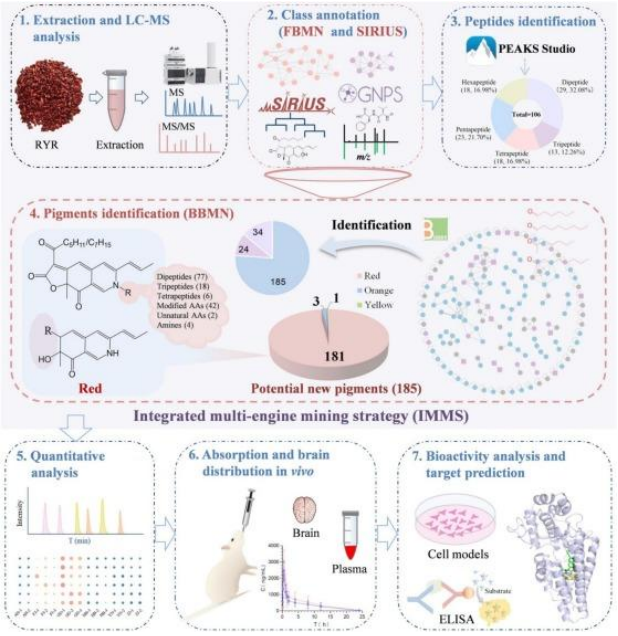
IL21: The Underappreciated Diversity of Functional Pigments in Red Yeast Rice Revealed by an Integrated Multi-Engine Mining Strategy

Yujuan Ban, Jianlin Wu*, Na Li*
State Key Laboratory of Mechanism and Quality of Chinese Medicine, Macau University of Science and Technology, Macau, China

Red yeast rice (RYR) is a popular functional food, while its functional components remain severely understudied. This study developed an integrated multi-engine mining strategy (IMMS) ingeniously combining feature-based molecular networking, building blocks-based molecular networking, SIRIUS, PEAKS, and BUDDY to comprehensively analyze RYR components. Employing IMMS, 219 pigments (208 red, 6 orange, 5 yellow) and 104 peptides were first identified, including 185 potential new pigments, with red and yellow pigments showing higher contents. Notably, red pigments demonstrated optimal plasma exposure and brain distribution in rats after oral RYR. Bioactivity analysis first revealed that six typical pigments, especially red, suppressed oxidative stress and neuroinflammation related to Alzheimer's disease in L-glu-induced HT-22 cells and LPS-induced BV-2 cells, potentially via the Keap1-Nrf2 and IDO1 pathways, respectively. These findings significantly expanded the pigment diversity and RYR components, facilitating the discovery of functional components and providing a foundation for RYR's development as an anti-Alzheimer's functional food.



Scheme 1. Workflow for the comprehensive identification of RYR components and the discovery of anti-Alzheimer's components.

IL22: Emerging Food-Processing Strategies for Reducing Allergenicity in Functional Foods and Beverages

Parisa Mostashari[1], Amin Mousavi Khaneghah[2]*
[1]Research and Development Unit, Dina Pharmed Pharmaceutical Co., Tehran, Iran
[2]Faculty of Food Science and Agrotechnology, Universiti Malaysia Terengganu, 21030 Kuala Nerus, Terengganu, Malaysia

Food allergies are a critical safety concern that affect the formulation and consumption of functional foods and beverages. Many plant-derived ingredients contain proteins that retain immunological activity even after minimal processing, particularly in fresh, cold-processed, or ready-to-consumer products. Conventional heating can reduce the activity of some allergens, but it may also adversely affect nutritional quality, sensory properties, and consumer acceptance. Consequently, attention is increasingly focused on alternative processing and formulation strategies that reduce allergenic potential while maintaining product quality. This presentation provides an overview of emerging approaches for allergen mitigation, including enzymatic treatment, fermentation, high-pressure processing, pulsed electric fields, ultrasound, cold plasma, controlled oxidation, and interactions between food proteins and naturally occurring phytochemicals. These interventions may modify protein structure, alter protein solubility or digestibility, and reduce the accessibility of antibody-binding regions. The effectiveness of each strategy depends on the allergen type, processing conditions, food composition, and interactions among proteins, carbohydrates, lipids, and bioactive compounds. Particular attention will be given to the role of the food matrix in determining allergen stability and immunological recognition. Rather than treating the matrix as an inert carrier, it may be deliberately designed to influence allergen behavior during processing, storage, and digestion. However, reduced antibody binding in laboratory assays does not necessarily indicate clinical safety. Reliable validation, therefore, requires complementary structural, immunochemical, digestive, cellular, and clinical investigations. The development of lower-allergenicity functional foods will depend on combining food-processing innovation with rigorous allergological assessment. Such an integrated approach may support safer product development without compromising nutritional and sensory quality.

IL23: Biosynthesis of a Volatile Organic Compound in Lavander Plants

Lin Chen[1], Guangli Li[1], Mathias Fontez[2], Yuxin Rao[1], Aurélie Rius-bony[2], Frédéric Jullien[2], Sandrine Moja[2], Natalia Dudareva[3,4,5], Benoît Boachon[2]*, Pan Liao[1,6,7]*
[1]Department of Biology, Hong Kong Baptist University, Kowloon Tong, Hong Kong SAR, China
[2]Laboratoire de Biotechnologies Végétales appliquées aux Plantes Aromatiques et Médicinales, CNRS, LBVpam UMR 5079, Université Jean Monnet, Saint-Étienne F-42023, France
[3]Department of Biochemistry, Purdue University, 175 South University St., West Lafayette, IN 47907, USA
[4]Purdue Center for Plant Biology, Purdue University, West Lafayette, IN 47907, USA
[5]Department of Horticulture and Landscape Architecture, Purdue University, 625 Agriculture Mall Dr., West Lafayette, IN 47907, USA
[6]State Key Laboratory of Agrobiotechnology (CUHK), Hong Kong SAR, China
[7]Institute of Systems Medicine and Health Sciences, Hong Kong Baptist University, Kowloon Tong, Hong Kong SAR, China

Lavender volatile organic compounds (VOCs) have been widely used in perfumery, essential oils and aromatherapy. Most VOCs from lavender plants are monoterpenes and have good activities like anti-bacterial, anti-inflammatory and even anti-cancer properties. Although the biosynthesis of many of them are already known, some remain unknown. A monoterpene VOC, an irregular monoterpene first identified in French lavender oil in 1942, caught our attention. It is the essential component of lavender essential oil and a potential insect pheromone. However, its amount is very low (0.1-3%) in most widely grown Lavandula species. Metabolic engineering provides a sustainable and alternative approach to produce it. However, the biosynthetic pathway should be firstly revealed before metabolic engineering can be performed. While Lavandula × intermedia LPPS is known to synthesize lavandulyl diphosphate (LPP) from the 5-carbon universal precursor DMAPP, how LPP is converted to lavandulol still unclear. In this work, we will introduce how integrated metabolic analysis, transcriptomics and biochemical techniques have been used to address the above scientific question. Our findings revealed a new molecular target for engineering lavender VOC in microbial or plant systems.

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IL24: Iron-Curcumin Nanozymes Hydrogels as a Dual Antibacterial and Cytoprotective Strategy for Wound Healing

Ching-Yee Loo*, Wing-Hin Lee
Faculty of Pharmacy and Health Sciences, Royal College of Medicine Perak, Universiti Kuala Lumpur (UniKL RCMP), 30450 Ipoh, Perak, Malaysia

The emergence of antibiotic-resistant bacteria in wound infections has become a major clinical challenge. Among the most common pathogens associated with chronic wounds, *Pseudomonas aeruginosa* and *Staphylococcus aureus* induce excessive production of inflammatory cytokines and oxidative stress, ultimately leading to cellular damage and impaired wound healing. An ideal wound therapeutic should therefore possess both antimicrobial and anti-inflammatory properties while effectively suppressing bacterial growth without compromising host cell viability. Iron-curcumin nanozymes represent a promising therapeutic strategy to effectively inhibit bacterial attachment and subsequent biofilm formation by *P.*

aeruginosa and *S. aureus*. Our iron-curcumin nanozymes-loaded hydrogel demonstrated superior antibacterial activity and significant inhibition of biofilm formation. Treatment of the bacterial-HaCaT co-culture system with iron-curcumin nanozymes hydrogel effectively reduced bacterial burden without compromising HaCaT cell viability. This is evident in improved cellular metabolic and oxidative stress profiles, including reduced lactate dehydrogenase release, reactive oxygen species, and enhanced ATP and MMP levels, compared with the curcumin-loaded hydrogel alone. In conclusion, the fabricated iron-curcumin nanozyme-loaded hydrogel effectively inhibited bacterial biofilm formation through its bactericidal activity while maintaining the viability of HaCaT cells.

IL25: *Polyopes constrictus*: A Red Seaweed with Potentials in Ameliorating Metabolic Syndrome

Md. Shahidul Islam*, S'thandiwe Magwaza
Department of Biochemistry, University of KwaZulu-Natal (Westville Campus), Durban 4000, South Africa

Oxidative stress and associated inflammations are one of major causal factors for the development of type 2 diabetes and its associated complications and ultimately metabolic syndrome. On the other hand, a number of seaweeds and their bioactive compounds have shown promising effects and ameliorated above metabolic abnormalities, when red seaweeds are in the forefront in this regard. Hence, the present study was investigated to examine the effects of a red seaweed, *Polyopes constrictus* on oxidative stress via scavenging various free radicals, anti-inflammatory activities, carbohydrate and lipid digestive enzyme inhibitory activities, inhibiting intestinal glucose absorption and enhancing muscle glucose uptake, hepatic oxidative damage, glucose metabolism and identification of its major bioactive compounds. The results of this study showed that both aqueous and ethanol extracts were effective ameliorating oxidative stress via scavenging DPPH free radicals when ethanol extract was effective in scavenging nitric oxide radicals. Both extracts were equally showed anti-inflammatory and carbohydrate and lipid digestive inhibitory activities in vitro. In ex vivo condition, both extracts were also effective in dose dependently inhibiting intestinal glucose absorption and increasing muscle glucose uptake as well ameliorating FeSO4 induced hepatic oxidative stress. The major compounds identified in the aqueous extract are Mulberrofuran A, Mulberrofuran A, 2,7,11-Cembratrien-4,6-diol, Oleanolate 3-O-beta-D-glucoside and in the ethanol, extract are Ascorbic acid ethyl ester, Stylisterol B, Absinthin and Pheophorbide a, when Stylisterol B has been found to be a stronger alpha-Glucosidase and pancreatic lipase inhibitor compared to standard drugs, acarbose and orlistat. The data of this study showed that *Polyopes constrictus* has potential bioactive compounds for the diabetes and obesity and may be for metabolic syndrome. Further studies in animal model are required to ascertain the results of this study.

IL26: Investigation of Innovative Technologies for Safety Evaluation in Medicinal Materials

Jinchao Wei*
Institute of Chinese Medical Sciences, University of Macau, Macau 999078, China

Medicinal materials is a vital component of national healthcare system and industry, characterized by original thinking and a unique theoretical framework. The robust growth of the TCM health sector relies on analyzing the material basis of medicinal ingredients and ensuring safety. The 2020 Chinese Pharmacopoeia now recommends enzyme-linked immunosorbent assay (ELISA) for rapid detection of mycotoxin residues in medicinal materials, reflecting recognition and demand for emerging rapid testing methods. As science and technology progress, rapid screening techniques evolve continuously. Addressing challenges such as detecting and accurately measuring common and trace exogenous harmful residues in medicinal materials, the author will show the research, development, and application of new safety control technologies, focusing on target discovery, molecular structure analysis, probe design, and analysis system development.

IL27: How Australian Native Plants and Our Gut Microbiome Could Revolutionise Cancer Therapy?

Indeewarie Hemamali Dissanayake[1], Kayla Jaye[1], Radwa Eladwy[1], Ahmad Al-Khazaleh[1], Wahida Tabassum[1], Muhammad Alsherbiny[2], Dennis Chang[1], Eshetu Mulisa Bobasa[3], Oladipupo Adiamo[3], Deep Jyoti Bhuyan[1]*
[1]NICM Health Research Institute, Western Sydney University, Penrith, NSW, Australia
[2]Thermo Fisher Scientific, Scoresby, Melbourne, Victoria, Australia
[3]Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Brisbane, Queensland, Australia

Australia's diverse flora, characterized by unique chemical profiles, has evolved in response to harsh climates, environmental stresses, and geographical isolation. These factors collectively endow Australian plants with significant potential for medicinal applications. Indigenous communities in Australia have utilised this rich flora as sources of food and medicine for millennia. Notably, Australian native plums such as Illawarra plum (*Podocarpus elatus)*, Kakadu plum (*Terminalia ferdinandiana*), and Davidson's plum (*Davidsonia pruriens*) are now commercially cultivated in Australia and possess polyphenol concentrations significantly higher than those found in most Western fruits[1]. Among these, Kakadu plum is recognised as the world's richest natural source of vitamin C, exceeding the content of both other native and Western fruits. We recently demonstrated the anti-proliferative effects of Australian native Kakadu plum, Illawarra plum, and Davidson's plum against MCF7 breast adenocarcinoma cells, attributable to the induction of apoptosis and strong antioxidant activities[2]. Additionally, our research identified abundant phenolic compounds as potential bioactive metabolites in Kakadu plum extracts [2]. Despite these promising results, the bioavailability and broad-spectrum therapeutic properties of Australian native fruits remain largely underexplored in the scientific literature.
The gut microbiota—comprising trillions of microorganisms residing in the human gastrointestinal tract—plays an essential role in food metabolism, nutrient and drug absorption, and in maintaining overall health and preventing disease. The specific composition of an individual's gut microbiota can significantly influence the absorption of nutrients, including phytochemicals. Approximately 95% of phenolic compounds that are not absorbed in the upper gastrointestinal tract can be metabolised by healthy gut microbiota into smaller phenolic metabolites, which are subsequently absorbed in the colon. Consequently, even with a nutritious diet or adequate nutrient intake, alterations in the gut microbiota may impede effective nutrient absorption. Although microbiome-targeted dietary interventions, such as prebiotics and probiotics, are widely available and show promise, their effectiveness is largely dependent on the adaptability of the gut microbiome. Restoring a disrupted gut microbiome, however, remains a considerable challenge due to the complex interplay of environmental (e.g., diet, antibiotics) and biological (e.g., individual variation, disease, ethnicity) factors. In this context, postbiotics represent an innovative approach to enhancing personalised nutrition and medicine. Our research group, along with others, has demonstrated that the gut microbiota exerts its functions by producing metabolites known as postbiotics (also referred to as gut microbial metabolites)[3,4]. Our recent work has expanded the understanding of postbiotics, such as butyrate, in cancer research[5-8]. Additionally, we are developing probiotic lactic acid bacteria (LAB)-based fermentation strategies to generate postbiotics with enhanced bioavailability and bioactivity from Australian native fruits, including Kakadu plum, Davidson's plum, and Illawarra plum[9]. This presentation will summarize our latest findings regarding the anticancer properties and chemical profiles of both LAB-fermented and unfermented Australian native fruit extracts and will address the current challenges and future directions in this emerging field of oncology and nutrition.

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IL28: Translating Bioactive Delivery Science into Commercial Functional Food Products: From Patents to Global Market Impact

Ali Rashidinejad
Associate Professor, Massey University, New Zealand

The growing global demand for health-promoting foods has accelerated the need for scientifically validated bioactive ingredients and effective delivery systems capable of preserving their functionality within complex food matrices. This invited lecture outlines an integrated research program that translates bioactive delivery science into commercially viable functional food products. The work spans the extraction and isolation of polyphenols, carotenoids, probiotics, and other bioactive compounds from diverse natural sources, including indigenous New Zealand botanicals, followed by the development of advanced micro- and nano-delivery systems such as liposomes, emulsions, protein self-assemblies, co-precipitates, and nanoparticles. These technologies enhance the stability, bioavailability, and targeted efficacy of bioactives, enabling their successful incorporation into next-generation food systems. A key focus in our research group is the application of these delivery innovations to functional dairy products and specialized foods designed for individuals with chronic health conditions. Notably, patented delivery platforms and prototype products emerging from this research have been licensed to industry partners for global commercialization, demonstrating a rare and impactful translation from laboratory innovation to market-ready solutions. Recent interdisciplinary collaborations, spanning chemical engineering, clinical nutrition, and Māori communities, further support the development of culturally grounded, clinically relevant, and sustainable functional food products. This presentation highlights the scientific foundations, technological advancements, and commercial pathways that collectively advance the “Food as Medicine” paradigm.

IL29: The Potential Effects of Berries on Skin Aging

Francesca Giampieri
Department of Clinical Sciences, Polytechnic University of Marche, Ancona Italy

Skin aging is a complex biological process driven by both intrinsic factors, such as immunosenescence and inflammation, and extrinsic factors, including ultraviolet radiation, pollution, tobacco exposure, and poor nutrition. These stimuli contribute to increased reactive oxygen species production and oxidative stress, promoting cellular damage, senescence, extracellular matrix remodeling, and impaired tissue repair. In this context, plant-based bioactive compounds from functional foods represent promising natural strategies to support healthy skin aging. This presentation summarizes the research experience of the Bioenergetics Lab at the Polytechnic University of Marche on strawberry-and blueberry-derived bioactive compounds and their application in skin health. Strawberries and blueberries are highlighted as valuable models due to their richness in vitamin C, folate, anthocyanins, and their high total antioxidant capacity. In vitro studies using human dermal fibroblasts, keratinocytes, and macrophages exposed to different oxidative, inflammatory, microbial, or UV-related stressors showed that berry-based formulations may improve cell viability, reduce apoptosis, decrease intracellular ROS levels, modulate inflammatory biomarkers, and support mitochondrial function. These findings supported the development of two pre-industrial skincare prototypes: a daily moisturizer and a sunscreen enriched with berry extracts and selected antioxidant compounds. Stability testing, antioxidant capacity assessment, patch testing, and photopatch testing conducted in human volunteers confirmed the safety and potential applicability of these formulations. Overall, this research supports the use of plant-based functional ingredients as innovative, natural, and eco-sustainable tools for healthy skin aging and cosmeceutical development.

IL30: Anti-Inflammatory and Anti-Osteoarthritis Effects of *Baccharis dracunculifolia* Intake in Rats

Alberto Carlos Pires Dias
CBMA – Centro de Biologia Molecular e Ambiental, Department of Biology, University of Minho, Campus de Gualtar, 4710– 057 Braga, Portugal

In arthritic disorders both inflammation and the progressive degeneration of joints persistently activate nociceptors, in periarticular structures, leading to the development of persistent pain and comorbid emotional impairments. Arthritis-induced peripheral sensitization leads to increased release of nociceptive molecules by primary afferents that activate neurones e glial cells in the spinal cord and supraspinal pain modulatory areas such as the amygdala (AMY) and the periaqueductal grey matter (PAG). *Baccharis dracunculifolia* DC (Asteraceae) (Bd) is a Brazilian plant, an important component of the green propolis, consumed worldwide and considered to be an important source of anti-inflammatory compounds. Adult 8 weeks old ovariectomized female Wistar rats weighting 210 ± 17 g were divided in four groups (n = 6 per group): (i) SHAM, (ii) ARTH, (iii) ARTH treated with Bd (50 mg/kg), and (iv) ARTH treated with Bd (100 mg/kg). Mechanical hyperalgesia in ARTH animals was assessed using the pressure application measurement apparatus, anhedonia using the sucrose preference test and learned helplessness using the forced swimming test. Activated microglia was stained with IBA-I and quantified in a subset of brain slides containing the target areas, the amygdala and the periaqueductal gray matter. A three-week oral treatment with Bd extract reversed ARTH-induced mechanical hyperalgesia and partly reserved depressive-like behaviour. Concomitantly, Bd decreased the number of activated microglia in the AMY and PAG of ARTH animals. Also, Bd consumption reduced significantly the degradation and inflammation of knee.

IL31: Targeting Obesity through Bitter Taste Receptors: The Role of Plant-Derived Specialized Metabolites

Luigi Milella
University of Basilicata, Department of Health Sciences, v.le dell'Ateneo Lucano Potenza – 85100, Italy

Bitter taste receptors (T2R or Tas2r) play a key role in regulating various physiological processes, including the modulation of enteroendocrine hormone secretion involved in appetite regulation. Bitter taste receptors (T2Rs), once thought to function only in the oral cavity, are now known to be widely expressed throughout the body, including in the gastrointestinal tract, lungs, and even the brain. These receptors are activated by a diverse range of bitter compounds, such as flavonoids, alkaloids, terpenes, and bitter acids, many of which are naturally occurring in plants. In the gut, for example, the activation of T2Rs by these compounds can stimulate the release of hormones that regulate appetite, glucose metabolism, and digestion. Their intestinal expression makes them potential therapeutic targets for controlling caloric intake and preventing obesity and overweight[1]. Our research activity aims to investigate the role of bitter compounds from hops (*Humulus lupulus* L.), such as α-acids, β-acids, and xanthohumol, in the secretion of anorexigenic hormones (GLP-1 and CCK) and in inducing the expression of T2R receptors in STC-1 intestinal cells[2]. This study thus provides a solid foundation for the development of T2R agonists based on bitter compounds from hops

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IL32: Oxygen-Driven Thermal Degradation of Isorhamnetin in Boiling Water and Its Lipid-Lowering Effects in *C. elegans*

Hui Cao
Universidade de Vigo, Nutrition and Bromatology Group, Department of Analytical and Food Chemistry, Faculty of Sciences, 32004 Ourense, Spain

Dietary flavonoids readily undergo structural transformations during thermal processing; however, it remains unclear whether the biological activities observed after heating are attributable to the residual parent compounds or to their thermal degradation products. This study constructed a time-resolved three-dimensional product-structure-activity network for isorhamnetin (ISO) in boiling water. A total of 12 products were identified and classified into phenolic acids, hydroxylated adducts, and dimers. Density functional theory (DFT) calculations supported a degradation mechanism involving quinone formation, nucleophilic attack at the C2 position, and cleavage of the C-ring. Further biological evaluation revealed that ISO and its major degradation products, phloroglucinol (PG) and 2,4,6-trihydroxybenzoic acid (THBA), alleviate glucose-induced metabolic reprogramming and lipid accumulation in *Caenorhabditis elegans* through a DAF-16/FOXO-dependent mechanism associated with H3K4me3/H3K27me3. Overall, this work provides a structural map of ISO under cooking-like conditions and offers new insights into the preservation of polyphenol bioactivity during thermal transformation (Figure 1).

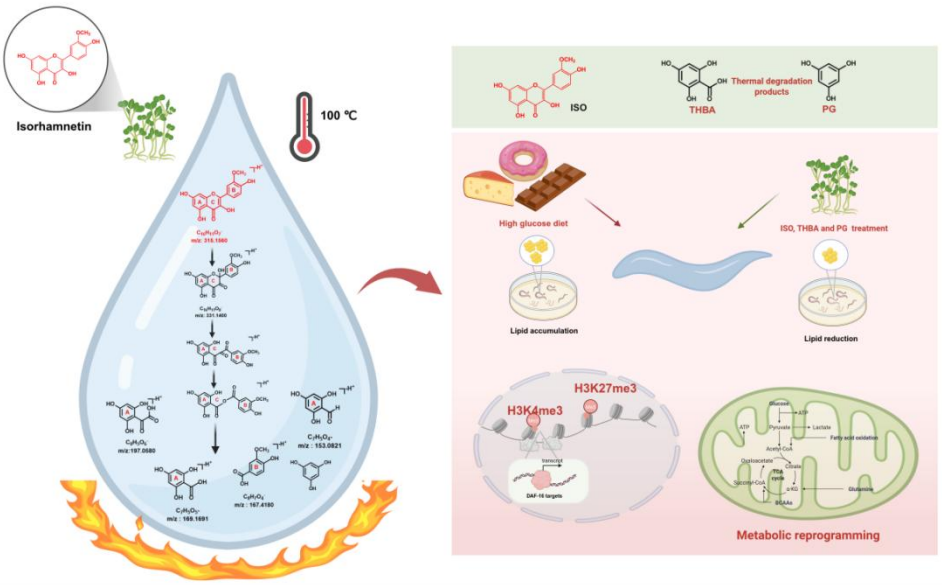

Figure 1. Mechanism of ISO and its thermal degradation products in alleviating lipid accumulation in *Caenorhabditis elegans*.

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IL33: Glucosinolate-Rich *Brassica rapa* as a Functional Food Candidate for Mitigating Diet-Induced Hepatic Steatosis

Seok-Geun Lee
Department of Biomedical Science and Technology, Kyung Hee University, Seoul 02447, Republic of Korea

Metabolic dysfunction-associated steatotic liver disease (MASLD) is a highly prevalent chronic liver disorder closely linked to obesity, insulin resistance, oxidative stress, and dysregulated hepatic lipid metabolism. Because no broadly approved pharmacological therapy is currently available, dietary approaches using functional food materials have attracted increasing attention. Glucosinolates are characteristic phytochemicals of cruciferous vegetables and are converted into bioactive isothiocyanates with antioxidant, anti-inflammatory, and metabolic regulatory activities. We previously developed high-glucosinolate (high-GSL) *Brassica rapa* lines through conventional breeding and demonstrated their enhanced antioxidant, anti-inflammatory, and anticancer activities. In the present study, we evaluated whether these high-GSL *B. rapa* lines could ameliorate hepatic steatosis using complementary in vitro and in vivo models. Two high-GSL *B. rapa* lines, DH014 and DH026, generated markedly higher levels of major isothiocyanates, including sulforaphane and phenethyl isothiocyanate, than conventional pak choi. In free fatty acid-induced steatotic HepG2 hepatocytes, treatment with DH014 or DH026 reduced intracellular lipid accumulation, triglyceride, cholesterol, free fatty acid levels, reactive oxygen species, and pro-inflammatory cytokine expression. Mechanistically, high-GSL *B. rapa* lines activated AMPK-SIRT1 and NRF2-related signaling, increased fatty acid oxidation-associated genes, and suppressed SREBP1c-mediated lipogenic gene expression. In high-fat diet-fed mice, oral supplementation with DH014 or DH026 attenuated body weight gain, visceral adipocyte, hepatic lipid deposition, NAFLD activity score, and dyslipidemia. These beneficial effects were accompanied by hepatic activation of AMPK/SIRT1 and NRF2 pathways, induction of antioxidant genes, and suppression of inflammatory markers. Collectively, these findings suggest that glucosinolate-rich *B. rapa* lines may serve as promising functional food resources for mitigating diet-induced hepatic steatosis by coordinating metabolic reprogramming and antioxidant defense. This work highlights the translational potential of phytochemical-enriched vegetables for dietary management of MASLD.
Note: This presentation is based on our recent publication: Kim et al., Food Bioscience, 2026, 78, 108487.

Oral Presentation

OL1: Development & Utilization of Lingnan *Citrus* Medicinal-Edible Resources:A Gonggan Mandarin Case

Liu Huifan[1]*, Wang Qin[1,2], Xiao Gengsheng[2], Xie Xi[1,2]
[1]Key Laboratory of Green Processing and Intelligent Manufacturing of Lingnan Specialty Food of Ministry and Rural Affairs, College of Light Industry and Food, Zhongkai University of Agriculture and Engineering, Guangzhou, China
[2]Guangdong Provincial Key Laboratory of Lingnan Specialty Food Science and Technology, Zhongkai University of Agriculture and Engineering, Guangzhou, China
[3]Lingnan Special Food-Medicine Homology Diet Nutrition and Health Engineering Research Center, Guangzhou, China
[4]State Key Laboratory of Food Science and Resources, Nanchang University, Nanchang, China

Lingnan citrus fruits are valuable medicinal–edible resources whose phytochemical composition strongly influences their nutritional quality, functional properties, and utilization potential. Using Gonggan mandarin as a representative Lingnan medicinal–edible citrus resource, this work examined how pectin structure and processing jointly determine cloudy-juice quality and broader utilization potential. Structural studies of Gonggan pectin polysaccharides established relationships among molecular architecture, branching, aggregation, and physicochemical behavior, providing the basis for subsequent processing research[1]. High-pressure homogenization promoted pectin solubilization and reshaped the volatile profile; treatment at 400 bar achieved a favorable balance between soluble pectin release and citrus aroma, whereas excessive pressure increased off-flavor formation[2]. Thermal sterilization induced simultaneous pectin depolymerization and aggregation, with treatment at 80oC better preserving colloidal stability and citrus–floral notes than higher temperatures[3]. Enzymatic hydrolysis loosened compact pectin assemblies, generated shorter and more flexible chains, and enhanced anti-inflammatory activity through suppression of MAPK/ERK signalling and downregulation of iNOS and COX-2. Beyond the Gonggan juice studies, process-compatible α-L-rhamnosidase and cold-active protease systems were developed for citrus debittering and mild whole-fruit conversion, including recyclable whole-cell catalysis and application in pomelo products[4]. A structure–activity-oriented data framework was further incorporated to support component screening, process optimization, and product development[5-5]. These studies connect molecular structure, processing response, biological function, and industrial application, providing a coherent route for the high-value utilization of Lingnan citrus resources.

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OL2: Improving Consumer Food Safety Practices: Opportunities to Reduce Food Waste, Support Public Health and Sustainability Goals

Maja Bensa[1]*, Mojca Jevšnik Podlesnik[2], Irena Vovk[3]
[1]Research Institute of Faculty of Health Sciences, Faculty of Health Sciences, University of Ljubljana, Ljubljana, Slovenia
[2]Department of Sanitary Engineering, Faculty of Health Sciences, University of Ljubljana, Ljubljana, Slovenia
[3]Laboratory for Food Chemistry, National Institute of Chemistry, Ljubljana, Slovenia

Food systems face increasing pressure from population growth, climate change and the need to reduce environmental impacts. At the same time, substantial amounts of food are lost and wasted throughout the food supply chain with estimates indicating that 13% of food is lost in the supply chain from harvest before retail and an additional 19% is wasted in retail, food service and households[1]. Consumer food safety practices can influence both food safety and food waste through food handling, storage and interpretation of date labels. The aim of this study was to investigate food safety knowledge, attitudes and practices among Slovenian consumers and identify behaviors that may contribute to food waste and public health risks. The Consumer Food Safety Study (CFSS) used a mixed methods approach with a validated online questionnaire (n=1621) and focus groups (n=40) to examine food safety knowledge, attitudes and practices of Slovenian consumers aged 18 years and older. Participants had varying demographics (gender, age, education). In the investigation of everyday consumer food handling, different consumer behaviors and food safety challenges that can contribute to food waste and public health risks were identified. Areas with room for improvement included using cooler bags for transportation when food shopping, understanding of expiration date labeling and handling of food with expired dates, reading and following storage and preparation instructions on food labels, knowing and measuring the temperatures in refrigerators, storing leftover foods, etc. Misinterpretation of "best before" and "use by" dates can lead to both premature food disposal and unsafe consumption. It is important that consumers take care of the temperature at which food is stored from purchase until consumption–especially for ready to eat and perishable foods–as this ensures food safety, prevents spoilage and helps preserve the nutritional content. An important guidance for ensuring food safety are also instructions for storage and food preparation included on labels of some food products on some food labels. The findings suggest that consumer food safety practices represent an important yet often overlooked leverage point for simultaneously improving food safety, reducing household food waste and supporting sustainability objectives. Consumer food safety practices not only affect the safety of their food but also influence the sustainability of the food system. Enhancing consumer food safety knowledge, attitudes and practices through targeted education campaigns could contribute to reaching public health and climate goals by maintaining food safety, preserving nutritional value and reducing food waste.

Acknowledgments
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OL3: Mechanistic Investigation of a Flavonoid-Enriched Fraction and Procyanidin C1 Derived from *Cynomorium songaricum* in Preserving Pancreatic β-cell Function under Diabetogenic Stress

Jihang Chen*, Xinyue Li, Zhihao Liu, Yuzi Jiang
Shenzhen Key Laboratory of Steroid Drug Discovery and Development, School of Medicine, The Chinese University of Hong Kong, Shenzhen, Guangdong, 518172, China

Type 2 diabetes mellitus (T2DM) is characterized by progressive pancreatic β-cell dysfunction, leading to impaired insulin secretion and persistent hyperglycemia1. Preserving β-cell function has therefore become an important therapeutic strategy for delaying disease progression2. Our previous studies demonstrated that a standardized flavonoid-enriched fraction from *Cynomorium songaricum* (CSF) effectively protects pancreatic β-cells against glucolipotoxicity-induced injury. Using an integrated transcriptomic analysis and network pharmacology-guided target identification strategy. In the present study, we screened the major constituents of CSF and identified procyanidin C1 (PCC1) as the most active compound for β-cell protection. The protective effects of both CSF and PCC1 were evaluated using high glucose/high palmitic acid-treated Min6 cells and a high-fat diet-induced diabetic mouse model. CSF significantly improved β-cell viability, reduced apoptosis, and restored glucose-stimulated insulin secretion (GSIS). Mechanistic studies demonstrated that CSF alleviated endoplasmic reticulum (ER) stress by suppressing activation of the PERK, IRE1α, and JNK pathways, while simultaneously improving mitochondrial function through restoration of mitochondrial membrane potential, oxidative phosphorylation capacity, and reduction of intracellular reactive oxygen species (ROS). In addition, CSF preserved β-cell identity by reversing dedifferentiation and maintaining mitochondria-associated membrane (MAM) homeostasis. To further elucidate the molecular basis of these protective effects, an integrated transcriptomic analysis combined with network pharmacology-guided target screening was performed, which identified SERCA2 as the most promising therapeutic target of CSF. Target engagement was subsequently confirmed by cellular thermal shift assay (CETSA), and pharmacological inhibition of SERCA2 largely abolished the protective effects of CSF, supporting a SERCA2-dependent mechanism. These protective effects were consistently observed in diabetic mice, where CSF improved glucose homeostasis and metabolic parameters and restored the expression of ER stress-, oxidative phosphorylation-, MAM-, and β-cell identity-related proteins in pancreatic tissues. Based on these findings, PCC1 was identified as the major bioactive constituent of CSF. Similar to CSF, PCC1 significantly increased Min6 cell viability, inhibited apoptosis, restored GSIS, improved mitochondrial function, attenuated ER stress, and prevented β-cell dedifferentiation under glucolipotoxic conditions. The comparable protective effects of PCC1 suggest that it contributes substantially to the pharmacological activity of CSF. Collectively, our findings demonstrate that both CSF and its active constituent PCC1 effectively preserve pancreatic β-cell function by alleviating ER stress, improving mitochondrial function, maintaining β-cell identity, and protecting against glucolipotoxicity-induced injury. These results provide mechanistic evidence supporting CSF as a promising botanical intervention for T2DM and identify PCC1 as a key bioactive constituent that may serve as a lead compound for future β-cell-protective drug development.

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OL4: Afternoon Shading of Grapevine Regulates Berry Development and Flavor Profile in Cabernet Sauvignon Grapes and Wines

Mengbo Tian[1,2], Ruiling Liu[1], Haiyan Gao[1], Jun Wang[2]*
[1]State Key Laboratory for Quality and Safety of Agro-Products, Zhejiang Key Laboratory of Intelligent Food Logistic and Processing, Key Laboratory of Post-Harvest Fruit Processing, Ministry of Agriculture and Rural Affairs, Institute of Food Science, Zhejiang Academy of Agricultural Sciences, Hangzhou 310021, China
[2]Center for Viticulture and Enology, College of Food Science and Nutritional Engineering, China Agricultural University, Beijing 100083, China

To mitigate the rapid ripening by afternoon high temperature in semi-arid wine regions, grapevine artificial shading was applied in a three-year experiment (2021-2023) in northwest China. The moderate shading (1.5 h, MD) and strong shading (2.5 h, SD) were applied in the afternoon. Climatic parameters were collected, flavonoids and volatiles of grapes and wines were determined by HPLC-MS and GC-MS. Results revealed that photosynthetic assimilation of grapevines was suppressed by 50% during shading, while photosynthesis during exposure and leaf area were enhanced. Shading reduced the berry surface temperature by up to 4 °C and delayed sugar accumulation, resulting in grapes with higher acidity (~1 g/L) and lower Brix (~0.5 °Brix) at harvest. Berry volatiles in MD and SD were 16% and 10% lower than CK at 2021 harvest but were enhanced in the latter two years. Linalool, hexanal, β-damascenone, and 6-methyl-5-hepten-2-one were key light-responsive biomarkers. MD and SD wines had lower flavonols, red hue, and anthocyanin derivates. Specific non-methylated anthocyanins and kaempferol-based flavonols were bioindicators of solar radiation. Shaded wines exhibited elevated levels of terpenoids and norisoprenoids, contributing to improved fruity-floral aromas and sensory scores in 2022 and 2023. Overall, afternoon shading delays grape ripening and regulates grape flavonoid and volatile profiles, thus modifies wine flavor and sensory distribution. This study provides insights into regulating grape and wine quality in semi-arid regions.

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OL5: Lactic Acid Bacteria as Edible Pickering Particles: Surface-Dependent Screening and Oleogel Stabilization Mechanisms

Xiaoyi Jiang, Ping Yin, Ying Wang, Yong Fang*
College of Food Science and Engineering, Nanjing University of Finance and Economics/Collaborative Innovation Center for Modern Grain Circulation and Safety, Nanjing 210023, China

Lactobacillus cells have recently emerged as promising natural Pickering stabilizers because of their amphiphilic surface characteristics and potential postbiotic functionality[1], offering new opportunities for the development of clean-label structured lipids[2,3]. However, despite increasing interest in bacteria-stabilized emulsions, the relationships between bacterial surface chemistry, emulsion stabilization, and the formation of emulsion-templated oleogels remain poorly understood. In this study, the surface properties of 42 *Lactobacillus* strains were first systematically characterized using complementary physicochemical techniques, including microbial adhesion to solvents, contact angle measurement, ζ-potential analysis, FTIR, and XPS. Multivariate analysis classified the strains into four representative groups, from which eight strains were selected to investigate the influence of surface properties on Pickering emulsion formation and stability. Based on their distinct emulsion characteristics, four representative strains were subsequently employed to fabricate emulsion-templated oleogels. The results demonstrated that bacterial hydrophobicity predominantly governed interfacial adsorption and emulsion-template stability, whereas surface charge regulated bacterial spatial distribution and the architecture of the resulting oleogel networks. Distinct stabilization pathways, including interfacial adsorption alone or in combination with bacterial aggregate-mediated droplet anchoring, produced markedly different network structures and mechanical properties[4]. Overall, this work establishes a comprehensive structure–function relationship linking bacterial surface chemistry to emulsion stabilization and oleogel performance. These findings provide mechanistic insight into the rational selection of bacterial strains and the design of clean-label, bacteria-based structured lipids for future functional food applications.

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OL6: Processing Characteristics, Functional Mechanisms, and High-Value Utilization of Buckwhea

Minglong Wang, Lan Zhang, Renzhi Lv, Yiming Zhou*
Faculty of Flavour Fragrance and Cosmetics, Shanghai Institute of Technology, Shanghai 201418, China

Buckwheat is rich in core functional components such as starch, protein, and flavonoids. It exhibits multiple physiological activities, including antioxidant effects, regulation of glucose and lipid metabolism, and modulation of intestinal health, making it a high-quality raw material for the development of functional foods and specialized diets. This work systematically analyzes the functional properties, interaction mechanisms, and processing modification rules of the three core components, and constructs a full-chain utilization technology system for buckwheat resources that enhances quality and efficiency, and realizes high value[1].

The three core components of buckwheat possess unique physicochemical and functional properties, and there exists a close mutual regulatory relationship among them[2]. Buckwheat starch can form an amylose-flavonoid complex, generating a low-digestibility structure. The derived resistant starch has excellent postprandial blood glucose regulation and intestinal modulation functions, and its digestion kinetics can be precisely regulated through various processing methods. Buckwheat protein has excellent functional properties, among which 13S globulin is the core functional and allergenic carrier. It can also be degraded to produce highly active antioxidant peptides, exerting a cell-protective effect; however, its allergenicity is a key pain point restricting its consumption. Flavonoid monomers such as rutin and quercetin in buckwheat can inhibit starch digestive enzymes and non-enzymatic glycosylation reactions, and have strong antioxidant activity, but their activity and bioaccessibility are easily affected by external conditions such as thermal processing.

The interaction between components is the core key to the quality and function regulation of buckwheat. Studies have shown that the interaction between protein and flavonoids can significantly change the spatial structure and functional properties of buckwheat protein. The complexation of starch and flavonoids can construct a stable low-digestibility system, effectively improving the low-GI characteristics and physiological activity of buckwheat products, and overcoming the processing shortcomings of starch, such as easy retrogradation and rapid digestion[3]. Meanwhile, processing modification technologies can positively regulate the component interaction effect. Technologies such as physical modification, microbial fermentation, and enzymatic hydrolysis can mediate flavonoid biotransformation, protein degradation and desensitization, and starch structure optimization, thereby enhancing the synergistic antioxidant and glucose-lipid metabolism regulation effects of the three components.

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OL7: Sinensetin Alleviates Metabolic Dysfunction-Associated Steatotic Liver Disease via Gut-Liver Axis in the High-Fat Diet Mice

Zuomin Hu*, Zhengwen Li, Zhongxing Chu, Yaping Zhou, Feijun Luo, Jiali Ren
Hunan Key Laboratory of Deeply Processing and Quality Control of Cereals and Oils, State Key Laboratory of Utilization of Woody Oil Resource, Hunan Key Laboratory of Forestry Edible Resources Safety and Processing, Central South University of Forestry and Technology, Changsha, 410004, Hunan, China

In recent years, the global prevalence of obesity has increased[1]. As the central organ for lipid metabolism, the liver is most adversely affected in obesity[2]. Metabolic dysfunction-associated steatotic liver disease (MASLD) is the primary hepatic disease resulting from prolonged lipid metabolism disorders. The prevalence of MASLD among the global overweight or obese population is approximately 50%[3]. In the early stages, MASLD patients typically do not exhibit noticeable symptoms. However, the disease can

easily progress to high-risk conditions or lead to complications[4,5]. Food-derived natural products are considered potential candidate agents for alleviating MASLD due to their accessibility and safety. Sinensetin (SIN) is a dietary flavonoid widely present in the citrus peel, and it has multiple biological functions[6]. However, the mechanism by which SIN alleviates MASLD remains unclear. Our research showed that SIN treatment ameliorated HFD-induced dyslipidemia and hepatic dysfunction, as well as pathological changes in the liver, epididymal fat pad and colon, while restoring gut barrier function. Furthermore, SIN suppressed the abnormal expression of HFD-induced lipogenic genes and inflammatory factors in the liver. Combined 16S rRNA and metabolomics analyses indicated that SIN improved gut microbiota dysbiosis and associated metabolic alterations in MASLD mice. KEGG analysis revealed that SIN affected lipid metabolism in the gut microbiota, as evidenced by changes in α-linolenic acid and linoleic acid metabolism. Gut microbiota analysis showed that SIN treatment increased the abundance of *Lactobacillus*_johnsonii and Limosilactobacillus_reuteri, which correlated with improved serum lipid profiles, enhanced gut barrier function and reduced hepatic lipid toxicity. Fecal samples collected from HFD+SIN group mice were used for fecal microbiota transplantation (FMT), which subsequently improved MASLD in recipient mice. Lipidomics suggested that SIN-modulated gut microbiota might alleviate MASLD by regulating glycerophospholipid metabolism in the liver. Collectively, these findings indicate that SIN might alleviate HFD-induced MASLD through regulation of the gut-liver axis.

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OL8: Transporter-Modulating Anthocyanin Nanoparticles for Stabilized and Efficient Delivery

Zhiying Li[1,2], Qilin Tian[1,2], Bin Li[1,2]*
[1]College of Food Science, Shenyang Agricultural University, Shenyang, Liaoning, 110866, China
[2]Key Laboratory of Healthy Food Nutrition and Innovative Manufacturing, Shenyang, Liaoning, 110866, China

Anthocyanins (ACNs) exhibit poor stability and low bioavailability[1,2]. These limitations restrict their functional activity and applications in food processing. In this study, we prepared ACNs-loaded nanoparticles by synthesizing thiolated hyaluronic acid and assembling THA/FA-zein@ACNs. The nanoparticles showed uniform spherical shape with a size of 91.35 nm (PDI=0.154 ± 0.023), and exhibited robust stability against processing and digestive stress. Caco-2 assays revealed their specific affinity for sodium-glucose cotransporter 1 (SGLT1), enabling active recognition, with SGLT1-mediated uptake being 2.3-fold higher than that mediated by glucose transporter 2 (GLUT2). The system effectively inhibited P-glycoprotein (P-gp)-mediated efflux, creating a "push-pull" mechanism that maximizes absorption[3,4]. Free ACNs exhibited a short half-life (0.528 ± 0.105) h, while THA/FA-zein@ACNs prolonged T1/2 to (1.611 ± 0.372) h. The nanoparticles also modulated gut microbiota and enhanced intestinal barrier function. This work provides a theoretical and practical foundation for the precise, high-efficiency delivery of functional bioactives.

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OL9: Characterisation and Screening Analysis of Haze-active Proteins in Thawed Cloudy Huyou (*Citrus changshanensis*) Juice Using a Data-independent Acquisition Proteomics Technique

Boyuan Guan[1,2,3,4], Qiong Huang[3], Wenjun Wang[1,2]*, Donghong Liu[1,2]*
[1]College of Biosystems Engineering and Food Science, Zhejiang University, Hangzhou 310058, China
[2]Innovation Center of Yangtze River Delta, Zhejiang University, Jiashan 314100, China
[3]Changshan Aijia Huyou Food Research and Development Center, Zhejiang Aijia Food Co., Ltd., Changshan 324200, China
[4]College of Food Science, Fujian Agriculture and Forestry University, Fuzhou, Fujian 350002, China

Turbidity loss is a significant issue in thawed huyou (*Citrus changshanensis*) juice, and understanding the composition of the precipitate is essential for effective control. In the present study, data-independent acquisition proteomics was used to investigate precipitation-related proteins in thawed cloudy huyou juice (TCHJ). A total of 1,268 precipitation-related proteins were identified, the majority of which were localised in the chloroplast and predominantly contained P-loop NTPase domains. By cross-referencing various bioinformatics algorithms, 33 pivotal haze-active proteins were identified. The three-dimensional structures of haze-active proteins were constructed using artificial intelligence algorithms, and molecular docking simulations revealed that these proteins interact with haze-active small molecules primarily through van der Waals forces and hydrogen bonds, leading to flocculation and precipitation in the TCHJ. Fluorescence spectroscopy analysis revealed that the primary static quenching mode exists between the precipitated protein and the haze-activated small molecules; the binding ability and stability between the precipitated protein with the haze-activated small molecules were clarified; and the non-covalent binding mechanism was verified. The findings of this study provide a deeper understanding of the precipitated protein system in TCHJ, providing technical support for future theoretical and process studies on the protein stability of TCHJ.

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OL10: Early Nutritional Intervention for Chronic Low-grade Inflammation and Construction of the Food Inflammation Index

Zhangtie Wang[1,2]*, Baiyi Lu[1,2]*
[1]Zhejiang University (ZJU) Hangzhou Global Scientific and Technological Innovation Center, Hangzhou, China
[2]College of Biosystems Engineering and Food Science, Key Laboratory for Agro-Products Nutritional Evaluation of the Ministry of Agriculture and Rural Affairs, Zhejiang University, Hangzhou, China

Diet is a primary driver of systemic chronic inflammation, yet quantitative assessments of the inflammatory potential of individual foods remain scarce. Crucially, current dietary frameworks often overlook the substantial variations in inflammatory effects among foods within the same food category. Here, we present a Food Inflammation Index (FII), derived from comprehensive Food Composition Tables, to systematically quantify and compare these effects. Our analysis reveals pronounced intra-group heterogeneity within standard dietary guidelines, showing that even strict adherence to a Mediterranean diet can harbor unanticipated inflammatory risks if intra-group variations are ignored. Utilizing the United States Department of Agriculture Food Composition Database, the FII identifies nuts and specific vegetable oils—abundant in flavonoids and n-3 polyunsaturated fatty acids—as potent anti-inflammatory agents, contrasting sharply with pro-inflammatory, saturated-fat-rich meats. These findings underscore that broad food classifications fail to capture the nuanced inflammatory profiles of foods, and that further subdivision of dietary categories is essential for precision nutrition. By quantifying the inflammatory footprint of whole foods, the FII serves as a robust public health tool to empower consumer choice, refine dietary guidelines, and guide clinical research. Furthermore, we review recent advances in early nutritional interventions targeting chronic low-grade inflammation—a critical, reversible precursor to chronic disease. We delineate five distinct mechanisms through which dietary components modulate inflammation: metabolic digestion and absorption, gut microbiota interactions, intracellular biochemical regulation, signal transduction pathways, and structural integration into cellular components. Ultimately, mapping these pathological and therapeutic pathways offers a blueprint for targeted dietary interventions across varying stages of chronic inflammation.

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OL11: Ginsenoside Rb1 Alleviates Aging by Regulating Mitochondrial Function

Meitong Liu[1], Yuyang Huang[2], Yang Li[1]*
[1]College of Food Science and Engineering, Jilin University, Changchun, Jilin 130062, China
[2]Key Laboratory for Food Science & Engineering, Harbin University of Commerce, Harbin 150076, China

Aging is accompanied by a progressive decline in mitochondrial energy metabolism, disruption of Ca^{2+} homeostasis, and impairment of mitochondrial quality control, which together contribute to functional deterioration in metabolically active tissues. Ginsenoside Rb1 is a major bioactive constituent of ginseng with reported antioxidant and metabolic regulatory activities, yet the mitochondrial mechanisms underlying its anti-aging effects remain incompletely understood. This study investigated whether Rb1 alleviates cellular aging by restoring mitochondrial Ca^{2+} uptake and promoting the clearance of damaged mitochondria. C2C12 myoblasts were differentiated into myotubes using 2% horse serum and exposed to 20 mmol/L D-galactose for 48 h to establish a cellular senescence model. Senescence-associated β-galactosidase staining, ATP measurement, mitochondrial Ca^{2+} imaging, mitochondrial membrane-potential analysis, mitochondrial reactive oxygen species detection, and Western blotting were used to evaluate cellular aging and mitochondrial function. Rb1 reduced the senescent phenotype of C2C12 myotubes, increased intracellular ATP levels, and restored the reduced mitochondrial Ca^{2+} content observed in aging cells. Rb1 also reversed aging-associated alterations in proteins involved in mitochondria-associated endoplasmic reticulum membrane signaling and mitochondrial Ca^{2+} transport, including IP3R, GRP75, VDAC1, and MICU1. In concanavalin A-treated HepG2 cells, Rb1 decreased mitochondrial reactive oxygen species accumulation, restored mitochondrial membrane potential, and increased the expression of LC3-II, PINK1, and Parkin, indicating enhanced PINK1/Parkin-associated mitophagy. Collectively, these findings suggest that Rb1 alleviates aging-related mitochondrial dysfunction by coordinating Ca^{2+}-dependent energy metabolism with mitochondrial quality control. This work provides a mechanistic basis for the potential application of ginsenoside Rb1 in functional foods and healthy-aging interventions.

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OL12: Tailoring Amylopectin Architecture for Ideal Thixotropic Starch Materials: A Comparative Study of Enzymatic Trimming by α-amylase and Maltogenic α-Amylase

Bo Zhang[1,2,3,4], Yuxiang Bai[1,2,3,4], Xiaoxiao Li[1,2,3], Yanli Wang[5], Jingjing Dong[1,2,3], Zhengyu Jin[1,2,3,4]*
[1]State Key Laboratory of Food Science and Resources, Jiangnan University, Wuxi, Jiangsu 214122, China
[2]School of Food Science and Technology, Jiangnan University, Wuxi, Jiangsu 214122, China
[3]Collaborative Innovation Center of Food Safety and Quality Control in Jiangsu Province, Jiangnan University, Wuxi, Jiangsu 214122, China
[4]International Joint Laboratory on Food Safety, Jiangnan University, Wuxi, Jiangsu 214122, China
[5]College of Food Science and Engineering, Ningbo University, Ningbo 315211, Zhejiang, China
[6]College of Food Science, Fujian Agriculture and Forestry University, Fuzhou, Fujian 350002, China

Starch-based products frequently encounter sudden deformation during processing, necessitating rapid structural recovery for stability and optimal performance. This study explores the enzymatic tailoring of amylopectin side-chain architecture to achieve ideal thixotropic properties, characterized by a small hysteresis loop area, which indicates a fast recovery rate after shear. Waxy maize starch (WMS) was modified using α-amylase (AM) and maltogenic α-amylase (MA) to produce gels with varying but controlled thixotropic loop areas. Our objective was to understand how the distinct chain-shortening patterns of these enzymes influence the gel network structure and subsequent rheological performance. Our findings reveal that while both enzymes effectively reduced the hysteresis loop area, the underlying gel networks were fundamentally different. AM primarily hydrolyzed longer internal chains (DP 12-36), while MA preferentially shortened shorter chains (DP 10-17), thereby retaining a higher proportion of long chains. Consequently, MA-modified starch gels exhibited a significantly lower entanglement concentration, higher gel strength (storage modulus, G'), and greater final viscosity compared to AM-modified gels with an identical thixotropic loop area. Microscopy and water mobility analyses further confirmed that MA gels formed a more robust honeycomb-like network. In conclusion, the study demonstrates that shortening the outer short chains of amylopectin while preserving its long internal chains is a viable strategy for synthesizing starch-based materials with superior thixotropic properties. The MA-modified samples, possessing a more resilient gel network alongside rapid structural recovery, more closely resemble the characteristics of an ideal thixotropic material. This work provides a crucial theoretical foundation for the targeted structural regulation of starch to meet the demands of diverse industrial applications.

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OL13: Metabolic Alterations in Streptozotocin–Nicotinamide-Induced Diabetic Rats Treated with 50% Ethanol *Muntingia calabura L.* extract via 1H-Nmr-Based Metabolomics

Nur Khaleeda Zulaikha Zolkeflee[1], Faridah Abas[2]
[1]Natural Medicines and Products Research Laboratory, Institute of Bioscience, Universiti Putra Malaysia, Serdang, Selangor Malaysia
[2]Department of Food Science, Faculty of Food Science and Technology, Universiti Putra Malaysia, Serdang, Selangor, Malaysia

Diabetes mellitus (DM) is a metabolic endocrine disorder caused by decreased insulin concentration or poor insulin response. People are turning to herbal therapies and superfoods diet for diabetes management instead of relying on synthetic drugs with potential side effects. *Muntingia calabura* L. (MC) has been used traditionally to reduce blood glucose levels. However, these herbal medicines lack proper quality control and standardization, resulting in inconsistent and potentially unsafe products. To validate the traditional claim, the present study aimed to profile the metabolites and investigate the antidiabetic properties of MC in streptozotocin–nicotinamide (STZ-NA)-induced diabetic rats model by using proton nuclear magnetic resonance (1H-NMR)-based metabolomics approach. The 50% ethanolic freeze-drying (FD) MC leaves extract (MCE) significantly gave the highest total phenolic content (TPC) (434.00 ± 11.33 mg GAE/g crude sample) and the lowest IC_{50} value for the 2,2-diphenyl-1-picrylhydrazyl (DPPH) scavenging (7.87 ± 0.16 µg/ml), α-glucosidase inhibitory (0.46 ± 0.05 µg/ml) and α-amylase inhibitory (26.39 ± 2.11 µg/ml) activities. In an attempt to standardize the active extract, the MCE was subjected to ultrahigh performance-liquid chromatography-mass spectrometry (UHPLC-ESI-MS/MS) analysis for compound identifications and UHPLC quantitative measurements. A total of 61 compounds were tentatively identified from the MCE, including flavonoids, anthocyanins, chalcones, quinones, lactones, alkaloids, sugars, terpenoids and ellagitannins. Geniposide, daidzein, quercitrin, 6-hydroxyflavanone, kaempferol, and formononetin were quantified in MCE via UHPLC quantitative analysis to establish standardization for the extract. Subsequently, the acute toxicity of the MCE was tested on male and female Sprague-Dawley rats at a single dose of 2000 mg/kg body weight (bw). Through physical observations, hematological, biochemical, histopathological analyses and ^{1}H-NMR-based urinary metabolomic toxicity evaluation methods revealed no signs of toxicity and the LD_{50} of MCE was until 2000 mg/kg bw. Then, the efficacy of the MCE was determined through application of 1H-NMR-based urinary metabolomics and serum biochemical analyses. Three dosages of MCE were tested including 100 mg/kg bw MCE (MCE 100), 250 mg/kg bw MCE (MCE 250) and 500 mg/kg bw MCE (MCE 500). The serum biochemical analyses revealed that the MCE 250 dosage treatment showed favorable serum creatinine, urea and glucose lowering capacity, which was comparable to standard drugs, metformin. The oral treatment with MCE 250 on diabetic rats induced with 110 mg/kg bw NA and 45 mg/kg bw STZ showed improvements in the altered carbohydrate metabolism within the TCA cycle, gluconeogenesis, and pyruvate metabolism, affected the metabolism of cofactors and vitamins, particularly in nicotinate and nicotinamide metabolism, and improved the compromised waste excretion system related to purine and homocysteine metabolism. In conclusion, the results have validated the traditional claim on hypoglycemic effect of MC leaves and set the preliminary step towards the development of this herb into an alternative DM management regimens.

OL14: Soybean Oil Body-Stabilized Self-Assembled Emulsions with High Curcumin Delivery Efficiency and Nutraceutical Functions

Wenwen Lv[1,2], Duoxia Xu[3], Lianxin Peng[1,2]*
[1]College of Food and Bioengineering, Chengdu University, Chengdu, China
[2]Key Laboratory of Coarse Cereal Processing, Ministry of Agriculture and Rural Affairs, Chengdu, China
[3]College of Food and Health, Beijing Technology and Business University, Beijing, China

Aiming at the bottlenecks of curcumin including poor water solubility, low bioavailability and susceptibility to degradation, as well as the drawbacks of conventional delivery systems such as high energy consumption and inferior stability, soybean oil bodies (SOBs) were adopted as natural delivery carriers in this study. A low-carbon and green integrated aqueous extraction approach was developed to isolate intact SOBs, followed by the fabrication of soybean oil body-curcumin self-assembled emulsions and protein-polysaccharide co-stabilized Pickering emulsions. Their structural characteristics, stabilization mechanisms, in vitro gastrointestinal digestion profiles, and nutritional and health-promoting functions were systematically investigated. The results demonstrated that aqueous-extracted SOBs possessed intact structural integrity and were abundant in bioactive components including unsaturated fatty acids, tocopherols, phytosterols and phospholipids. The as-prepared nanoemulsions remarkably improved the photothermal and storage stability of curcumin, with its degradation half-life prolonged by 12 times; hydrogen bonding and hydrophobic interactions were identified as the predominant driving forces for emulsion stabilization. In vitro simulated digestion experiments revealed that the delivery matrix effectively shielded curcumin from pepsin-induced degradation. The Pickering emulsions achieved a maximum curcumin bioaccessibility of 83.96%. Moreover, the emulsions facilitated the transmembrane transport of calcium, iron and zinc via upregulating specific peptides, yielding a calcium bioaccessibility as high as 96.55%. In vivo animal assays verified that the delivery system alleviated colitis symptoms in mice, repaired intestinal barrier integrity, mitigated oxidative stress and the secretion of pro-inflammatory cytokines, and reshaped the composition of gut microbiota. Its anti-inflammatory activity was mediated by suppressing the PI3K/AKT-NF-κB signaling pathway. This study established a green and high-efficiency oil body-based delivery technology, providing theoretical basis and technical support for the high-value utilization of curcumin and other bioactive factors, as well as the development of functional foods for general health.

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OL15: Applications of Numerical Simulation in Ultrasonic Processing of Plant Proteins

Yue Wu[1]*, Yang Tao[1], Muthupandian Ashokkumar[2]
[1]College of Food Science and Technology, Whole Grain Food Engineering Research Center, Nanjing Agricultural University, Nanjing 210095, Jiangsu, China
[2]Sonochemistry Group, School of Chemistry, The University of Melbourne, Parkville, Victoria 3010, Australia

As a non-thermal processing technology, ultrasound has been adopted to boost the efficiency of food processing, shorten processing duration, enhance product quality and cut down energy consumption. Such processing performances are closely associated with the acoustic cavitation effect of ultrasound, which facilitates heat and mass transfer throughout processing operations. Based on classical thermodynamic and mechanical laws, computer-aided modeling enables the visualization of heat and mass transfer during processing. Taking plant proteins as the research object, the speaker elaborates on the applications of numerical simulation technology in revealing the cavitation characteristics of ultrasound-enhanced plant protein extraction, adsorption and desorption. This provides a theoretical foundation for in-depth understanding of ultrasound action mechanisms, scaling up ultrasonic effects, and realizing process reproducibility across different ultrasonic equipment.

OL16: PSGL-1 Mediated Biomimetic Drug Delivery System for Targeted and Immune Treatment of Atherosclerosis

Lingchao Miao[1,2]*, Xutao Zhang[2], Zhong Guo[3], Wai San Cheang[2]*
[1]GuangDong Engineering Technology Research Center of Medicine-Food Homologous Foods, Food Science School, Guangdong Pharmaceutical University, Zhongshan, 528400, China
[2]State Key Laboratory of Quality Research in Chinese Medicine, Institute of Chinese Medical Sciences, University of Macau, Macao SAR, 999078, China
[3]Center for Biological Science and Technology, Faculty of Arts and Sciences, Beijing Normal University, Zhuhai, 519087, China

Atherosclerosis (AS) is the main pathological basis of cardiovascular diseases, which is the leading cause of death worldwide. In recent years, immunotherapy has increasingly demonstrated its advantages in the treatment strategy for AS. P-selectin, as a receptor specifically expressed at AS plaques (both endothelial cells and platelets), is a key functional molecule that drives the development of AS pathology. It recruits and adheres to immune cells (P-selectin on endothelial cell), driving the development of the early AS inflammatory micro-environment, as well as leading to the aggravation of thrombosis and instability of the plaque (P-selectin on platelet) in the middle and late stages of AS. According to the 'ligand-receptor' relationship between PSGL-1 and P-selectin, we constructed an MS1 cell line overexpressing PSGL-1 through genetic engineering, extracted biomimetic membrane to encapsulate the atorvastatin (ATV) nanocores, and constructed a PSGL-1 biomimetic drug delivery system (Cm-ATV-NPs) to target and treat AS plaques. Based on this, we can precisely target AS plaques with Cm-ATV-NPs, which slowly release ATV, in order to increase the circulation time of ATV in the body and to reduce the dosage, thereby minimizing side effects. Moreover, the biomimetic system mediated by PSGL-1 can itself achieve dual targeting of P-selectin through endothelial cells and platelets, competing with immune cells throughout the entire process of AS to bind plaques. This can suppress inflammation, prevent thrombosis and stabilize the plaques, leading to the inhibition of AS development. Ultimately, it can achieve the synergistic treatment of AS through the combined effects of immunotherapy and precise targeted administration of ATV, reducing toxicity and enhancing efficacy. This project will provide a new strategy for the precise intervention of AS with ATV and immune modulation, providing significant theoretical and application values.

OL17: Large Language Model-Guided Intelligent Screening and Mechanism Study of Antihyperuricemic Peptides from Plant Proteins

Liling Zhang[1], Fan Mo[1], Shuai Jiang[1]*, Ling Jiang[1,2]*
[1]College of Food Science and Light Industry, Nanjing Tech University, Nanjing 211816, China
[2]State Key Laboratory of Materials-Oriented Chemical Engineering, Nanjing Tech University, Nanjing, 211816, China

Hyperuricemia has emerged as the fourth major "high" metabolic disorder following hypertension, hyperlipidemia and hyperglycemia, and current urate-lowering drugs such as allopurinol and febuxostat are limited by hepatotoxicity and hypersensitivity reactions, driving growing interest in food-derived bioactive peptides as safer dietary interventions. However, conventional multienzyme hydrolysis strategies rely on extensive trial-and-error screening, resulting in low efficiency and high cost. In this respect, large language model (LLM)-guided multienzyme hydrolysis strategies attract profound interest as an intelligent alternative for peptide screening. We employed an LLaMA-based model, fine-tuned via LoRA on 86 enzyme-substrate-activity data points, to guide multienzyme hydrolysis of chickpea protein. The optimal combination (MGI) exhibited a xanthine oxidase (XO) inhibitory rate of 94.1% and retained 91.5% of its activity after simulated gastrointestinal digestion; in adenosine-induced HK-2 hyperuricemic cells, MGI reduced intracellular uric acid levels and alleviated oxidative stress and inflammation. Four core tripeptides (LLF, GFM, FSF and SWL), identified via LC-MS/MS combined with LLM-assisted computational screening, formed stable hydrogen bonds with the XO active-site residue Ser876. Building on this framework, an expanded LLM strategy using the larger Qwen3-8B model was subsequently applied to walnut protein, screening eight candidate enzyme combinations and identifying WH1 as the optimal hydrolysate. Cellular mechanism analysis was extended to direct ROS quantification and flow-cytometric apoptosis assays, and a hyperuricemic mouse model was introduced to provide in vivo evidence. Beyond static molecular docking of nine candidate peptides against five key XO residues, molecular dynamics simulations further confirmed the dynamic structural stability of the peptide–XO complexes, with LLF independently identified as an active peptide in both systems. These results support LLM-guided multienzyme hydrolysis as a feasible and generalizable strategy for screening antihyperuricemic peptides from plant proteins, providing a theoretical and technical basis for the development of plant-protein-derived antihyperuricemic functional foods.

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OL18: Electrochemical Biosensing Technology Based on CRISPR-Cas Systems for Pathogenic Microorganism Detection

Ye Li*, Zhaofan Zhou, Chaojie Liao, Ni Li, Jun Huang*
School of Biological and Chemical Engineering, Zhejiang University of Science and Technology, Hangzhou, China

CRISPR-Cas-based biosensing technology, with its exceptional specificity, sensitivity, and operational simplicity, has emerged as a promising tool for the rapid detection of pathogenic microorganisms, particularly suitable for on-site testing of animal-derived and aquatic pathogens. This study focuses on the CRISPR-Cas13a and Cas14a1 systems to develop a series of high-performance electrochemical biosensors. Specifically, we established electrochemical detection methods for bovine viral diarrhea virus and porcine epidemic diarrhea virus using CRISPR-Cas13a, with the latter further enhanced by integrating nanocomposite materials for improved signal response[1,2]. Concurrently, we constructed a CRISPR-Cas14a1-based biosensor for aquatic pathogens, effectively expanding the detection target range. Furthermore, through molecular engineering of the LwaCas13a protein, we screened and obtained mutants with significantly enhanced trans-cleavage activity, and applied them to the rapid detection of RNA viruses, substantially improving assay sensitivity. Looking ahead, we aim to elucidate the molecular mechanisms governing the trans-cleavage activity of CRISPR-Cas13a and develop highly sensitive electrochemical biosensors based on the activity-enhanced mutants, thereby providing more efficient technical support for food safety monitoring and epidemic disease prevention and control.

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OL19: Bioinformatics-Guided Discovery and Mechanistic Evaluation of the Oyster-Derived Antithrombotic Peptide P-2-CG

Shuzhen Cheng[1,2,3], Ming Du[1,2,3]*
[1]School of Food Science and Technology, Dalian Polytechnic University, Dalian 116034, China
[2]National Engineering Research Center of Seafood, Dalian Polytechnic University, Dalian 116034, China
[3]State Key Laboratory of Marine Food Processing and Safety Control, Dalian 116034, China

Thrombosis is a central pathological process underlying ischemic cardiovascular and cerebrovascular disorders, and coagulation-centered intervention remains a major strategy for reducing thrombotic risk. Marine food proteins are valuable reservoirs of bioactive peptides; however, antithrombotic peptides from oyster proteins remain insufficiently explored, particularly with respect to target-oriented discovery and mechanism-defined validation. In this study, a bioinformatics-guided workflow was established to identify and evaluate an oyster-derived antithrombotic peptide. Oyster myosin heavy chain was virtually digested with trypsin using PeptideCutter, generating 317 theoretical peptides, including 53 peptides with lengths of 10-15 amino acids. Using the thrombin Exosite I-binding regions of HIRV-2 and bivalirudin as structural references, these peptides were docked to thrombin Exosite I and further screened according to physicochemical properties. P-2-CG, with the sequence IEELEEELEAER, was selected due to its acidic character, strong negative net charge, hydrophilicity, and favorable docking score. The peptide was identified in the actual tryptic hydrolysate of oyster protein with a peptide identification score of 78.46 and was subsequently obtained by solid-phase synthesis with a purity of 98.55%. Functional assays showed that P-2-CG inhibited multiple coagulation factors, with a particularly pronounced effect on FIXa, and reduced FXa formation in both intrinsic and extrinsic tenase systems. P-2-CG also attenuated thrombin generation in the FXa-FVa-PCPS-mediated prothrombin activation system. In endothelial cells, P-2-CG alleviated thrombin-induced barrier dysfunction, preserved VE-cadherin organization, reduced F-actin stress fiber formation, prolonged plasma clotting time from 288 s to 337 s, decreased the FXa generation rate from 0.059 to 0.019 nM FXa/min, and lowered thrombin-induced tissue factor expression from 8.1-fold to 4.2-fold. In mouse models, P-2-CG reduced carrageenan-induced tail thrombosis and improved survival after thrombin-induced acute pulmonary embolism. These results indicate that P-2-CG acts at the coagulation-endothelium interface by suppressing tenase-mediated FXa generation, thrombin formation, and endothelial procoagulant activation. This work provides a target-guided strategy for the efficient discovery, preparation, and mechanistic evaluation of marine food protein-derived antithrombotic peptides.

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OL20: Oral Microbiome Signatures Predict Biological Age and Host Health

Huilin Yu
Zhejiang Agriculture and Forestry University, China

Identifying robust, non-invasive biomarkers of biological age is key to preventive medicine. While gut aging clocks exist, the oral microbiome remains underexplored as a quantitative biomarker. Using oral microbiome data from two NHANES cohorts (N = 4,675), we identified 64 age-dependent bacterial genera and developed a machine learning model predicting chronological age, with generalizability in an independent external cohort (N = 1,293). We derived an Oral Microbiome Aging Acceleration (OMAA) Score as the residual of predicted age against chronological age. The OMAA Score independently predicted all-cause mortality (HR = 1.05, P = 0.024) and frailty (OR = 1.05, P = 0.008), correlated with impaired kidney function (lower eGFR: $\beta = -0.066$, P = 5.22×10-4), and enhanced risk prediction for cancer (AUC 0.70 vs. 0.67, P = 0.009) and heart attack (AUC 0.79 vs. 0.76, P = 0.016) beyond conventional risk factors. Diet and medication had minimal association. The OMAA Score offers a scalable, non-invasive tool to identify high-risk individuals for age-related morbidity and mortality.

OL21: Multi-Omics-Guided Identification and Functional Characterization of Two Zn_2Cys_6 Transcription Factors Regulating Ganoderic Acid Biosynthesis in *Ganoderma lucidum*

Yihong Li
Zhejiang University of Technology, China

Ganoderma lucidum (*G. lucidum*) is a well-known medicinal and edible mushroom, and its major bioactive constituents, ganoderic acids (GAs), exhibit diverse pharmacological activities, including antitumor, anti-inflammatory, hepatoprotective, and immunomodulatory effects. However, the naturally low abundance of GAs in fruiting bodies remains a major obstacle to their industrial production and the development of functional foods and pharmaceuticals. Elucidating the regulatory mechanisms underlying GA biosynthesis is therefore essential for improving GA production through metabolic engineering and synthetic biology.
In this study, an integrated multi-omics strategy combining metabolomics, transcriptomics, and proteomics was employed to investigate four *G. lucidum* strains across six developmental stages. Quantitative metabolite profiling revealed dynamic and stage-dependent accumulation of 18 representative ganoderic acids, with the highest levels detected during fruiting body maturation and sporulation. Weighted gene co-expression network analysis (WGCNA), together with transcriptomic and proteomic analyses, enabled the construction of a regulatory network associated with GA biosynthesis and led to the identification of 22 candidate cytochrome P450 genes and 27 transcription factors. Among them, two Zn2Cys6 family transcription factors, Zn2Cys6_61 and Zn2Cys6_82, were identified as key positive regulators of GA biosynthesis.
Functional characterization demonstrated that overexpression of either Zn2Cys6_61 or Zn2Cys6_82 significantly increased total triterpenoid accumulation, whereas gene silencing produced the opposite effect. Subcellular localization confirmed that both proteins were localized in the nucleus. Yeast one-hybrid, dual-luciferase reporter, and electrophoretic mobility shift assays (EMSA) further demonstrated that both transcription factors directly bind to and activate the promoter of the squalene synthase (SQS) gene, thereby promoting triterpenoid biosynthesis. Transcriptome analysis further indicated that these transcription factors coordinately regulate multiple genes involved in the GA biosynthetic pathway, highlighting their central regulatory roles in metabolic flux toward GA production.
Overall, this study provides a comprehensive multi-omics framework for elucidating the regulatory network governing ganoderic acid biosynthesis and identifies Zn2Cys6_61 and Zn2Cys6_82 as promising genetic targets for enhancing GA production. These findings not only advance our understanding of specialized metabolism in medicinal fungi but also provide valuable genetic resources for the metabolic engineering of *G. lucidum* and the sustainable biomanufacturing of high-value bioactive natural products for applications in medicine and functional foods.

OL22: Calcium-Peptide Chelate: A Potential Calcium Supplement and Its Chelation Mechanism

Xiaochen Liu[1,2]*; Ruixia Chen[2,3], Xinyan Wei[2], Leif H. Skibsted[4], Weizheng Sun[2], Dapeng Li[1]*
[1]School of Food Science and Engineering, Shandong Agriculture University, Daizong Street 61, 271018 Tai'an, Shandong, China
[2]School of Food Science and Engineering, South China University of Technology, 510641 Guangzhou, China
[3]Institute of Agrochemistry and Food Technology (CSIC), 46980 Paterna, Valencia, Spain
[4]Department of Food Science, University of Copenhagen, Rolighedsvej 30, DK-1958 Frederiksberg C, Denmark

This work investigates peptides and their calcium chelates derived from soybean meal and spent hen to address prevalent calcium deficiency in China, where daily intake reaches merely 50% of recommended levels. Traditional supplements exhibit low bioavailability and gastric discomfort, necessitating innovative alternatives. This study elucidates the coordination mechanism whereby acidic amino acids (Asp and Glu) bind calcium via side-chain carboxyl groups, with enhanced binding ability under alkaline conditions due to deprotonation. Molecular docking demonstrates improved binding stability with TRPV6 calcium channels, suggesting enhanced targeting efficiency for calcium absorption. Optimized enzymatic hydrolysis using Papain and Flavourzyme, followed by ethanol fractionation, yielded small-molecular-weight peptide fractions achieving calcium-binding capacity of 69 mg/g protein for spent hen. Characterization through FTIR, XRD, and ITC confirmed carboxyl groups as primary exothermic binding sites, with analysis revealing a positive correlation between acidic amino acid residues and binding capacity. Molecular simulations identified hydrogen bonds, electrostatic interactions, and salt bridges as key stabilizing forces. Ultimately, this research establishes a strategic framework for high-value utilization of low-value proteins and provides a theoretical foundation for developing targeted mineral nutritional supplements.

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OL23: Quantitative NMR (qNMR) Analysis of Bioactive Compounds in Biopolymer-Encapsulated Kombucha Tea

Nor Arifah Mat Nor, Hazrulrizawati Abd Hamid*
Faculty of Industrial Sciences & Technology, Universiti Malaysia Pahang Al-Sultan Abdullah, Malaysia.

Quantitative nuclear magnetic resonance (qNMR) spectroscopy is increasingly recognized as a robust and non-destructive tool for the direct quantification of bioactive compounds in complex food systems. Recent advances have highlighted its significant role in foodomics and metabolomics for the comprehensive characterization of functional foods[1]. This study investigates the application of qNMR for profiling and monitoring key metabolites in freeze-dried encapsulated kombucha tea, a functional beverage rich in organic acids and phenolic compounds[2]. Encapsulation was performed using biopolymer-based carriers comprising whey protein isolate (WPI), Arabic gum (AG), and pectin (PEC), formulated at varying concentrations and compositional ratios. Freeze drying was employed to enhance the stability of thermolabile compounds while improving shelf life. The approach demonstrated clear capability in differentiating formulations and assessing the influence of carrier composition on metabolite preservation. Variations in carrier ratios were associated with distinct metabolite profiles, highlighting the importance of matrix design in functional food development. The study underscores the potential of integrating freeze-drying encapsulation with qNMR analysis as a rapid and reliable strategy for quality assessment, formulation optimization, and standardization of kombucha-based products. The findings support broader applications of qNMR in functional beverage innovation and advanced food characterization.

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OL24: Exposure to Grilled Lamb-Borne Carbon Quantum Dots Induces Intrahepatic Cholestasis by Activating the Intestinal Microbial-Derived Lipopolysaccharide-TLR4 Pathway

Jingwen Xu*, Ning Guo, Guoliang Li*
School of Food Science and Engineering, School of Biological and Pharmaceutical Sciences, Shanxi University of Science & Technology, Xi'an, China

The by-products of thermally processed foods, carbon quantum dots (CQDs), pose unpredictable risks to human health due to their nanoscale size and abundant surface functional groups that can readily accumulate in organs[1]. Herein, mice were oral exposed to grilled lamb-derived CQDs (25 mg kg-1) for 9 weeks. The results indicated that CQDs exposure resulted in liver and intestinal barrier injury, as well as an increase in intestinal microbiota-derived lipopolysaccharide (LPS). CQDs exposure directly and indirectly upregulated the expression of bile acid (BA) synthesis genes (Cyp7a1, Cyp8b1, and Cyp27a1) by activating MyD88 in the intestinal LPS-TLR4 pathway, as well as MyD88 and NFκB, downstream molecules of LPS-TLR4 pathway in the liver, leading to increased BA synthesis[2]. Concurrently, the expression of BA excretion genes Bsep and Mrp2 was downregulated, contributing to cholestasis. With prolonged exposure, the levels of the farnesoid X receptor (FXR) inhibitor tauro-β-muricholic acid increased, while that of agonists chenodeoxycholic acid and taurochenodeoxycholic acid decreased, further exacerbating cholestasis. Supplementation with *Lactiplantibacillus plantarum* ATCC8014 mitigated cholestasis by reducing the relative abundance of g_Flexispira, increasing the relative abundance of g_Adlercreutzia, and remodeling the intestinal barrier[3]. This study provides substantial evidence for the comprehensive assessment, control, and intervention regarding the hepatotoxicity of foodborne CQDs.

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OL25: Intelligent Materials for Food Freshness Based on Anthocyanins: From Color Sensitization to Functional Integration

Xu Si, Yiwen Bao, Jiaxin Li, Yao Ma, Fan Wang, Bin Li*
Shenyang Agricultural University, College of Food Science, Shenyang, China

As global food safety and nutritional health issues become increas ingly prominent, achieving real-time monitoring and effective man agement of food quality has emerged as a critical challenge requiring urgent solutions. Statistics reveal that the economic losses and environmental burdens caused by food spoilage and waste each year are extremely severex[1]. While traditional physicochemical testing methods are accurate, they often rely on expensive equipment and specialized operations, making them difficult to apply in daily consumption and distribution channels where rapid, low-cost solutions are needed. Against this backdrop, intelligent packaging, as an emerging technology for food preservation and quality monitoring, is gaining widespread attention from both academia and industry due to its convenience, intuitiveness, and consumer-friendly characteristics[2, 3]. However, low color sensitivity and stability and poor indication of sub-fresh level of the existing pH-sensitive indicator films with anthocyanin as indicator have yet to be improved. We have applied co-pigmentations for anthocyanins based on the ionic complexes between anthocyanins flavonoid ion and the sulfuric acid groups of chondroitin sulfate[4]. The sensitivity and stabilizing effect in starch-based labels was further enhanced by 3D printing technology through controlling nozzle size for smooth and homogeneous gel structure[5]. To realize sub-freshness indication, operations of pH shift in film-forming solution solved the limitation of chitosan-based packaging films in undistinguishable colorimetric endpoints[6]. Furthermore, Dual-function starch-based intelligent label with reversible responsiveness and sustained bacteriostat-releasing for food preservation and monitoring was explored[7]. Results showed that β-cyclodextrin encapsulation of cinnamon essential oil performed a high growth-inhibition rate in *E. coli* and *S. aureus* of almost 100%. For functional integration, with 1-methylcyclopropene as a preservative, and acetylated starch with pullulan as matrices, a core-shell structural fiber membrane with indication and freshness-keeping functions was prepared via coaxial electrospinning technology. successful encapsulation of 1-methylcyclopropene in the core layer and its sustainable-release for 96 h. The functional fiber membrane treatment significantly slowed the degradation of soluble solids and vitamin C, reduced total phenolic consumption, and extended the shelf life of fresh-cut kiwifruit by 66% during storage[7]. The above intelligent labels have good biosafety and degradability, and responded efficiently to the freshness of fresh food with high protein and water activity. When the colorimetric monitoring reflection was transferred to digitized freshness color signals by recognizing RGB values via APP, inter-individual differences in visual recognition will be reduced.

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OL26: Construction of Probiotic Coating System Induced by Metal Ions and Its Relief Mechanism against Intestinal Injury

Yanming Ren[1,2], Guangzhi Xu[1], Qinxue Ni[1], Youzuo Zhang[1], Xingqian Ye[2]*, Jinhu Tian[2]*
[1]College of Food and Health, Zhejiang A & F University, Hangzhou 311300, China
[2]College of Biosystems Engineering and Food Science, Zhejiang University, Hangzhou 310058, China

Probiotics have emerged as a promising dietary intervention for gastrointestinal disorders, with well-documented efficacy in preserving intestinal barrier integrity and restoring gut microbiota homeostasis. However, oral probiotic delivery remains severely challenged by harsh upper gastrointestinal conditions (gastric acid, bile salts) and poor mucosal adhesion, leading to insufficient viable cells reaching the colon and compromised functional performance. Accordingly, developing biocompatible delivery systems to enhance probiotic survivability and intestinal retention is a critical focus in food and nutritional science. Metal-phenolic networks (MPNs), self-assembled from natural polyphenols and metal ions, represent an attractive coating strategy owing to their superior mucoadhesion and biosafety. In this study, we fabricated a double-layer probiotic coating via metal ion-induced self-assembly, composed of a protocatechuic acid-Fe^{3+} MPN inner adhesion layer and a calcium-crosslinked sodium alginate outer barrier layer, using *Lactiplantibacillus plantarum* (LP) as the model strain. In vitro characterization demonstrated that coated LP exhibited ~100-fold higher survival than free cells under simulated gastric exposure, along with enhanced tolerance to bile salts, antibiotics and ethanol. In vivo assays further confirmed that the coating significantly improved LP viability along the mouse gastrointestinal tract, strengthened intestinal adhesion and prolonged colonic retention, with favorable biosafety validated by cytotoxicity, hemolysis and histopathological analyses. In dextran sulfate sodium (DSS)-induced ulcerative colitis model, coated LP administration markedly alleviated disease phenotypes including weight loss, bloody diarrhea and colon shortening, restored intestinal barrier function via upregulating tight junction proteins and mucin, and reshaped gut microbiota with elevated beneficial bacteria and increased short-chain fatty acid production. Mechanistically, the protective effect was primarily mediated by inhibiting the TLR4-NLRP3 inflammatory signaling pathway and modulating the Bax/Bcl-2 apoptosis axis, accompanied by reprogramming of serum metabolic profiles related to nucleotide and tryptophan metabolism.

OL27: Anthocyanin Oral Film: Homeostatic Protection, Structural Design, and Functional Modulation

Yiwen Bao, Bin Li*
College of Food Science, Shenyang Agricultural University, 110866, China

With the development of functional foods toward greater convenience, personalization, and precision delivery, oral films have emerged as promising carriers for food bioactives because they require no water for administration, offer flexible and adjustable dosing, and enable localized oral release with potential mucosal delivery. On this basis, a series of studies was conducted using anthocyanins as the core bioactive, focusing on homeostatic protection, structural design, and functional modulation in oral films. First, blueberry anthocyanins were complexed with sulfated polysaccharides to improve their color and content stability while modulating release behavior. Subsequently, a natural polychromatic system composed of anthocyanins and phycocyanin was integrated with a starch–κ-carrageenan printing ink, enabling personalized control of film color, shape, thickness, and nutritional dosage through 3D printing. Electrospun fibers films with distinct pore structures were then fabricated using octenylsuccinylated starch and pullulan, revealing the regulatory role of film architecture in anthocyanin delivery. Dense structures enhanced mechanical performance, storage stability, and sustained release, whereas loose structures promoted rapid release and improved penetration through mucus and oral mucosal models. The delivery platform was further extended to postbiotics. The resulting postbiotic-loaded fibers films exhibited antibacterial, beneficial-bacteria-promoting, antioxidant, cytoprotective, and anti-inflammatory activities. Furthermore, co-loading postbiotics and anthocyanins enabled coordinated modulation of oral microorganisms, oxidative stress, and inflammatory responses. Collectively, these studies established a progressive research framework encompassing homeostatic protection, structural design, controlled delivery, and functional modulation, providing a theoretical basis and technical support for the development of anthocyanin oral films in personalized nutrition and oral health applications.

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OL28: Hypericin Blocks the Function of HSV-1 UL12 and Suppresses Viral Replication

Kang Cao[1], Yan Zhang[1,2], Qian Yao[3], Yanjuan Peng[4], Qu Pan[1], Qiuxia Jiao[1], Ke Ren[5], Fenghui Sun[1], Qian Zhang[6], Ran Guo[7], Jiali Zhang[7], Tian Chen[1]*
[1]Department of Pathogen Biology, Chengdu Medical College, Chengdu, China
[2]Department of Pathology, Fourth People's Hospital of Zhenjiang City, Zhenjiang, China
[3]Key Laboratory of Medicinal and Edible Plants Resources Development of Sichuan Education Department, Sichuan Industrial Institute of Antibiotics, School of Pharmacy, Chengdu University, Chengdu, China
[4]Department of Pharmacology, Chengdu Medical College, Chengdu, China
[5]School of Laboratory Medicine, Chengdu Medical College, Chengdu, China
[6]Department of Nursing, The Second People's Hospital of Xindu District, Chengdu, China
[7]Grade 2019 of Clinical Medicine, Chengdu Medical College, Chengdu, China

Herpes simplex virus type 1 (HSV-1) is a prevalent pathogen with significant global health implications. Due to the emergence of drug resistance against the nucleoside analogues, there is an urgent need to find novel antiviral agents and antiviral targets. The alkaline nuclease (AN) encoded by the HSV-1 UL12 gene is essential for viral genome processing and capsid egress, making it a promising antiviral target. This study aimed to identify that hypericin can inhibit AN and suppresses the viral replication. Bioinformatics screening predicted that hypericin, a major active component of *Hypericum perforatum L.*, interacts with AN. Recombinant AN was expressed in *Pichia pastoris* to validate this prediction. In vitro enzymatic assays demonstrated that hypericin inhibited both the exonuclease and endonuclease activities of AN in a dose-dependent manner. Immunohistochemical analysis revealed that hypericin treatment caused the accumulation of viral nucleocapsids within the nucleus, indicating that hypericin inhibits the intracellular function of AN. Furthermore, hypericin significantly downregulated the expression of many key viral genes (UL12, ICP27, ICP8, gD, UL53) and reduced the synthesis of the viral proteins (ICP4, ICP8, gD). Plaque assays showed the potent antiviral activity of hypericin, with EC50 values of 2.59 ± 0.08 μM against HSV-1 F strain and 2.94 ± 0.10 μM against the clinical SM44 strain. Time-of-addition assay indicated that hypericin primarily suppresses viral replication at the early stages. Additionally, hypericin exhibited virucidal activity and inhibited viral adsorption and penetration. In conclusion, hypericin suppresses HSV-1 replication by blocking the function of AN, revealing a novel intracellular antiviral mechanism for its antiherpetic effect and highlighting its potential as a candidate for anti-HSV therapy.

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OL29: Sinensetin Ameliorates Lipopolysaccharide-induced Liver Injury by Targeting the TLR4/NF-κB/NLRP3 Pathway and Restoring Intestinal Barrier Function

Zhuoqun Meng[1,2], Qin Zhang[1,2], Ranran Zhang[5], Guirong Liu[1,2], Wenliang Xiang[1,2], and Yang He[4], Qing Zhang[1,2], Jie Tang[1,2,3]*
[1]School of Food and Bioengineering, Xihua University, Chengdu 610039, Sichuan, China
[2]Food Microbiology Key Laboratory of Sichuan Province, Xihua University, Chengdu, 610039, Sichuan, China
[3]Chongqing Key Laboratory of Speciality Food Co-Built by Sichuan and Chongqing, Xihua University, Chengdu 610039, Sichuan, China
[4]College of Medical Technology, State Key Laboratory of Characteristic Chinese Medicine Resources in Southwest China, Chengdu University of Traditional Chinese Medicine, Chengdu 611137, China; 5. Department of Food Quality and Safety, College of Food Science and Engineering, Jilin University, Changchun, Jilin 130062, P. R. China

Acute liver injury (ALI) caused by lipopolysaccharide (LPS) is a disease characterized by congenital immune system dysfunction and liver cell damage. Due to its increased mortality rate, it has attracted widespread clinical attention. The focus of the research work is to elucidate the potential mechanisms involved in this process. Sinensetin is a multi methoxy flavonoid that is abundant in the peel of citrus fruits. In addition to exhibiting biological activities such as antioxidant, anti-inflammatory, lipid-lowering, and anticancer, it also has significant liver protective effects. There is evidence to suggest that sinensetin may help reduce acute liver injury caused by LPS and acetaminophen. However, it is currently unclear whether sinensetin can reduce LPS induced liver injury through innovative mechanisms involving the gut liver axis, and what the potential mechanisms of its action are. The results of this study indicate that administration of sinensetin can reduce liver tissue damage, decrease the release of inflammatory cytokines, alleviate oxidative stress, and inhibit LPS induced activation of toll-like receptor 4 (TLR4)/nuclear factor-κB (NF-κB)/NLR family pyrin domain containing 3 (NLRP3) signaling pathway. Sinensetin significantly improved abnormal histopathological changes in the intestine and restored the function of the intestinal barrier. In addition, examination of the microbiota showed that sinensetin remedied the ecological imbalance present in the gut microbiota, while also increasing the concentration of short chain fatty acids (SCFAs). Overall, this study examined the interaction between phytochemicals and virulence factors, revealing that sinensetin significantly alleviates LPS induced liver disease by inhibiting the inflammatory cascade of the gut liver axis mediated by the gut microbiota. It provides new ideas and targets for utilizing functional factors in food to improve LPS induced liver injury.

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OL30: Regulation Mechanisms of Amino Acid Crosslinking in Protein-Based Food Processing

Haining Xu[1], Xinyang Wang[1], Yingchun Ma[1], Yan Ye[1], Xueyue Huang[2]*, Ronghai He[3], Jun Tian[1]*
[1]School of Life Sciences, Jiangsu Normal University, 221116 Xuzhou, China
[2]WuXi AppTec (Suzhou) Co., Ltd., 215104 Suzhou, China
[3]School of Food and Biological Engineering, Jiangsu University, 212013 Zhenjiang, China

Amino acid crosslinking frequently occurs in protein-based foods during industrial production and processing, including alkaline fermentation, alkaline extraction, heat treatment, and pH-shift modification[1]. Among the relevant reactions, amino acid racemization and β-elimination represent typical unfavorable crosslinking pathways[2,3]. These reactions produce dehydroalanine (DHA) intermediates and lysinoalanine (LAL) end products, which reduce protein digestibility and may even induce renal lesions in humans[3]. Early studies have revealed that chemical synthetic reagents such as liquid ammonia, sulfites and sulfhydryl compounds can inhibit the formation of DHA and LAL[4]; however, these additives compromise food flavor and nutritional value, failing to meet the "green and healthy" development requirements of the modern food industry. This study investigated the effects of glycation, ultrasonication and amino acid oxidation on LAL crosslinking. Glycation experiments demonstrated that monosaccharides (xylose) and disaccharides (maltose) competitively hinder the binding between DHA and amino groups via strong Maillard carbonyl-amino interactions[5,6]. Sodium alginate polysaccharides enhance the steric hindrance of the reaction system by inducing covalent/non-covalent protein aggregation, thereby increasing the activation energy of amino acid crosslinking reactions[7]. Ultrasonication improves both the efficiency and degree of glycation; meanwhile, it facilitates the conversion of disulfide bonds to sulfhydryl groups and promotes DHA-sulfhydryl binding, thus inhibiting LAL formation[5,6,7]. Recent findings further indicate that amino acid oxidation serves as an alternative reaction pathway for LAL crosslinking during the thermal processing of proteins. This research provides a theoretical foundation and green technical strategies for the nutritional quality regulation of protein-based foods.

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OL31: Targeting the Mitotic Machinery with Maackiain: A Natural-Product Strategy Against Lung Cancer

Rajeev Kumar
Institutes for Systems Genetics, West China Hospital, Sichuan University, Chengdu, China

Maackiain is a naturally occurring pterocarpan with diverse biological activities, but its anticancer potential and selectivity toward malignant lung cells remain incompletely understood. We combined phytochemical characterization, patient-derived transcriptomic analysis, molecular modeling, and cellular experiments to investigate its activity in lung adenocarcinoma. Maackiain inhibited A549 cell viability, promoted apoptosis, and reduced wound closure, while producing weaker cytotoxicity in non-malignant BEAS-2B bronchial epithelial cells. The respective IC_{50} values were 276.00 ± 11.53 and 402.33 ± 53.50 μM, indicating modest cancer-cell selectivity. Analyses of independent lung cancer transcriptomic cohorts consistently highlighted dysregulation of E2F, G2/M, and mitotic programs, supporting the investigation of the kinesin Eg5/KIF11 as a candidate mechanistic node. Molecular docking and 100-ns molecular dynamics simulations suggested a plausible interaction between Maackiain and Eg5, whereas Western blotting, RT-qPCR, and cellular thermal shift assays demonstrated Eg5-associated molecular responses accompanied by modulation of NRF2/KEAP1 and ERK signaling. These findings position Maackiain as a mechanistically informative natural-product lead targeting mitotic vulnerability. However, its modest potency and limited in vitro selectivity indicate that structural optimization and more rigorous target-validation studies are required before further translational development.

OL32: Selenium Biofortification and Phytochemical Enhancement in Germinated Barley: Effects of Selenium Forms and Calcium Regulation

Chao Cheng
Institute of Food and Marine Bio-resources, College of Biological Science and Engineering, Fuzhou University, Fuzhou 350108, China

Selenium (Se) biofortification of cereals offers a food-based strategy for improving dietary Se supply, but its nutritional value depends on Se chemical form, tissue distribution, metabolic conversion, and phytotoxicity control. A series of studies was conducted using germinating barley (*Hordeum vulgare L.*) to investigate how Se forms, Se concentrations, and calcium supplementation regulate Se accumulation, biotransformation, nutritional quality, and oxidative stress. Barley grains were treated with selenate, selenite, or selenomethionine (SeMet), followed by analyses of Se accumulation, tissue translocation, Se speciation, protein-bound Se, phenolic acids, redox responses, and the expression of genes involved in Se transport and metabolism. Se accumulation followed the order SeMet > selenite > selenate and reached its maximum near the end of steeping[1]. During germination, Se was redistributed from the husk and endosperm to the acrospire and rootlets, and the proportion of organic Se exceeded 86% by day 4. Se was predominantly enriched in protein fractions, with SeMet treatment resulting in the highest protein-bound Se concentration and the greatest accumulation of free and bound phenolic acids[2]. The response to selenite was dose-dependent: 150 μM selenite was tolerated without marked disruption of seedling growth or redox homeostasis, whereas 600 μM selenite increased reactive oxygen species and lipid peroxidation and inhibited rootlet growth[3]. Supplementation with 0.5-4 mM Ca^{2+} increased total Se accumulation by 15-39%, with the maximum Se concentration of 10.13 mg kg^{-1} dry weight observed at 4 mM Ca^{2+}. Calcium also altered the tissue and subcellular distribution of Se and regulated genes involved in Se transport and assimilation. By contrast, 8 mM Ca^{2+} reduced fresh weight and respiration[4]. Collectively, these results demonstrate that barley germination promotes Se biotransformation and phenolic accumulation, while appropriate Ca^{2+} supplementation further enhances Se accumulation without compromising early seedling growth.

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PhD student's forum

GL1: Probiotic Lactobacillus Plantarum Potentiates Innate Immunity through Purine Metabolic Remodeling

Yuxi Wen[1], Jianbo Xiao[2]*, Chao Zhao[1]*
[1]College of Marine Sciences, Fujian Agriculture and Forestry University, Fuzhou 350002, China
[2]University of Vigo, Nutrition and Bromatology Group, Department of Analytical Chemistry and Food Science, Faculty of Science, E32004 Ourense, Spain

A low or dysfunctional immune system weakens resistance to pathogens. Therefore, improving immunity is vital for keeping the body healthy[1,2]. The present study centers on *Lactobacillus plantarum*, with a dedicated effort to thoroughly probe into the mechanisms underpinning its function in bolstering the innate immunity of *Caenorhabditis elegans*. *L. plantarum* effectively inhibits *Pseudomonas aeruginosa* PA14 colonization and upregulates clc-1 to strengthen gut barrier function. Metabolomics analysis suggests that *L. plantarum* may enhance the immune capacity of *C. elegans* by reprogramming the purine metabolism pathway, thus improving its resistance to pathogenic bacteria. Moreover, the supplementation of exogenous uric acid (UA) and xanthine both significantly enhanced the immunity of the *C. elegans*. *L. plantarum* and UA regulate immune regulatory effects through the DAF-2/AGE-1/DAF-16/SKN-1 pathway. The results show that the *L. plantarum*-induced UA metabolic changes modulate oxidative stress and immune balance via DAF-2/DAF-16/SKN-1, and thus optimize the health status of *C. elegans*.

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GL2: Preconception Dietary EGCG Prevents Bubble Tea-Induced Intergenerational Obesity and Oxidative Stress via Vitellogenin-Mediated Nutrient Transport in *Caenorhabditis elegans*

Xincheng Wu[1,2], Shiye Lin[1,2], Jesus Simal-Gandara[1,2]*, Hui Cao[1,2]*, Jianbo Xiao[1,2,3]*
[1]Universidade de Vigo, Nutrition and Bromatology Group, Department of Analytical Chemistry and Food Science, Faculty of Science, 32004 Ourense, Spain
[2]Instituto de Agroecoloxía e Alimentación (IAA), Universidade de Vigo, Campus Auga, 32004 Ourense, Spain
[3]Research Group on Food, Nutritional Biochemistry and Health, Universidad Europea del Atlántico, Isabel Torres 21, 39011 Santander, Spain

Maternal nutrition is increasingly recognized as a determinant of offspring metabolic health[1], yet whether bubble tea (BT), a sugar- and saturated fat-rich dietary matrix, induces intergenerational obesity together with oxidative stress and whether such effects can be prevented remain unclear. Using *Caenorhabditis elegans*, we investigated maternal BT exposure and the preventive role of preconception epigallocatechin gallate (EGCG). Chemical characterization showed that BT was enriched in sucrose and saturated fatty acids, mainly C12:0 and C18:0. Maternal BT exposure increased lipid accumulation, glucose and triglyceride levels, impaired physiological performance, reduced oxidative stress resistance, decreased SOD and CAT activities, and disrupted central carbon metabolism, with these phenotypes persisting into the F1 generation. Preconception EGCG significantly attenuated these changes and also protected against lipid accumulation induced by representative single sugar (glucose, fructose) and fatty acid (lauric acid) components. Mechanistically, the intergenerational lipid-lowering and antioxidative effects of EGCG depended on DAF-16/FOXO signalling and were associated with the histone marks H3K4me3 and H3K9me2. Notably, EGCG reduced vitellogenin synthesis and yolk protein abundance (YP170, YP115), and its protective effect was abolished in vit-2 and vit-5 mutants, indicating a central role for vitellogenin-mediated maternal nutrient transport[2]. These findings identify a vitellogenin-centred nutrient axis as a key mechanism by which preconception EGCG prevents maternal BT-induced intergenerational obesity and oxidative stress, providing a mechanistic basis for dietary polyphenol intervention before conception.

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GL3: Effect of Microgreens and Spices on Sensory Properties of Bean-based Product

Helena M. Todorović[1,2]*, Nikola S. Tomić[2], Danijela Ratkov Žebeljan[2], Svetlana Roljević Nikolić[1], Jelena Popović-Đorđević[2]
[1]Tamiš Research and Development Institute, Pančevo, Serbia
[2]University of Belgrade, Faculty of Agriculture, Belgrade, Serbia

The growing demand for gluten-free, vegan, and vegetarian products is associated with ethical reasons, religious practices, and medical conditions such as celiac disease[1,2]. Beans are widely recognized as valuable plant-based protein sources due to their high nutritional value[2]. The addition of microgreens and spices to bean-based products may improve their nutritional and sensory characteristics, potentially affecting consumer acceptance.
The aim of this study was to evaluate sensory properties of a fermented bean-based product enriched with different types of microgreens and spices. The prepared samples (BB-beans/basil microgreens; BP – beans/pea microgreens; BR-beans/radish microgreens; BRpC-beans/red pepper/chives microgreens; BSR – beans/saffron/radish microgreens) were evaluated using the CATA (check-all-that-apply) procedure and acceptance tests. All sensory tests were conducted in the sensory testing laboratory at the University of Belgrade, and the obtained data were analyzed using correspondence analysis and ANOVA.
Participants were able to identify the taste of microgreens and sweet bell pepper flavor in the samples. However, 68% of participants checked the descriptor "leather/new shoes" when evaluating the sample with saffron. Among the tested samples, BRpC sample was liked by more than 70% of participants, and the highest willingness to buy was expressed for BRpC and BB products. On a 9-point hedonic scale, the overall acceptability scores showed that the highest acceptance was observed for BRpC (6.3±2.3) and BB (5.6±2.3) samples. As samples with chive and basil microgreens coating were favorable in terms of overall acceptability and purchase intention, while samples with radish microgreens coating were recognized as more bitter and less acceptable in flavor, the findings highlight that microgreen type strongly influences flavor perception and consumer acceptance. Additionally, a considerable proportion of participants (≥ 20% and up to 53%) were perceived all evaluated products as "too sour" which indicate that the fermentation process should be controlled in some way.

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GL4: Discovery of the Natural MALT1 Inhibitor and Its Beneficial Effect on Intestinal Health

Son Hung Tran[1,2], Siqi Zhang[1,2], Uyen Tran Tu Nguyen[1,2], Won Young Bae[1], Suk Woo Kang[1], Keunwan Park[1], Joonki Kim[1,2], Kyungsu Kang[1,2]*
[1]Gangneung Institute of Natural Products, Korea Institute of Science and Technology, Gangwon-do, 25451, South Korea
[2]Natural Product Applied Science, KIST School, University of Science and Technology (UST), Gangneung, Gangwon-do, 25451, South Korea

The mucosa-associated lymphoid tissue lymphoma translocation protein 1 (MALT1) is a key regulator of immune responses and inflammatory signaling through activation of the NF-κB pathway[1]. Dysregulated MALT1 activity has been increasingly recognized as a critical contributor to chronic intestinal inflammation, epithelial barrier disruption, and the development of intestinal disorders, including inflammatory bowel disease (IBD)[2]. Consequently, pharmacological inhibition of MALT1 has emerged as a promising therapeutic strategy for restoring intestinal homeostasis. While several synthetic MALT1 inhibitors have demonstrated encouraging efficacy in preclinical studies, their long-term safety and clinical applicability remain concerns. In the present study, we screened and identified novel MALT1 inhibitors from natural sources and investigated their protective effects on intestinal epithelial function. Functional studies revealed that novel MALT1 inhibitors effectively suppressed cytokine-induced NF-κB activation, reduced IL-8 production, and attenuated the expression of inflammatory mediators in intestinal epithelial cells. Furthermore, treatment with the compounds markedly improved epithelial barrier integrity by restoring transepithelial electrical resistance, reducing FITC-dextran permeability, and increasing the expression of tight junction proteins. Consistent protective effects were also observed in the *Caenorhabditis elegans* model, where the compounds significantly alleviated *P. aeruginosa*-induced epithelial barrier dysfunction. Collectively, this study provides mechanistic insights into the therapeutic potential of targeting MALT1 with natural products and highlights MALT1 inhibition as a promising strategy for the prevention and treatment of intestinal disorders.

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GL5: Microencapsulation of Tuna Oil Using Vanillin-Crosslinked Fish Gelatin–Pectin Complex Coacervates: Physicochemical Characterization, Flavor Improvement, and Digestion Properties

Qiang Zhang[1], Qiuyu Xia[1,2]*, Shucheng Liu[1,2,3]
[1]College of Food Science and Technology of Guangdong Ocean University, Guangdong Provincial Key Laboratory of Aquatic Product Processing and Safety, Guangdong Provincial Engineering Technology Research Center of Seafood; Guangdong Province Engineering Laboratory for Marine Biological Products, Key Laboratory of Advanced Processing of Aquatic Product of Guangdong Higher Education Institution, Zhanjiang, Guangdong, 524088, China
[2]Guangdong Laboratory of Southern Marine Science and Engineering (Zhanjiang), Zhanjiang, Guangdong, 524025, China
[3]Collaborative Innovation Center of Seafood Deep Processing, Dalian Polytechnic University, Dalian, Liaoning, 116034, China

In this study, microcapsules were prepared using the co-precipitation method, with fish gelatin and pectin as the shell materials and tuna oil as the core material. Vanillin (Va) was introduced as a cross-linking agent, and a group treated with transaminase (TGse) served as the control, to systematically investigate the mechanisms governing the physicochemical and delivery properties of the microcapsules. The results indicate that the optimal pH for the double-coagulation process in this system is 4.2. In terms of cross-linking regulation, the 4% Va group exhibited the best overall performance: the smallest particle size, the highest encapsulation rate (98.39%) and loading efficiency (73.09%), and the lowest surface oil (1.61%) and water (2.32%) content. Characterisation by scanning electron microscopy and atomic force microscopy confirmed that this group formed a dense, uniform, three-dimensional porous gel network scaffold with the highest surface smoothness. In vitro simulated digestion indicated that the 4% Va group possessed both excellent gastric tolerance and the ability for precise targeted release in the intestine, exhibiting the highest fatty acid release rate constant ($k = 0.0319\ min^{-1}$) during the small intestine phase. Furthermore, the fishy odor was effectively masked and a distinctive vanilla flavor was imparted to the microcapsules by 4% Va cross-linking, as indicated by flavor analysis. This study provides a theoretical basis for the use of vanillin to regulate lipid encapsulation, flavour enhancement and targeted release.

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GL6: Lychee Pulp-derived Arabinogalactan Protects Intestinal Mucosal Barrier to Alleviate Colitis in Mice Through Enriching *Bacteroides Thetaiotaomicron*

Guitao Huang, Ruifen Zhang*, Mingwei Zhang*
Sericultural & Agri-Food Research Institute Guangdong Academy of Agricultural Sciences/Key Laboratory of Functional Foods, Ministry of Agriculture and Rural Affairs/Guangdong Key Laboratory of Agricultural Products Processing, Guangzhou 510610, P.R. China

Intestinal mucosal homeostasis constitutes a primary line of host defense against gut pathogens. Plant polysaccharide-mediated regulation of intestinal mucosal homeostasis can effectively alleviate the development of intestinal inflammation. Previous studies have shown that lychee pulp polysaccharides improve intestinal mucosal homeostasis, but the underlying mechanisms remain unclear. Herein, the major component isolated from lychee pulp polysaccharides was characterized as an arabinogalactan, with a backbone structure of T-Araf-(1→5)-α-L-Araf-(1→2,5)-α-L-Araf-(1→2,5)-α-L-Araf-(1→3)-β-D-Galp-(1→3,6)-β-D-Galp-(1→3,6)-β-D-Galp-(1→6)-β-D-Galp-(1→. FLP1B-a intervention effectively alleviated intestinal mucosal damage and promoted the abundance of *Bacteroides thetaiotaomicron* in DSS-induced colitis mice. Through microbiota profiling, bacterial isolation, and mono-colonization validation, *B. thetaiotaomicron* was confimed as the pivotal microbial species responsible for the protective effect of FLP1B-a against intestinal mucosal injury. Mechanistically, FLP1B-a-enriched B. *thetaiotaomicron* promoted goblet cell differentiation by upregulating Spdef/Klf4 expression and alleviated endoplasmic reticulum stress by suppressing the Perk/Atf4 signaling pathway, thereby enhancing Muc-2 synthesis, restoring intestinal mucosal homeostasis, and ultimately ameliorating inflammation in mice.

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GL7: Antibacterial Efficacy of Calamansi Residue Extracts on *Staphylococcus aureus*

Chunrong Ling, Min Du, Wenqing Ge, Fang Chen, Xiaosong Hu, Li Dong*
College of Food Science and Nutritional Engineering, National Engineering Research Centre for Fruits and Vegetables Processing, Key Laboratory of Fruits and Vegetables, Processing, Ministry of Agriculture, Engineering Research Centre for Fruits and Vegetables Processing, Ministry of Education, China Agricultural University, Beijing, 100083, China

Foodborne illnesses caused by *Staphylococcus aureus* (*S. aureus*) remain a significant public health concern, exacerbated by the rapid emergence of antibiotic resistance. and the rapid emergence of antibiotic resistance has further intensified challenges in food safety management. Valorization of agricultural by-products offers a sustainable countermeasure. Processing of calamansi (*Citrus reticulata* × *Citrus japonica*) produces large amounts of peel and seed residues that are rich in bioactive phytochemicals with antioxidant and antimicrobial potential. Although calamansi processing yields abundant peel and seed residues rich in bioactive phytochemical, the specific antimicrobial constituents of residues remain largely uncharacterized. In this study, calamansi residues (CR) were extracted using different solvents to obtain calamansi residue extracts (CREs), and their antioxidant capacities and antibacterial activities were systematically evaluated. Among the texted extracts, the ethanol extract (CREE) exhibited the strongest antioxidant activity, while the defatted aqueous extract (CRDAE) showed the most pronounced antibacterial effect, with minimum inhibitory concentration (MIC) of 6.25 mg/mL and minimum bactericidal concentration (MBC) of 12.5 mg/mL values of and against *S. aureus*, respectively. To elucidate the chemical basis underlying these functional differences, non-targeted metabolomic profiling based on UPLC-QE-MS was conducted to characterize and discriminate the CREs. Tangeretin and quinic acid were identified as major metabolites consistently present across all extracts.
Integrated KEGG pathway analysis further highlighted dibutyl phthalate, phlorizin, hesperidin and kojic acid as candidate bioactive compounds associated with antibacterial activity. Subsequent validation assays demonstrated that kojic acid exerted the strongest inhibitory effect against *S. aureus*, suggesting its contribution as a key antimicrobial metabolite in CREs. Overall, this study provides new insights into the chemical composition and antibacterial mechanisms of CR and supports their potential application as natural antimicrobial agents in food systems.

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GL8: Flavoromic Comparison of Naturally and Industrially Fermented Sichuan Pickled Peppers

Xinyu Zhang
College of Food Science and Nutritional Engineering, China Agricultural University, Beijing 100083, China

Pickled pepper is a representative fermented vegetable product in Southwest China, where naturally fermented pickled pepper (NFP) and industrially fermented pickled pepper (IFP) exhibit different processing regimes and microbial ecologies[1,2]. NFP relies on aged brine and indigenous microbiota, whereas IFP is produced with standardized formulations and controlled processing, leading to noticeable differences in aroma complexity and taste-related metabolites. Here, eight NFP and eight IFP samples collected in Sichuan were compared by headspace solid-phase microextraction gas chromatography-mass spectrometry (HS-SPME-GC-MS) and non-targeted LC-MS metabolomics. Complementary 16S rRNA gene sequencing was used to characterize microbial community differences. NFP contained a higher average number of volatile compounds than IFP (approximately 88 vs. 62 compounds per sample), together with substantially more odor-active compounds (OAV > 1: 40.1 vs. 17.4; OAV >= 10: 24.9 vs. 6.0). Eight NFP-enriched markers - alpha-terpineol, p-cymene, eucalyptol, D-limonene, linalool, beta-myrcene, ethyl acetate and phenylethyl alcohol - collectively indicated a floral, citrusy, fruity and fermentation-associated aroma profile. In contrast, IFP showed a less complex but more acid-spicy and seasoning-associated volatile profile. Non-targeted metabolomics detected 5,159 features. After multivariate and univariate screening, 493 stringent differential features met the criteria $P < 0.01$, VIP > 1.5 and FC > 2 or FC < 0.5; high-confidence food-relevant metabolites were further prioritized. Pathway annotation highlighted lysine degradation among the significantly altered pathways associated with NFP-upregulated metabolites, suggesting that amino-acid catabolism and succinate-related metabolism may contribute to the nonvolatile differentiation of NFP. Overall, the study identifies a fruitier and more aroma-rich NFP signature in contrast to the more acid-spicy and processing-associated IFP signature, providing chemical and microbial targets for quality differentiation and future flavor-oriented process optimization.

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GL9: Green Alga Enteromorpha Prolifera Oligosaccharide Exerts Antiaging Effects through Targeted Modulation of Protein O-GlcNAcylation

Shuo Shan , Weichao Chen , Weihao Wu , Wenbo Zhang , Jingyi Liu , Wei Liao , Yuxi Wen , Chao Zhao
Fujian Agriculture and Forestry University · Universidade de Vigo

Backgrounds

Aging and type 2 diabetes reinforce one another through shared metabolic dysregulation. Protein O-GlcNAcylation, a dynamic post-translational modification driven by the OGT/OGA cycle, links hyperglycemia to insulin resistance, proteostasis failure, and cellular senescence. This study examines whether Enteromorpha prolifera oligosaccharide (EPO) counters aging-related metabolic decline by targeting O-GlcNAcylation.

Approach

An aging-diabetic rat model (high-fat/high-sugar diet + D-galactose + streptozotocin) was compared with Normal and EPO-treated (125 mg/kg) groups. Methods integrated:

- 4D label-free glycoproteomics of jejunal O-GlcNAc sites, plus GEO-dataset (GSE155903/GSE156472) and PPI network mining;
- Cellular senescence models (D-gal-induced CCD-18Co, HepG2) with shRNA knockdown of OGA, FLNA, and HCF1, the OGA inhibitor Thiamet-G, ROS and cell-cycle assays;
- C. elegans hcf-1 mutant lifespan, lipofuscin, lipid, and glycogen assays; molecular docking of EPO with OGA, OGT, and HCF1.

Key Findings

- EPO lowered jejunal O-GlcNAc levels, improved glucose tolerance/insulin, and boosted antioxidant capacity (↑T-SOD, ↓MDA/H_2O_2) versus the model group.
- OGA is a primary ROS/cell-cycle driver: shOGA increased ROS by 77.0% and shortened S phase (→G2/M arrest, 12.2%); the OGA inhibitor TMG mimicked this effect, and EPO co-treatment reversed it.
- FLNA and HCF1 as downstream effectors: FLNA expression, suppressed in aging, was restored by EPO; HCF1 knockdown lowered ROS (48.8%→28.3%) but drove strong G2/M arrest and cut glucose uptake ~17%.
- hcf-1(pk924) worms showed shortened lifespan, elevated lipofuscin, disrupted lipid metabolism, and reduced glycogen — confirming HCF1's conserved role in aging and carbohydrate metabolism.

Docking confirmed EPO forms stable hydrogen bonds within the active sites of OGA, OGT, and HCF1, supporting direct enzyme/regulator engagement as the structural basis for its effects.

Conclusion & Significance

EPO mitigates diabetic aging by rebalancing the O-GlcNAc cycle — restraining OGA-driven ROS and cell- cycle arrest while restoring FLNA and HCF1-dependent glucose metabolism. Together with amino-acid metabolism rebalancing, these mechanisms position EPO as a natural, food-based candidate for antiaging and antidiabetic intervention, with O-GlcNAcylation emerging as an actionable therapeutic node linking metabolic dysfunction to cellular senescence.

GL10：Saikosaponin A Induces Apoptosis in HCT116 Colorectal Cancer Cells via ROS-Mediated ER Stress and p38/JNK MAPK Pathway Activation: In Vitro and In Vivo Evidence

Xiu Xiu Zhang[1], Wang Wei Zhang[1], Yuan Song[1,2,3], Run Hui Ma[2,3], Zhi Jing Ni[2,3], Kiran Thakur[2,3], Jian Guo Zhang[1,3]*, Zhao Jun Wei[1,2,3]*
[1]School of Food and Biological Engineering, Hefei University of Technology, Hefei 230009, People's Republic of China
[2]School of Biological Science and Engineering, Specialty Food Nutrition and Health Innovation Team of Ningxia Hui Autonomous Region, North Minzu University, Yinchuan 750021, People's Republic of

China
[3]Ningxia Key Laboratory of Development and Utilization of Specialty Food Resources, Yinchuan 750021, People's Republic of China

Colorectal cancer (CRC) is the third most prevalent cancer globally, with limited effective treatment options and significant chemotherapy resistance. Saikosaponin A (SSA), a triterpenoid saponin from Radix Bupleuri, exhibits anti-inflammatory and antitumor properties, but its mechanism of action in CRC remains undefined. This study aims to investigate SSA's antitumor effects against HCT116 CRC cells and elucidate the underlying molecular mechanisms through integrated omics analysis and functional validation. SSA selectively inhibited HCT116 proliferation and colony formation with minimal toxicity to HEK293 cells. SSA suppressed xenograft tumor growth by 54% (10 mg/kg) without affecting body weight or organ histology. Integrated omics revealed 6,033 DEGs and 39 DEMs, with 81 genes and 37 miRNAs significantly enriched in the MAPK pathway. SSA induced apoptosis in a dose-dependent manner, increasing ROS production 3.2-fold and decreasing MMP. Mechanistically, SSA activated p38 and JNK MAPK pathways, upregulated CHOP-mediated ER stress, and modulated apoptosis proteins (decreased Bcl-2, increased cleaved caspase-3 and -9). Network analysis identified miR-132-3p as a key regulator of MAPK hub genes (KRAS, SOS1, BRAF). SSA exerts potent antitumor activity against HCT116 CRC cells, representing a promising therapeutic candidate for CRC treatment.

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GL11：Carbon-efficient Upcycling of Agrifood Waste into Fatty Acid Ester by Engineered *Clostridium* Tyrobutyricum

Zhenlei Liu[1], Ling Jiang[2]*
[1]College of Biotechnology and Pharmaceutical Engineering, Nanjing Tech University, Nanjing, China
[2]College of Food Science and Light Industry, Nanjing Tech University, Nanjing, China

Microbial conversion of renewable feedstocks into biofuels is gaining interest due to its sustainability. In this research article, we develop a carbon-and cost-efficient fermentation route in *Clostridium tyrobutyricum* to produce the biofuel butyl butyrate (BB) from abundant, low-cost agrifood waste. Using iterative, multimodule strain engineering—promoter engineering, multienzyme colocalization, nonoxidative glycolysis-driven carbon conservation, and cofac-tor engineering—we achieved high-selectivity BB production from rice straw hydrolysate and shrimp shell waste. The best strain delivered a 49.5-fold improvement, reaching 31.16 g/l BB with 98.4% selectivity and a productivity of 0.325 g/l/h in5-l batch fermentations. Techno-economic and carbon-footprint analyses indicate that, compared with conventional sugar biorefineries, agrifood-waste biorefineries cut feedstock costs by 53.6% and life-cycle carbon emissions by 63.4% perton of BB produced. These results show that engineered *C. tyrobutyricum* enables carbon-efficient upcycling of agrifood waste into high-yield BB and provides a blueprint for the biosynthesis of other biofuels.

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GL12: Improving Soluble Expression of Sweet Protein Thaumatin II through Directed Evolution in *Escherichia Coli*

Lefei Wang[1], Ling Jiang[2]*
[1]College of Biotechnology and Pharmaceutical Engineering, Nanjing Tech University, Nanjing, China
[2]College of Food Science and Light Industry, Nanjing Tech University, Nanjing, China

Thaumatin is a natural sweet protein valued for its intense sweetness, long-lasting effect, low-calorie content, and safety[1]. However, limited solubility and low yields hinder microbial fermentation[2]. To overcome these challenges, we engineered *Escherichia coli* to express thaumatin II and implemented three strategies to improve its solubility, then co-expression with molecular chaperones has proved to be the most effective in significantly enhancing the soluble expression of thaumatin II. Furthermore, we applied directed evolution to further refine thaumatin II, resulting in the M-882 mutant, which achieved a thaumatin titer of 42 mg/L, representing a 45% increase compared to the original protein yield. Structural analysis revealed that disruption of two adjacent disulfide bonds in the M-882 mutant minimized mispairing during peptide folding, thereby improving protein solubility. Additionally, molecular dynamics simulations showed that the M-882 variant enhanced solvent accessibility and structural flexibility, both of which contributed to improved solubility. The interaction between thaumatin II and sweet taste receptors, as well as the analysis of surface positive charges, indicates that the M-882 variant is capable of binding to the receptors, thereby retaining its sweetness[3]. Overall, this study not only offers valuable insights into optimizing thaumatin expression but establishes a foundation for engineering other sweet proteins with broad industrial applications.

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GL13: Multi-Omics Elucidation of the Trade-off between Quality and Stress Tolerance in *Anoectochilus roxburghii*

Yanqin Zhu[1,2], Aimin Lv[1,2]*, Qingsong Shao[1,2]*
[1]State Key Laboratory for Development and Utilization of Forest Food Resources, Zhejiang A&F University, Hangzhou, 311300, China
[2]Zhejiang Provincial Key Laboratory of Resources Protection and Innovation of Traditional Chinese Medicine, Zhejiang A&F University, Hangzhou 311300, China

Anoectochilus roxburghii, a precious medicinal plant of the Orchidaceae, is widely used in functional foods and nutraceutical products. Its primary bioactive components, kinsenoside and flavonoids, exhibit antioxidant and hypoglycemic effects. However, abiotic stresses such as cold frequently impair plant growth and reduce the accumulation of these secondary metabolites, thereby compromising the edible and medicinal values. In this study, a total of 55 flavonoid metabolites were identified between two A. *roxburghii* cultivars 'ArKF06' (Cold-Sensitive, CS) and 'ArZN09' (Cold-Tolerant, CT) under low-temperature (4℃) conditions. Among these, kaempferol and quercetin-3-O-glucoside showed the most substantial changes at 3 d. Transcriptomic analysis identified 2102 differentially expressed genes (DEGs), among which 27 favonoid biosynthesis genes (PAL, 4CL, CHS, F3H, F3'H, F5H and FLS) and 17 transcription factors were identified. Furthermore, weighted gene co-expression network analysis identified two distinct modules, and the turquoise module exhibited a robust positive correlation with numerous flavonoid metabolites. Specially, four flavonoid-related genes, including F3'H, F3H, were closely associated with ArNAC2. ArNAC2, a nuclear-localized protein responsive to low temperature, was highly expressed in leaves. Transient overexpression of ArNAC2 significantly increased flavonoid content and stress tolerance, whereas RNA interference (RNAi) -mediated knockdown of ArNAC2 reduced the levels of kaempferol and quercetin-3-O-glucoside. Yeast one-hybrid assays confirmed that ArNAC2 directly binds to the promoter of ArF3'H. Collectively, these findings demonstrated that ArNAC2 transcriptionally regulates ArF3'H to promote flavonol accumulation, thereby ensuring quality stability of *A. roxburghii* under cold conditions. This study provides a key candidate gene for the metabolic regulaton aimed at improving the quality and edible value of *A. roxburghii* under stress conditions.

GL14: Pickering Emulsions Stabilized by Whey Protein Isolate-Sodium Alginate Composite Nanoparticles for Enhanced Delivery of Subcritical Goji Berry Extract (LDP): Formation, Stability, and Bioaccessibility

Qian Ma[1], Kiran Thakur[1], Jian-guo Zhang[1], Fei Hu[1], Zhao-Jun Wei[2]
[1]School of Food and Biological Engineering, Hefei University of Technology, Hefei 230009, PR. China
[2]School of Biological Science and Engineering, North Minzu University, Yinchuan 750021, PR. China

As a carotenoid ester, the subcritical extract of goji berries (LDP) exhibits low water solubility and insufficient chemical stability. While Pickering emulsions offer superior protection for LDP compared to conventional surfactant-stabilized systems, their food-grade application remains limited due to challenges in controlling particle size and amphiphilicity. To address this, we developed a food-grade Pickering emulsion using whey protein isolate (WPI) and sodium alginate (SA) composite nanoparticles to stabilize a ternary LDP-loaded system. Under optimal conditions (pH 4.0, 0.6 wt% WPI, 5% oil-to-water ratio), a stable emulsion with a droplet size of 0.93 μm was successfully formulated. The resulting emulsion demonstrated excellent thermal stability (78.6% LDP retention after 1 h at 90°C) and good storage stability (80.7% retention after 28 days at 4°C). Furthermore, in vitro digestion assays revealed that the emulsion achieved 90% of the theoretical maximal cumulative free fatty acid release at 120 min, with an LDP bioaccessibility of 89.91%. Finally, the encapsulated LDP exhibited significantly enhanced antioxidant activity compared to its free form, underscoring the protective effect of the emulsion system. This work provides a promising platform for constructing food-grade Pickering emulsions, thereby enabling broader application of carotenoid esters in functional foods and pharmaceutical preparations.

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GL15：6-Hydroxykaempferol-3-O-β-D-glucopyranoside From *Carthamus* Tinctorius L. Induces Cell Apoptosis and Autophagy in Human Colon Cancer HCT116 Cells

Yuan Song[1], Zhao Jun Wei[1,2*]
[1]School of Food and Biological Engineering, Hefei University of Technology, Hefei 230601, China
[2]School of Biological Science and Engineering, Ningxia Key Laboratory of Development and Utilization of Specialty Food Resources, North Minzu University, Yinchuan 750021, China

Background & Aim： The global incidence of colorectal cancer (CRC) has been rising continuously. It is of great research significance to explore natural flavonoid anticancer lead compounds with low toxicity from *Carthamus tinctorius* L. (safflower). This study aimed to investigate the antiproliferative effect of 6-Hydroxykaempferol-3-O-β-D-glucopyranoside (HK3G), a flavonoid glycoside isolated from safflower, on human colon cancer HCT116 cells, and to elucidate its molecular regulatory network across multiple dimensions including oxidative stress, ferroptosis, apoptosis and autophagy.

Methods： HCT116 cells were used as the in vitro research model. The inhibitory effect of HK3G on cell proliferation was evaluated by cell morphological observation and colony formation assay. Flow cytometry was performed to detect cell cycle arrest and apoptosis levels; activation of the mitochondrial apoptosis pathway was verified by mitochondrial membrane potential (ΔΨm) assay and intracellular calcium ion (Ca^{2+}) fluorescence staining. Cell migration and invasion capacities were determined via Transwell assay. Fluorescent probes and commercial biochemical kits were applied to measure intracellular levels of reactive oxygen species (ROS), ferrous ions (Fe^{2+}), glutathione (GSH) and malondialdehyde (MDA); ferroptosis activation was confirmed by glutathione peroxidase 4 (GPX4) immunofluorescence staining and ferrostatin-1 (Fer-1) rescue assay. The formation of intracellular autolysosomes was observed by transmission electron microscopy (TEM). Integrated miRNAomics and transcriptomics analysis was conducted to screen differentially expressed genes and key miRNA-mRNA regulatory axes associated with apoptosis, ferroptosis and autophagy under HK3G treatment.

Results： HK3G inhibited the proliferation, colony formation, migration and invasion of HCT116 cells in a concentration-dependent manner, and induced G2/M phase cell cycle arrest. HK3G disrupted mitochondrial membrane homeostasis, triggered calcium overload and excessive ROS accumulation, and significantly promoted cell apoptosis. In response to oxidative stress, cells initiated a compensatory defense mechanism, leading to a marked elevation of intracellular GSH content. However, HK3G concurrently downregulated the expression of GPX4, the core executor of ferroptosis. As a result, GSH as the major antioxidant substrate failed to efficiently scavenge lipid peroxides, ultimately causing remarkable increases in MDA and Fe^{2+} levels. The ferroptosis inhibitor Fer-1 partially reversed HK3G-induced ROS accumulation and lipid peroxidation damage. Abundant autolysosome structures were visualized under TEM, indicating that HK3G simultaneously activated cellular autophagy. The integrated omics analysis identified multiple key miRNA-mRNA interaction pathways regulating oxidative stress, ferroptosis, apoptosis and autophagy.

Conclusion： Safflower-derived HK3G exerts anti-colorectal cancer activity through multiple synergistic mechanisms: it triggers severe oxidative stress, induces compensatory GSH elevation but inactivates the GPX4-mediated lipid peroxide clearance pathway, and co-activates ferroptosis, mitochondrial apoptosis and lethal autophagy. This study provides solid in vitro experimental evidence and omics-based molecular mechanistic support for HK3G as a promising natural candidate agent against colorectal cancer.

GL16: Polysaccharides from *Coreopsis tinctoria* Buds Enhance the Hypoglycemic Effect of Metformin

Shang Gao, Rui Bo Jia, Saiyi Zhong*
College of Food Science and Technology, Guangdong Ocean University, Guangdong Provincial Key Laboratory of Aquatic Product Processing and Safety, Guangdong Province Engineering Laboratory for Marine Biological Products, Guangdong Provincial Engineering Technology Research Center of Seafood, Guangdong Provincial Engineering Technology Research Center of Prefabricated Seafood Processing and Quality Control, Zhanjiang 524088, China

Diabetes has become a global public health challenge owing to its rising incidence and prevalence, and metformin, despite being a first-line therapy, cannot completely halt disease progression or cure the disease [1,2]. Combination therapy with polysaccharides as adjuvants has shown promise in enhancing the efficacy of antidiabetic drugs while enabling dose reduction[3,4]. *Coreopsis tinctoria* buds polysaccharides exhibit α-glucosidase inhibitory activity in vitro, yet systematic in vivo studies on their hypoglycemic adjuvant potential remain lacking[5]. In this study, we investigated whether polysaccharides extracted with sodium hydroxide from *Coreopsis tinctoria* buds (Al) could enhance the hypoglycemic effect of low-dose metformin (LMET) in streptozotocin-induced diabetic mice, and explored the underlying mechanisms via gut microbiota and metabolomics. The results showed that both metformin and LMET+Al alleviated weight loss and hyperglycemia; however, LMET+Al more effectively reduced fasting blood glucose, improved glucose tolerance, promoted glycogen synthesis, restored islet function, and stimulated insulin secretion. Notably, LMET+Al better prevented islet cell atrophy by inhibiting cleaved Caspase-3 and the NLRP3 inflammasome. Gut microbiota analysis revealed a higher abundance of the probiotic Ligilactobacillus in the LMET+Al group compared to metformin alone. Metabolite profiling indicated that LMET+Al regulated diabetic mice through aspartate metabolism and sphingolipid metabolism pathways. Correlation analysis further demonstrated that sphingosine was positively correlated with Muribaculum and Alistipes_A, and negatively correlated with Acinetobacter, highlighting multi-omics interactions that collectively contribute to host health. These findings suggest that Al may serve as a useful adjunct hypoglycemic agent for metformin, offering a potential combination strategy for diabetes management.

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GL17: Enhancing Effect of Ultrasound-Assisted Natural Deep Eutectic Solvent Extraction on the Stability of R-Phycoerythrin and Its Thermodynamic

Ziyu Li, Shang Gao, Saiyi Zhong*
College of Food Science and Technology, Guangdong Ocean University, Guangdong Provincial Key Laboratory of Aquatic Product Processing and Safety, Guangdong Province Engineering Laboratory for Marine Biological Products, Guangdong Provincial Engineering Technology Research Center of Seafood, Guangdong Provincial Engineering Technology Research Center of Prefabricated Seafood Processing and Quality Control, Zhanjiang 524088, China

R-Phycoerythrin (R-PE), a red algae-derived pigment-protein complex with excellent fluorescence and bioactivity, has broad prospects in food, cosmetics, and medicine[1]. However, traditional extraction/purification is complex and costly[2], and R-PE is highly sensitive to heat, light, and pH[3], limiting its application. This study developed a green ultrasonic-assisted natural deep eutectic solvent (NADES) extraction coupled with aqueous two-phase system (ATPS) purification, and evaluated product stability and thermodynamic conformational mechanism. Using choline chloride-glucose (2:1, 33.1% water) as the solvent, the crude yield of R-PE reached 2.44% with a purity (A_{565}/A_{280}) of 0.45. After purification by PEG 2000-sodium potassium tartrate ATPS, A_{565}/A_{280} reached 3.15, meeting pharmaceutical-grade standards[4]. Stability tests showed the NADES extract (UADP) retained significantly more pigment than the water extract (UAWP) under thermal, light, pH, and storage stresses. UADP fully preserved the protein backbone and subunits, with α-helix content (79.9%)[5] far exceeding UAWP (34.2%). Thermodynamic fitting revealed UADP's second-step unfolding enthalpy (ΔH_2 = 339.5 kJ/mol) and melting temperature were markedly higher, with total synergy 54% greater than UAWP. DSC and fluorescence spectroscopy confirmed tighter hydrophobic core packing and stronger intramolecular cooperative forces. NADES reshapes the solvent microenvironment, reinforcing the internal hydrogen bond network and hydrophobic packing, thereby enhancing conformational rigidity[6]. After removal of the NADES, UADP still maintained high α-helix and tight conformation; together with NADES's water-dependent fluctuation inhibition[7], this confirms a persistent conformational lock rather than mere external protection[8].This work provides theoretical basis and technical support for green, efficient preparation of highly stable R-PE.

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GL18: Dual Antiglycation and Neuroprotective Actions of Siraitia Grosvenorii Polysaccharide Through Direct AGEs Inhibition and Gut-Brain Axis Modulation

Hui Long[1,2], Jie Wang[1,2], Wenjuan Yang[1,2], Pin Gong[1,2]*
[1]School of Food science and Engineering, Shaanxi University of Science and Technology, Xi'an 710021, China
[2]Key Laboratory of Precision Nutrition and Functional Product Development in Xi'an, Xi'an 710021, China

Dietary advanced glycation end products (dAGEs) are food-derived harmful compounds generated through non-enzymatic glycation between reducing sugars and proteins or lipids, and their accumulation is associated with oxidative stress, chronic inflammation, and metabolic disorders[1]. Natural AGEs inhibitors have attracted increasing attention for food safety and health intervention[2]. *Siraitia grosvenorii* polysaccharide (SGP), a bioactive polysaccharide with antioxidant and gut microbiota-regulating properties, has shown potential antiglycation activity[3]; however, its underlying mechanisms remain unclear. This study aimed to investigate the antiglycation effects of SGP and its protective mechanisms against dAGEs-induced neuroinflammation using food models, an in vitro BSA-fructose (BSA-Fru) glycation system, and an dAGEs-induced mouse model. SGP significantly inhibited dAGEs formation in cocoa biscuits, indicating its potential application in functional food processing[4]. In the BSA-Fru model, SGP suppressed the formation of fructosamine, dicarbonyl compounds, and fluorescent AGEs through metal ion chelation and competitive interaction with key BSA residues, particularly Asp108 and Arg144. In dAGEs-challenged mice, SGP supplementation improved behavioral impairments, restored intestinal barrier integrity, reduced colonic inflammation, and decreased hippocampal accumulation of AGEs and lipopolysaccharide (LPS). Moreover, SGP enhanced PSD95 and brain-derived neurotrophic factor (BDNF) expression, thereby alleviating neuroinflammatory responses. Multi-omics analysis integrating 16S rRNA sequencing and untargeted metabolomics revealed that dAGEs exposure induced gut microbiota dysbiosis and metabolic disturbance, characterized by enrichment of *Ruminococcus gnavus* and accumulation of isopentylamine. SGP intervention promoted the enrichment of beneficial bacteria, including *Parabacteroides gordonii*, and increased propionate production, which was associated with attenuated neuroinflammation. Collectively, SGP functions as both a direct dAGEs inhibitor and a microbiota-targeting functional ingredient, providing a promising strategy for functional food development and dAGEs-associated health intervention through antiglycation activity and gut–brain axis modulation.

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GL19: Network Pharmacology and Molecular Docking Analysis of *Astragalus* against Atherosclerosis

Xiao Mei Ma[1], Zhao Jun Wei[1,2]*
[1]School of Food and Biological Engineering, Hefei University of Technology, Hefei 230601, China
[2]School of Biological Science and Engineering, Ningxia Key Laboratory of Development and Utilization of Specialty Food Resources, North Minzu University, Yinchuan，750021, China

Background & Aim: Atherosclerosis (AS) is a major pathological basis of cardiovascular and cerebrovascular diseases, involving lipid deposition, oxidative stress, inflammation, endothelial dysfunction, and metabolic disturbance. *Astragalus membranaceus* is a medicinal and food-related plant resource with potential cardiovascular benefits, but its key anti-AS constituents and core targets remain unclear. This study aimed to construct a component-target-pathway evidence chain for *Astragalus* against AS using network pharmacology and molecular docking, and to identify candidate compounds and targets for further mechanistic validation.
Methods: Active constituents and predicted targets of *Astragalus* were screened from TCMSP using oral bioavailability (OB) >= 30% and drug-likeness (DL) >= 0.18 as criteria. AS-related targets were collected from GeneCards and OMIM, and shared targets were obtained by intersection. STRING was used to construct the protein-protein interaction (PPI) network, while DAVID was used for GO and KEGG enrichment analyses. Keap1, eNOS, Caspase-3, LOX-1, and PFKFB3 were selected as representative docking targets according to the network results and key AS pathological processes.
Results: A total of 20 active constituents were obtained, of which 17 had predictable targets. Overall, 209 drug targets, 2,561 AS-related targets, and 113 shared targets were identified. PPI and functional analyses indicated that the shared targets were mainly enriched in inflammation and immunity, vascular function and coagulation, lipid metabolism, oxidative stress, apoptosis, and signal transduction. GO enrichment yielded 817 terms, and KEGG enrichment identified 159 pathways, mainly including AGE-RAGE, PI3K-Akt, TNF, HIF-1, NF-kappaB, MAPK, and PPAR signaling pathways, which are closely related to vascular inflammation, metabolic stress, and plaque progression. The component-target network suggested that calycosin was associated with PTGS2, PTGS1, NOS2, RXRA, DPP4, PPARG, ADRB2, and MAPK14, covering inflammation, oxidative stress, lipid metabolism, and vasodilation. Docking analysis showed that calycosin bound well to eNOS, Keap1, PFKFB3, Caspase-3, and LOX-1, with binding energies of -9.2, -8.7, -8.7, -8.0, and -7.2 kcal/mol, respectively.
Conclusion: These findings suggest that *Astragalus* may exert anti-AS effects through multi-component, multi-target, and multi-pathway regulation involving anti-inflammatory activity, antioxidative stress, endothelial protection, lipid uptake regulation, and glycolytic reprogramming. Calycosin is a representative candidate constituent with both network relevance and multi-target binding potential, while PFKFB3 may link metabolic reprogramming with vascular inflammation. This study provides compound, target, and pathway evidence for subsequent validation of the calycosin-PFKFB3 axis.

GL20: Resistant Starch Induces Gut Barrier Failure and Secondary Renal JAK2-STAT3 Activation through Exocytosis

Hongting Deng, Lei Chen, Hui Teng*
[1]College of Food Science and Technology, Guangdong Ocean University, Zhanjiang, Guangdong 524000, People's Republic of China
[2]Guangdong Provincial Key Laboratory of Aquatic Product Processing and Safety, Zhanjiang, Guangdong 524000, People's Republic of China
[3]Guangdong Province Engineering Laboratory for Marine Biological Products, Zhanjiang, Guangdong 524000, People's Republic of China

Resistant starch (RS) is widely used in functional foods, yet its potential toxicity at high doses remains unclear. This study investigated the dose-dependent effects of highly branched corn starch (RCS), a type of RS, on colonic barrier function and subsequent kidney injury, and elucidated the underlying mechanisms. Mice were orally administered RCS at 0.5, 1.0, and 2.0 g/kg for three weeks, with or without the exocytosis inhibitor Vacuolin-1. The 0.5 g/kg RCS caused no significant changes, whereas 1.0 and 2.0 g/kg RCS disrupted colonic integrity, as evidenced by histological damage, elevated serum D-Lac and DAO, and reduced Occludin and ZO-1 expression, accompanied by decreased beneficial bacteria and increased opportunistic pathogens. Mechanistically, RCS activated exocytosis, which triggered renal NLRP3 inflammasome assembly and JAK2/STAT3 phosphorylation, leading to inflammatory cytokine release (IL-1β, IL-18), oxidative stress (SOD/CAT decline, MDA/H_2O_2 rise), and fibrotic responses (α-SMA, Collagen I upregulation), ultimately resulting in elevated serum BUN and CRE and renal histopathological damage. Vacuolin-1 co-administration reversed all these alterations. Correlation analyses confirmed significant associations between colonic barrier disruption and renal injury markers. These findings reveal that RCS induces dose-dependent colonic barrier dysfunction via exocytosis, subsequently activating renal NLRP3 and JAK2/STAT3 pathways through the gut–kidney axis. This study uncovers a novel gut–kidney toxicity pathway for RS and highlights the importance of dose optimization in RS-containing products.

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GL21: Bilayer Nanoencapsulation of Riboflavin-Producing Lactobacillus Plantarum B2 Improves Gastrointestinal Survival, Mucoadhesion, and Therapeutic Efficacy in Colitis

Wang Wei Zhang[1], Xiu Xiu Zhang[1], Yuan Song[1,2,3], Run Hui Ma[2,3], Zhi Jing Ni[2,3], Kiran Thakur[2,3], Jian Guo Zhang[1,3], Yi Long Ma[1,3], and Zhao Jun Wei[1,2,3]*
[1]School of Food and Biological Engineering, Hefei University of Technology, Hefei 230009, People's Republic of China
[2]School of Biological Science and Engineering, Specialty Food Nutrition and Health Innovation Team of Ningxia Hui Autonomous Region, North Minzu University, Yinchuan 750021, People's Republic of China
[3]Ningxia Key Laboratory of Development and Utilization of Specialty Food Resources, Yinchuan 750021, People's Republic of China

Oral administration of probiotic bacteria represents a promising strategy for the prevention and alleviation of colitis; however, its translational potential is frequently constrained by low bacterial viability under gastrointestinal conditions, inadequate mucosal adhesion, oxidative stress, and suboptimal host–microbe interactions at inflamed mucosal sites. To address these limitations, we developed a bilayer nanoencapsulation system for riboflavin-producing *L. plantarum* B2, consisting of an inner gallic acid–Ca^{2+} metal–polyphenol network and an outer coating of either hyaluronic acid (HA) or bovine serum albumin (BSA). Successful formation of uniform, conformal nanocoatings on the bacterial surface was confirmed by transmission electron microscopy (TEM), scanning electron microscopy (SEM), atomic force microscopy (AFM), zeta potential and particle size analyses, and laser scanning confocal microscopy (LSCM). Among the coated formulations, HA-coated *L. plantarum* B2 (H-G-*L. plantarum* B2) exhibited markedly improved storage stability, enhanced resistance to simulated gastrointestinal fluids, and greater tolerance to hydrogen peroxide-induced oxidative stress, while largely preserving bacterial growth kinetics, acidification capacity, riboflavin production, and isoflavone biotransformation activity during soymilk fermentation. Furthermore, HA-based nanoencapsulation significantly enhanced bacterial adhesion to Caco-2 intestinal epithelial monolayers in vitro and prolonged gastrointestinal retention in mice. In a dextran sulfate sodium (DSS)-induced colitis model, oral administration of nanoencapsulated *L. plantarum* B2 attenuated body weight loss, colon shortening, histopathological injury, and colonic oxidative stress. Mechanistically, the treatment suppressed the levels of TNF-α, IL-1β, calprotectin, MPO, and MDA; elevated IL-10, CAT, and reduced GSH; restored the expression of tight junction proteins ZO-1 and occludin; and modulated gut microbiota composition. These findings establish bilayer nanoencapsulation as an effective and biocompatible strategy to enhance probiotic oral delivery and highlight the therapeutic potential of riboflavin-producing *L. plantarum* B2 as a microbiome-targeted intervention for colitis management.

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GL22: Preparation of Composite Film Incorporating Pomegranate Peel Polyphenols/Ginger Essential Oil/Sodium Alginate/Nano TiO 2 Application in Post-Harvest Grapes Preservation

Elam Elnur[1,3], Wei Wang[2], Kiran Thakur[1,2], Wen-Ping Ma[2], Zhi-Jing Ni [2]*, Zhao Jun Wei[1,2]*
[1]School of Food and Biological Engineering, Hefei University of Technology, Hefei 230009, China
[2]School of Biological Science and Engineering, Specialty Food Nutrition and Health Innovation Team of Ningxia Hui Autonomous Region, North Minzu University, Yinchuan 750021, China
[3]Ningxia Key Laboratory of Development and Utilization of Specialty Food Resources, Yinchuan 750021, China

A composite film was prepared using sodium alginate as the substrate, supplemented with nano-TiO_2 and antimicrobial agents consisting of pomegranate peel polyphenols and ginger essential oil at different ratios. The film was fabricated via cast-film method as a pomegranate peel polyphenol/ ginger essential oil/sodium algi nate/nano-TiO_2 composite. Its properties were characterized, and the film's effects on grape storage quality in dicators were evaluated. The results showed the P6 composite film exhibited optimal mechanical properties, with a tensile strength of 6.13 MPa and an elongation at break of 200.88%. Its soil degradation rate reached 10.74% after 15 d. It effectively suppressed quality loss in grapes and significantly reduced rot rates, while better maintaining hardness, ascorbic acid content, soluble solids content, and titratable acidity, thereby extending the grape storage life. This study demonstrates that the composite film extends fruit shelf life, reduces packaging costs for greater economic benefit, and minimizes packaging waste and plastic pollution, offering significant environmental advantages.

GL23: Pre-acidification Modulates Stretchability of Casein Gels via Multi-Scale Structural Remodeling Mechanisms of Hydrogen Bonding-Calcium Phosphate Network Coupling

Zhaorui Li[1,2], Yixiao Wang[1,2], Baifeng Fu[1,2], Jinxiu Xu[1,2], Shuzhen Cheng[1,2]*, Ming Du[1,2,3]*
[1]State Key Laboratory of Marine Food Processing & Safety Control, School of Food Science and Technology, Dalian Polytechnic University, Dalian, 116034, China
[2]National Engineering Research Center of Seafood, School of Food Science and Technology, Dalian Polytechnic University, Dalian 116034, China
[3]College of Food Science and Engineering, Dalian Ocean University, Dalian 116023, China

Stretchable dairy products rely crucially on the structural plasticity of casein gels, yet the multi-scale regulatory mechanisms of pre-acidification on their stretchability remain unclear. This study employed multi-scale characterization to investigate how pre-acidification (pH 6.0-5.0) modulates stretchability of casein gels. A critical transition occurred at pH 5.2, where gels showed maximum extensibility (24.33 mm, 121.7% elongation), and a 20-fold increase in thermal stretchability compared with pH 6.0. Weakened hydrogen bonding and rearrangement of hydrophobic environments (indicated by slight shifts in the amide A and -CH_3 bands), together with dissolution of colloidal calcium phosphate nanoclusters (CCPs), jointly drove network reorganization and enabled the redistribution of water toward weakly bound states (T20). Rheological analysis revealed reduced elasticity (low modulus), enhanced chain mobility (high Jmax and low percentage of elasticity), and controlled viscous flow (η_0= 0.93), supported by Confocal Laser Scanning Microscopy showing well-aligned fibrous structures. Excessive acidification (pH 5.0) caused a 58.3% decline in extensibility due to disordered networks. Overall, this study establishes a regulatory framework linking pre-acidification degree to intermolecular forces, network topology, and stretchability, providing novel insights for designing stretchable dairy products and functional protein materials.

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GL25: Xanthurenic Acid Alleviates Acrylamide-induced Neuroinflammation Through TLR4-NLRP3-GSDMD Axis

Xiangning Ma, Jianwei Gao, Lujia Zhang, Fang Chen*
National Engineering Research Center for Fruits and Vegetables Processing, College of Food Science and Nutritional Engineering, China Agricultural University, Beijing 100083, China

Acrylamide (AA), a neurotoxic contaminant commonly encountered in food and the environment, can impair brain function by promoting oxidative injury and inflammatory responses. Xanthurenic acid (XA), a metabolite generated through the tryptophan pathway, has been implicated in the regulation of neuronal activity, metabolism, and immunity. Here, we evaluated whether XA could protect rats against AA-induced neurological damage. Preventive treatment with XA at 50 mg/kg/day markedly improved synaptic integrity and reduced oxidative stress and neuroinflammation following AA exposure. Transcriptomic analysis further showed that XA reversed the expression changes of a broad range of genes associated with inflammasome activation and inflammatory signaling. Mechanistically, XA restrained TLR4-dependent signaling, disrupted NLRP3 inflammasome formation, and limited caspase-1 activation. These effects consequently decreased GSDMD cleavage and suppressed pyroptotic cell death. XA also reduced the overall expression of GSDMD, suggesting an additional regulatory effect on the principal executor of pyroptosis. Taken together, these results indicate that XA protects against AA-induced neurological injury by limiting oxidative stress, neuroinflammation, and pyroptosis, primarily through modulation of the TLR4/NLRP3/GSDMD signaling axis.

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GL26: Myricetin Attenuates Inherited Lipid Accumulation and Metabolic Dysfunction Induced by Parental High-glucose Exposure in *Caenorhabditis Elegans*

Wanning Ma[1,2], Rui Lu[1,2], Jingyimei Liang[1,2], Yuxuan Zhao[1], Hui Cao[1]*, Jianbo Xiao[1]*
[1]Universidade de Vigo, Nutrition and Bromatology Group, Department of Analytical Chemistry and Food Science, Instituto de Agroecoloxía e Alimentación (IAA) – CITEXVI, 36310 Vigo, Spain
[2]College of Food Science and Technology, Northwest University, Xi'an, 710069, China

High-calorie and high-energy diets are major contributors to obesity and metabolic disorders. Recent evidence suggests that parental dietary exposure can not only disturb lipid metabolism in the exposed generation, but also influence lipid accumulation and metabolic susceptibility in subsequent offspring1. However, whether food-derived phytochemicals can alleviate parental diet-induced obesity-like phenotypes and limit their inheritance remains unclear. Here, we established a parental high-glucose-induced inherited obesity model in *Caenorhabditis elegans* (*C. elegans*) and evaluated the protective effects of myricetin, a naturally occurring dietary flavonol.
Synchronized parental worms were exposed to a normal diet, high-glucose diet, or high-glucose diet supplemented with myricetin. Lipid accumulation was assessed by Oil Red O staining in parental, F1 and F2 generations, while body size and locomotor activity were examined to evaluate broader physiological consequences. To explore the potential mechanisms involved, we further analyzed lipid metabolism-related gene expression, targeted metabolic profiles, oxidative stress-associated responses and H3K4me3-related chromatin changes.
Parental high-glucose exposure markedly increased lipid deposition in *C. elegans*, and elevated lipid accumulation was still observed in F1 and F2 descendants raised under normal conditions, suggesting the inheritance of a parental diet-induced obesity-like phenotype. Myricetin supplementation reduced lipid accumulation in parental worms and partially attenuated the inherited lipid deposition in offspring. These effects were accompanied by improved physiological performance, suppression of lipogenic gene expression, modulation of the IIS–DAF-16 axis, and restoration of glucose-related metabolic balance. In addition, altered H3K4me3-associated signals suggest that chromatin remodeling may contribute to the establishment and attenuation of parental high-glucose-induced metabolic memory.
Together, these findings indicate that myricetin mitigates parental high-glucose-induced lipid accumulation and metabolic dysfunction in *C. elegans*, highlighting its potential as a functional food-derived phytochemical for modulating inherited metabolic disorders.

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GL27: Ammonia-Sensitive Enhanced Intelligent System for Freshness Grading Monitoring of High-Protein Foods

Yuxiao Hu, Zhijian Tan*
Institute of Bast Fiber Crops & Center of Southern Economic Crops, Chinese Academy of Agricultural Sciences, Changsha 410205, China

To address key bottlenecks in early spoilage monitoring of high-protein foods—low volatile basic nitrogen (VBN) levels, poor sensitivity of traditional sensors, and inaccurate freshness grading—this work constructs high-sensitivity visual sensing systems for alkaline volatile gases via porous enrichment using cyclodextrin metal–organic frameworks (CD-MOFs)[1], fluorescence amplification[2], and multi-site synergistic capture with deep eutectic solvents (DESs)[3]. First, CD-MOF-derived porous enrichment and host-guest protection accelerate ammonia response and color shift of curcumin films, realizing three-grade precise freshness evaluation for shrimp. Second, self-adhesive solid-state fluorescent sensors are engineered; energy level modulation by fluorescent chaperones achieves turn-on fluorescence enhancement and resolves stability/adhesion defects under high humidity. Third, a multi-functional DES strategy relying on multi-site hydrogen bonding strengthens ammonia capture to fabricate flexible sensing tags with high sensitivity, low LOD and superior environmental tolerance. This study systematically elucidates performance-boosting mechanisms of porous architectures, molecular energy levels and active sites, providing integrated theoretical frameworks and technical routes for in-situ visual graded freshness intelligent packaging of high-protein foods.

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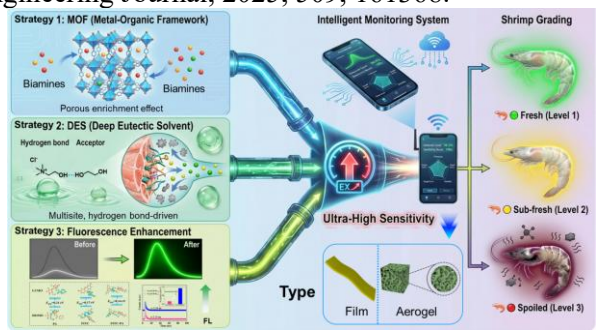

Figure 1. Construction of sensitivity-enhanced intelligent monitoring systems via three strategies for graded freshness detection of high-protein foods.

GL28: Smartphone App-assisted Colorimetric Sensing Based on 4-MPBA-Au@AgNPs for Instrument-Free Discrimination of Enshi Yulu Tea Grades

Wang Siyu[1], Long Wanjun[2], Fu Haiyan[1,2]*
[1]Hubei Provincial Key Laboratory for Protection and Application of Special Plants in Wuling Area of China, College of Life Sciences, South-Central Minzu University, Wuhan 430074, PR China
[2]The Modernization Engineering Technology Research Center of Ethnic Minority Medicine of Hubei Province, School of Pharmaceutical Sciences, South-Central Minzu University, Wuhan 430074, PR China

Enshi Yulu green tea (ESYL) is the most representative traditional steamed green tea in Enshi, Hubei[1,2]. Different ESYL grades exhibit distinct ffavors, tastes, and prices[3,4]. In this study, a visual sensor based on 4-MPBA Au@AgNPs was developed for the rapid and accurate identiffcation of ESYL grades. The recognition mechanism involved the binding of 4-MPBA Au@AgNPs with polyphenolic compounds in ESYL to form borate esters and the conversion of Ag+ to Ag0, with the generated Ag0 depositing on the surface of 4-MPBA Au@AgNPs. The results showed that the sensor can amplify the color differences of different grades of ESYL. The visual results were also validated by the partial least squares discriminant analysis model, demonstrating an enhancement in recognition accuracy from 68.2 % to 95.5 % compared to the original extraction solution. Furthermore, to further achieve instrument-free on-site visual discrimination of green tea grades, a smartphone app was integrated, with core functions including RGB extraction, Enshi Yulu grade classification model, and premium Enshi Yulu identification model. It classified and identified Enshi Yulu with different grades and verified premium Enshi Yulu, with an average accuracy of 97.0%. The results indicate that the constructed colorimetric sensor and smartphone app enable rapid and accurate instrument-free visual discrimination of Enshi Yulu with different grades, and provide new insights for the authenticity research of other polyphenol-rich foods[5].

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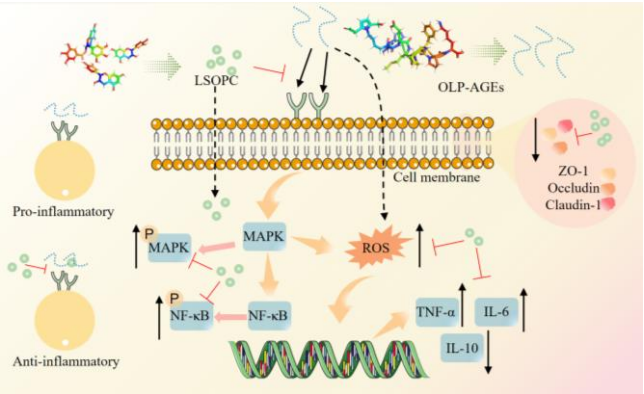
GL29: Procyanidins Target AGEs-RAGE Interaction to Alleviate Dietary AGEs-induced Intestinal Injury

Jia Yan[1], Gaohui Huang[1], Boran Zhang[1], Jianbo Xiao[3], Qian Wu[1,2]*, Haiyan Fu[2]*
[1]Hubei Key Laboratory of Industrial Microbiology, Hubei University of Technology, Wuhan, Hubei, 430068, China
[2]The Modernization Engineering Technology Research Center of Ethnic Minority Medicine of Hubei Province, School of Pharmaceutical Sciences, South-Central Minzu University, Wuhan, 430074, China
[3]Faculty of Sciences, Department of Analytical and Food Chemistry, Universidade de Vigo, Nutrition and Bromatology Group, Ourense, 32448, Spain

Dietary advanced glycation end products (AGEs) generated during thermal food processing are linked to intestinal inflammation[1]. After digestion, food-derived AGEs become oligopeptide-AGEs (OLP-AGEs), the true gut exposure form. The RAGE V domain (RAGE-V) is the key region that initiates OLP-AGEs-driven inflammatory signaling[2]. Human cohort data (NHANES) show higher AGEs intake is associated with abnormal bowel habits. Using surface plasmon resonance, fluorescence quenching, and molecular dynamics simulations, lotus seedpod oligomeric procyanidins (LSOPC), a sustainable agricultural by-product[3], are shown to directly bind RAGE-V with high affinity (KD = 1.338 μM) and competitively inhibit OLP-AGEs binding. This antagonism suppresses RAGE/NF-κB signaling in Caco-2 cells, extends healthspan in *Caenorhabditis elegans*, and alleviates OLP-AGEs-induced intestinal injury, barrier dysfunction, and gut dysbiosis in mice. This study thus provides the first molecular-level evidence that a natural polyphenol from an agricultural by-product acts as a direct RAGE-V antagonist, offering a mechanistic dietary strategy against dietary AGEs-induced intestinal inflammation.



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GL30: Integrated miRNA and mRNA Omics Reveal Neferine Induced Autophagy-Dependent Ferroptosis in Human Endometrial Cancer in Vivo and in Vitro

Feifei Ma[1,2], Rui Lu[1], Runhui Ma[1,3], Kiran Thakur[3], Jianguo Zhang[4], Jesus simal Gandara[1], Zhaojun Wei[3,4]*, Hui Cao[1]*

[1]Nutrition and Bromatology Group, Department of Analytical Chemistry and Food Science, Institute of Agroecology and Alimentasian (IAA)–CITEXVI, University of Vigo, Vigo, 36310, Spain

[2]School of Food Engineering, Anhui Science and Technology University, Chuzhou, 233100, People's Republic of China

[3]School of Biological Science and Engineering, Ningxia Key Laboratory for the Development and Application of Microbial Resources in Extreme Environments, North Minzu University, Yinchuan, 750021, China

[4]School of Food and Biological Engineering, Hefei University of Technology, Hefei 230009, People's Republic of China

The most frequent type of gynecological cancer, endometrial cancer, seriously jeopardizes the health of women. Lotus seed embryos contain large amounts of the compound neferine (Nef), which has demonstrated strong anticancer properties. Nevertheless, its impacts and defense mechanisms against Endometrial cancer (EC) are still unknown. In order to identify the putative anti-cancer pathways that Nef targets, we combined mRNA-seq and miRNA-seq analyses and assessed the effects of Nef on EC both in vivo and in vitro. The integrative analysis of miRNA and mRNA omics data identified autophagy and ferroptosis as the primary anti-cancer pathways targeted by Nef. Nef stimulated the production of autophagosomes and autolysosomes, so initiating cell autophagy, as demonstrated by transmission electron microscopy. Furthermore, Nef altered Fe2+ concentration, GSH, and MDA levels, promoting ferroptosis. Molecular data indicated that Nef activated the AMPK/mTOR and SLC7A11/GPX4 pathways in vitro and in vivo, inducing autophagy and ferroptosis. The use of the 3-Methyladenine (3-MA) and Ferrostatin-1 (Fer-1) reversed Nef-induced reactive oxygen species (ROS) generation and GPX4 expression levels, confirming that Nef suppresses Ishikawa cell growth through autophagy-dependent ferroptosis. These results indicate that Nef is a viable functional food for the treatment of EC, as it can dramatically promote autophagy-dependent ferroptosis in Ishikawa cells.

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GL31: Multi-Strain Fermentation of Whole Grains: Structural Remodeling, Flavor Modulation, and Development of Low-GI Functional Bakery Products

Jinchen Li, Yiming Zhou*, Minglong Wang, Lan Zhang, Renzhi Lv
Faculty of Flavour Fragrance and Cosmetics, Shanghai Institute of Technology, Shanghai, 201418, China

Whole grains are rich in dietary fiber, resistant starch, and polyphenols, which have been shown to reduce the risk of type 2 diabetes and cardiovascular diseases, as well as to improve gut microbiota composition. However, traditional whole grain products often suffer from coarse texture, poor palatability, and unsatisfactory processing properties due to the use of single and conventional processing methods, thus failing to meet the dual consumer demands for both palatable taste and nutritional quality. Lactic acid bacteria fermentation offers an innovative solution to these challenges. Nevertheless, the complex molecular mechanisms underlying the interactions between lactic acid bacteria and whole grain substrates during fermentation remain insufficiently elucidated, which limits the full exploitation of their potential advantages.

In this study, we systematically investigated the effects of fermentation with *Lactiplantibacillus plantarum* on the multiscale structure of coarse grain flours (tartary buckwheat, highland barley, and oat), as well as its subsequent impacts on dough processing performance, bread quality, and starch digestibility. Our results demonstrated that fermentation simultaneously improved the processing properties and nutritional functionality of coarse grain flours by remodeling starch crystalline structures and inducing a conformational transition of protein secondary structures from random coils to thermodynamically stable β-sheets. On this basis, we further employed a multi-strain synergistic fermentation strategy and isolated five lactic acid bacteria strains with outstanding acid- and ester-producing capacities. Through integrated volatile flavor compound analysis and metabolomic profiling, pyruvate, acetyl-CoA, valine, leucine, and isoleucine were identified as key nodes in the flavor metabolic network, enabling the establishment of a precision quality regulation model. Additionally, lactic acid bacteria fermentation was found to achieve simultaneous degradation of acrylamide and endogenous gluten allergens generated during processing.

Breads prepared with the fermented coarse grain flours exhibited significantly increased specific volume and retarded staling rates. In vitro digestion assays further revealed that the estimated glycemic index (eGI) of these breads was reduced to 52.03–55.17, meeting the criteria for low-GI foods. Collectively, this study systematically established a core technological system for whole grain fermented foods encompassing structural modification, flavor regulation, and safety hazard mitigation. Our findings provide a robust scientific foundation for the development of high-value-added functional whole grain products and facilitate the sustainable advancement of the whole grain industry toward health-oriented and quality-enhanced directions.

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GL32: Maternal Quercetin Induces Female-specific Intergenerational Lifespan Extension Associated with Glycine-centered Metabolic Remodeling in Drosophila Melanogaster

Quanyong Wu[1], Boya Ouyang[1], Yi Yuan[2], Min Zhang[3], Jesus Simal-Gandara[1]*, Hui Cao [1]*
[1]Universidade de Vigo, Nutrition and Bromatology Group, Department of Analytical Chemistry and Food Science, Instituto de Agroecoloxía e Alimentación (IAA), Vigo, Spain
[2]College of Biological Science and Engineering, Fuzhou University, Fuzhou 350108, China
[3]College of Oceanology and Food Science, Quanzhou Normal University, Quanzhou 362000, China

Quercetin is a natural polyphenol with reported anti-aging properties; however, its stage-specific and intergenerational effects on lifespan regulation remain unclear[1,2]. This study investigated the effects of quercetin exposure at different developmental stages on lifespan regulation in *Drosophila melanogaster* and evaluated the intergenerational impact of parental exposure on offspring lifespan and metabolic homeostasis. Quercetin was administered during embryonic or adult stages in *Drosophila melanogaster*. Lifespan, locomotor activity, antioxidant capacity, transcriptomic, metabolomic, and epigenetic changes were analyzed. Intergenerational effects were assessed in F1 and F2 offspring, and glycine supplementation experiments were performed to explore the underlying metabolic mechanisms. Embryonic exposure altered developmental timing and endocrine regulation but did not significantly extend adult lifespan. In contrast, adult-stage quercetin treatment selectively prolonged lifespan in female flies and improved locomotor performance and antioxidant capacity. Quercetin activated energy-sensing, autophagy, immune homeostasis, and stress-response pathways, accompanied by metabolic remodeling involving glycolysis, pentose phosphate pathway activity, TCA cycle intermediates, and one-carbon metabolism. Glycine was consistently altered in both treated parental flies and offspring. Glycine supplementation partially reproduced the lifespan extension and metabolic remodeling observed in offspring from quercetin-treated maternal flies. Maternal quercetin treatment induced a female-specific lifespan extension and substantial metabolic remodeling in F1 offspring, whereas these effects were attenuated in the F2 generation. Quercetin regulates lifespan in a stage-dependent and sex-specific manner through coordinated metabolic and epigenetic remodeling. Maternal quercetin exposure induces a female-specific intergenerational longevity effect that is associated with glycine-related metabolic remodeling.

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GL33: Polysaccharides from *Cynanchum auriculatum* Royle Ex Wight Ameliorate Symptoms of Hyperglycemia by Regulating Gut Microbiota in Type 2 Diabetes Mellitus Mice

Jiawei Zhang[1], Ligen Chen[2], Rong Shao[2], Wei Xu[2]*
[1]College of Biotechnology and Pharmaceutical Engineering, Nanjing Tech University, Nanjing, 211816, China
[2]College of Marine and Bioengineering, Yancheng Institute of Technology, Yancheng, 224051, China

Type 2 diabetes mellitus (T2DM) represents a chronic metabolic disorder characterized by disrupted carbohydrate and lipid balance, resulting in hyperglycemia[1,2]. This study evaluated the impact of polysaccharides derived from *Cynanchum auriculatum* Royle ex Wight (CRP) on mitigating hyperglycemia and modulating intestinal microbiota in T2DM mice[3]. Findings indicated that CRP is mainly linked by →6)α-D-Glcp-(1→ and CRP-H demonstrated greater efficacy than CRP-L in regulating hypoglycemic-related indicators such as serum high-density lipoprotein cholesterol (HDL-c) level. Additionally, CRP at varying doses enhanced the mRNA expression of insulin receptor substrate 1 (IRS-1), phosphatidylinositol 3-kinase (PI3K), protein kinase B (AKT-1), and glucose transporter 2 (GLUT-2). Following a 4-week CRP-H treatment, a significant reduction in the Firmicutes/Bacteroidetes ratio at the phylum level was observed, alongside a marked increase in the relative abundance of beneficial genera such as Limosillactobacillus and Prevotella. Overall, CRP-H displayed enhanced hypoglycemic properties by activating the IRS-1/PI3K/AKT-1/GLUT-2 pathway and enriching beneficial gut bacteria, including Prevotella and Limosillactobacillus[4,5]. This study establishes a foundational framework for further development and application of *Cynanchum auriculatum* Royle ex Wight resources, emphasizing the hypoglycemic potential of CRP.

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GL34: Study on the Protective Effect of *Rhodiola rosea* L.-Red Ginseng Combined Fermentation on Acute Liver Injury by APAP

Tingting Hu[1], Shuang Liu[2], Xin Qi[2], Chengbi Cui[1,2]*
[1]College of Pharmacy, Yanbian University, Yanji, Jilin Province, 133002, China
[2]College of Agriculture, Yanbian University, Yanji, Jilin Province,133002, China

Rhodiola rosea L. and Red ginseng, as medicinal and edible herbs, have been proven effective in treating liver-related diseases[1,2]. However, the mechanism by which the mixed fermentation of *Rhodiola rosea L.* and Red ginseng (F-R+R) affects acute liver injury (ALI) is still unclear. The study aims to investigate the protective effect of F-R+R on ALI induced by acetaminophen (APAP). Mixed fermentation extraction was carried out using *L. plantarum* and *Pediococcus acidilactici*[3]. Identify the main compounds by HPLC and determine their antioxidant activity. Using the APAP induction model, liver function, inflammatory factors, pathological morphology of liver tissue, expression of PI3K/AKT/Bax/Bcl-2 related proteins, and gut microbiota were measured to explore the protective effect of F-R+R on the liver[4,5]. The results indicate that F-R+R can regulate inflammatory response by inhibiting abnormal activation of the PI3K/AKT signaling pathway, thereby reducing cell apoptosis, improving gut microbiota, and protecting the liver from APAP damage.

Acknowledgments
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GL35: *Anoectochilus Roxburghii* (Wall.) Lindl-Derived Nanovesicles Attenuate Colitis-Associated Colorectal Cancer via Gut Microbiota-Dependent Reprogramming of Tryptophan Metabolism

Xiaoxiao Han[1], Xinyue Huang[1], Yusha Zhang[1], Xipeng Song[1], Yi Sun[1,2], Xuecheng Yu[1], Yanan Yu[1], Shengqian Deng[1], Zonghui Xu[1], Huizhe Ding[1], Man Li[1], Chengtao Sun[1]*, Guoyin Kai[1]*
[1]Zhejiang Provincial International S&T Cooperation Base for Active Ingredients of Medicinal and Edible Plants and Health, Zhejiang Provincial Key TCM Laboratory for Chinese Resource Innovation and Transformation, School of Pharmaceutical Sciences, Jinhua Academy, Zhejiang Chinese Medical University, Hangzhou, Zhejiang, 310053, China
[2]Innovative Institute of Chinese Medicine and Pharmacy, Shandong University of Traditional Chinese Medicine, Jinan, Shandong, 250355, China

Gut microbiota dysbiosis and metabolic disturbances are critically involved in the development of colitis-associated colorectal cancer (CAC)[1,2]. Whether *Anoectochilus roxburghii* (Wall.) Lindl (AR)-derived nanovesicles (ARNVs) mitigate AOM/DSS-induced CAC through microbiota remodeling and tryptophan metabolic reprogramming remains unclear. Here, we show that orally administered ARNVs markedly suppress CAC progression with high intestinal tropism and favorable biosafety. ARNVs treatment induces a causal remodeling of the gut microbiota, particularly by decreasing Amulumruptor abundance and enriching CAG-485 abundance. Antibiotic depletion and fecal microbiota transplantation demonstrate that enhanced activation of the indole branch of tryptophan metabolism, characterized by increased levels of tryptamine and tryptophol. Correlation analysis showed that CAG-485 abundance was positively associated with tryptamine and tryptophol levels, whereas Amulumruptor was negatively correlated with tryptophol, suggesting that ARNVs promote indole metabolite production via selective microbial remodeling. Mechanistically, ARNVs-driven microbiota remodeling redirects tryptophan metabolism toward antitumor indole derivatives, including tryptamine and tryptophol, which attenuate colorectal cancer progression by suppressing SPP1 expression and inhibiting ECM-EMT signaling axis. Collectively, ARNVs modulate specific microbial taxa and enhancing indole-dependent tryptophan metabolism to attenuate CAC progression. These findings provide mechanistic insight into the therapeutic potential of ARNVs and identify microbiota-metabolite signatures that may serve as candidate biomarkers for CAC intervention.

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GL36: Study on the Physiological and Biochemical Characteristics and Gut Microbiota Effects of Type 3 Lotus Seed Resistant Starch on OVA Induced Food Allergy Rats

Zhiyun Wang
College of Food Science, Fujian Agriculture and Forestry University, Fuzhou 350002, China

Abstract: Food allergies have become a global high incidence food safety and immune health issue. In order to clarify how natural food macromolecule type 3 lotus seed resistant starch (LRS3) affects physiological, biochemical, and intestinal microbiota in alleviating OVA induced food allergies in rats, this study prepared LRS3 using a hydrothermal/enzymatic method for in vivo animal intervention. An OVA induced food allergy model was constructed in BN rats to systematically explore the physiological, pathological, and intestinal microbiota evolution laws of LRS3 intervention in alleviating allergies. The results showed that the OVA model rats had slower growth, higher anal temperature, significantly increased serum Th2 cytokines (IL-4, IL-5, IL-13, IL-25), specific IgE/IgM, mast cell activation mediators (histamine, CMA1), and intestinal injury markers (TNF-α, TSBAP1) ($P<0.05$), and a large amount of inflammatory cell infiltration and crypt structure destruction in the colonic mucosa. LRS3 intervention can significantly restore feeding and body weight in rats, reduce allergy symptom scores, inhibit Th2 immune overactivation, downregulate allergen release, repair colon mucosal integrity, and is safer than the glucocorticoid dexamethasone. The results of gut microbiota analysis showed that OVA sensitization disrupted the stability of colonic microbiota, reduced the abundance of short chain fatty acid synthesis bacteria and mucus degrading bacteria; LRS3 can reshape the microbial community structure, increase the relative abundance of beneficial bacteria such as Pseudoflavonifractor and Candidatus_Faecousia, upregulate GH family starch degrading glycoside hydrolase, and enhance polysaccharide fermentation and SCFA production. The research results provide theoretical basis and experimental support for the development of LRS3 as a natural functional food and nutritional intervention for food allergies.

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GL37: Monosodium Glutamate Disrupts Methionine Metabolism to Induce Transgenerational Infection Susceptibility in *C. elegans*

Shiye Lin, Hui Cao, Jianbo Xiao
Universidade de Vigo, Nutrition and Bromatology Group, Department of Analytical and Food Chemistry, Faculty of Sciences, 32004 Ourense, Spain

Monosodium glutamate (MSG) is a widely used food additive, and its potential health effects under excessive or chronic dietary exposure remain controversial. Here, using *Caenorhabditis elegans* as a model, we show that parental MSG exposure reduces host resistance to *Pseudomonas aeruginosa* PA14 infection and impairs learning behavior, with these effects persisting for two subsequent generations. Mechanistically, MSG perturbs one-carbon metabolism, reducing glucose-derived methionine and thereby suppressing S-adenosylmethionine (SAM) generation. This leads to reduced tri-methylation at the 4th lysine residue of the histone H3 protein (H3K4me3) levels and transcriptional downregulation of foxo/daf-16 in both parents and offspring. Dietary supplementation with SAM or tetrahydrofolate mixed with methionine improves immunity in F1 offspring. Furthermore, metabolic changes in MSG-exposed *Escherichia coli* suggest that microbial metabolism may contribute to transgenerational phenotype. Together, these results reveal a potential pathway by which parental dietary MSG intake can shape offspring health status by influencing microbial and host metabolism and epigenetic programming, highlighting evidence for how the potential long-term risks of food additives can negatively impact on transgenerational health.

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GL38: Quercetin Alleviates MSG-Induced Oxidative Toxicity and Functional Decline in Caenorhabditis Elegans

Boya Ouyang[1], Hui Cao[1], Jesus Simal-Gandara[1]*, Jianbo Xiao[1,3]*
[1]Universidade de Vigo, Nutrition and Bromatology Group, Department of Analytical Chemistry and Food Science, Instituto de Agroecoloxía e Alimentación (IAA) - CITEXVI, 36310 Vigo, Spain
[2]Research Group on Food, Nutritional Biochemistry and Health, Universidad Europea del Atlántico, Isabel Torres 21, 39011 Santander, Spain

Monosodium glutamate (MSG) is a widely used food additive [1]. However, the long-term consequences of early-life MSG exposure on aging-associated physiological homeostasis remain poorly understood. This study investigated whether developmental MSG exposure induces persistent oxidative toxicity and functional decline in *Caenorhabditis elegans* and evaluated the protective effects of quercetin (Que).
Synchronized worms were exposed to MSG during larval development (L1–L4) and subsequently treated with Que during early adulthood. Lifespan, locomotor activity, reproductive performance, stress resistance, oxidative stress biomarkers, targeted metabolomics, transcriptomic profiling, and pathway-associated functional analyses were performed.
Developmental MSG exposure significantly shortened lifespan, impaired locomotor performance, and altered reproductive patterns without affecting body length. These physiological impairments were accompanied by increased reactive oxygen species accumulation, reduced antioxidant capacity, and decreased resistance to heat and oxidative stress. Targeted metabolomics revealed widespread metabolic remodeling, including reductions in multiple amino acids and tricarboxylic acid cycle intermediates, indicating disrupted metabolic homeostasis and energy metabolism. Transcriptomic analysis further demonstrated alterations in glutathione metabolism, xenobiotic detoxification, and stress-response pathways. Functional analyses using a gst-4p:GFP reporter strain showed impaired gst-4-associated detoxification responses following MSG exposure, whereas Que partially restored detoxification capacity. Furthermore, the lifespan-protective effect of Que was markedly attenuated in daf-16 (mu86) mutants, supporting the involvement of DAF-16-dependent stress resilience.
Collectively, these findings demonstrate that developmental MSG exposure induces persistent oxidative stress, metabolic remodeling, and functional decline, whereas Que partially alleviates these adverse effects by modulating redox homeostasis, metabolic balance, and stress-response pathways.

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GL39: Finger Citron (*Citrus medica L. var.* Sarcodactylis Swingle) and Its Characteristic Component Limettin Alleviated Diet-Induced Obesity via Modulating Gut Microbiota and Steroid Hormone Biosynthesis

Hui Xu[1], Jiebiao Chen[1], Xinyu Shen[1], Yunyi Chen[1], Jiaojiao Liang[1], Yan Liu[2], Jinping Cao[1], Li-Shu Wang, Baiyi Lu[3], Chongde Sun[1]* and Yue Wang[1]*
[1]Fruit Science Institute, College of Agriculture and Biotechnology, Zhejiang University, Hangzhou 310058, People's Republic of China
[2]Division of Hematology and Oncology, Department of Medicine, Medical College of Wisconsin, Milwaukee, Wisconsin 53226, United States
[3]College of Biosystems Engineering and Food Science, Key Laboratory for Quality Evaluation and Health Benefit of Agro-Products of Ministry of Agriculture and Rural Affairs, Key Laboratory for Quality and Safety Risk Assessment of Agro-Products Storage and Preservation of Ministry of Agriculture and Rural Affairs, Zhejiang University, Hangzhou 310058, People's Republic of China

This study investigated the antiobesity effects and underlying mechanisms of finger citron extract (FC) and its characteristic compound limettin (LMT) in high-fat diet (HFD)-induced obese mice. FC and LMT significantly reduced body weight gain and improved glucose and lipid homeostasis in obese mice. Fecal 16S rRNA sequencing revealed that both treatments reversed HFD-induced gut dysbiosis, enriching norank_f__norank_o__Clostridia_UCG-014, while FC uniquely increased Akkermansia and decreased Rikenella. Serum metabolomics indicated that FC and LMT markedly activated the steroid hormone biosynthesis pathway, elevating 11β-hydroxyprogesterone, 17α-hydroxyprogesterone, and 11-deoxycorticosterone. Colon transcriptomics further confirmed altered local steroid synthesis and metabolism in the colon. Antibiotic depletion and fecal microbiota transplantation verified the indispensable role of gut microbiota in FC/LMT-mediated metabolic protection. Collectively, FC and LMT ameliorated diet-induced obesity by modulating steroid hormone biosynthesis through gut microbiota regulation, highlighting their potential as functional dietary supplements for obesity prevention.

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GL40: Interannual variation in tea stable isotopes and climate-informed data augmentation

Menglin Zhang[1,2,3], Jianbo Xiao[2,3]*, Chunlin Li[1]*
[1]State Key Laboratory for Quality and Safety of Agro-Products, Institute of Agro-Products Safety and Nutrition, Zhejiang Academy of Agricultural Sciences, Hangzhou 310021, China
[2]Universidade de Vigo, Nutrition and Bromatology Group, Department of Analytical Chemistry and Food Science, Faculty of Science, 32004, Ourense, Spain
[3]Instituto de Agroecoloxía e Alimentación (IAA), Universidade de Vigo, Campus Auga, 32004 Ourense, Spain

Stable-isotope geographic authentication is widely used because isotopic fingerprints are often assumed to remain more temporally persistent than many conventional compositional markers[1,2]. However, the extent to which climate-driven isotope variability affects the long-term transferability of authentication frameworks remains poorly understood, particularly in perennial crops exposed to multi-year environmental variability[3]. A seven-year multi-isotope dataset from tea cultivated in monsoon-dominated northern China is used to evaluate how interannual climatic variability reshapes isotope-space structure and influences geographic authentication across years. Although isotope fingerprints achieve strong within-year discrimination in 2024 (recall = 0.982), direct application to 2022–2023 samples result in substantial performance declines (recall = 0.543 and 0.560), indicating pronounced temporal instability. Multiscale climate analyses reveal a strong antecedent climate-memory effect, with isotope–climate coupling peaking 1–3 months before harvest, suggesting that isotope signatures integrate hydroclimatic forcing over extended periods. These results highlight three limitations of current authentication frameworks: assumptions of multi-year baseline stability, insufficient consideration of antecedent climate effects, and the lack of mechanisms for updating temporally shifting isotope baselines. To address these limitations, a climate-informed virtual isotope reconstruction framework is developed to infer year-specific isotope baselines from climatic predictors. Reconstruction improves cross-year membership recovery (recall > 0.8), providing a pathway toward more robust authentication under increasing environmental variability.

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GL41: Cloud Algorithms Enhanced ZAIS@GSH Fluorescence Colorimetric Sensing Combined with Mobile Phone App for Visual Detection of Paraquat in Food

Xueqing Zeng[1,2], Hengye Chen[1], She Yuanbin[3]*, Haiyan Fu[1,2]*
[1]Hubei Provincial Key Laboratory for Protection and Application of Special Plants in Wuling Area of China, College of Life Sciences, South-Central Minzu University, Wuhan, China
[2]The Modernization Engineering Technology Research Center of Ethnic Minority Medicine of Hubei Province, School of Pharmaceutical Sciences, South-Central Minzu University,
Wuhan 430074, PR China
[3]State Key Laboratory Breeding Base of Green Chemistry-Synthesis Technology, College of Chemical Engineering, Zhejiang University of Technology, Hangzhou 310032, PR China

Paraquat, as a highly efficient and broad-spectrum herbicide widely used around the world, plays a crucial role during the cultivation and harvest of crops. However, due to its strong toxicity, even a small amount of residue can cause irreversible damage to the human body. In this work, a fluorescence colorimetric sensor based on Zn-Ag-In-S@GSH (ZAIS@GSH) for accurately detecting PQ was constructed. The photoinduced electron transfer (PET) effect mediated by electrostatic adsorption between ZAIS@GSH and PQ selectively quenches the fluorescence emission peak at 540 nm of quantum dots and generates rich fluorescence color changes. The results show that the linear fitting coefficient of PQ concentration and fluorescence intensity within the range of 1 μg/L -10 μg/L is greater than 0.99, and the calculated LOD is as low as 5.6 × 10-2 μg/L. Furthermore, the RF regression algorithm was used to fit the linear relationship between the RGB values of the color response and the PQ concentration. The R2 of both the training set and the prediction set were above 0.99. The recovery rates calculated based on the PQ concentrations predicted by the mobile phone APP based on this fitting model are generally between 83% and 120%, and the RSD is within 15%. The cloud-based algorithm-enhanced fluorescence colorimetric sensor constructed in this work, combined with the mobile phone APP method, accurately predicted the PQ concentration, providing a new idea for the detection of harmful substances in agricultural products.

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GL42: A Voting Model Weighting Algorithm-Driven Multi-Algorithm Framework Enhances Intelligent Point-of-Care Testing for Edible Oil Safety

Zhiqiang Li[1,2], Wen Zhang[2], Qi Zhang[2], Peiwu Li[2], Xiaoqian Tang[2]*, Wei Wang[1,2]*
[1]College of Engineering, China Agricultural University, Beijing, China
[2]Oil Crops Research Institute, Chinese Academy of Agricultural Sciences, Wuhan, China

Dibutyl phthalate (DBP) and benzo[a]pyrene (BaP) are typical hazardous contaminants in edible oils, which show high toxicity, wide distribution and serious threats to human health[1-3]. Conventional point-of-care testing methods suffer from subjective judgment, poor accuracy and matrix interference, failing to meet the demand for rapid and precise on-site screening[4-6]. We developed a bimetallic porous carbon nanomaterial Pt-Zn-CN with excellent photothermal and antibody-loading properties as signal probes, and established a dual-mode lateral flow immunoassay. Combined with a voting model weighting algorithm-driven multi-algorithm framework, an intelligent edible oil safety detection platform was constructed, realizing high-precision, high-speed and visualized quantitative detection of DBP and BaP with ultra-low detection limits. After systematic optimization, the LODs reached 0.184 ng/mL for DBP and 0.096 ng/mL for BaP. Combined with ant colony optimization, DBSCAN clustering and weighted voting fusion, the platform achieved 97.6% contour recognition, 95.7% accuracy within 0.03 s. It features high sensitivity, speed and intelligence, providing a reliable tool for rapid on-site screening.

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GL43: Procyanidin C1 From Cynomorium Songaricum Targets SERCA2b to Alleviate Endoplasmic Reticulum Stress in T2DM

Zhihao Liu[1,2], Jihang Chen[1,2]*
[1]Shenzhen Key Laboratory of Steroid Drug Discovery and Development, Department of Pharmaceutical Science, Division of Biomedical Health Sciences, School of Medicine, The Chinese University of Hong Kong, Shenzhen, Guangdong, PR China
[2]The Chinese University of Hong Kong, Shenzhen Futian Biomedical Innovation R&D Center, Shenzhen, Guangdong, PR China

Cynomorium songaricum Rupr., a traditional edible and medicinal plant in China, exhibits hypoglycemic potential, yet its active constituents, direct targets, and mechanisms in endoplasmic reticulum (ER) stress-associated type 2 diabetes remain unclear. This study investigated the pharmacological basis of a polyphenol-enriched fraction from Cynomorii Herba (CSF) and its major bioactive constituents. UPLC/ESI-LTQ-Orbitrap-MS profiling, network pharmacology, and functional screening in high-insulin/high-glucose and palmitic acid/oleic acid-induced HepG2 cell models identified ER stress attenuation as a principal mechanism of CSF action. This effect was further supported in a 5-month high-fat diet-induced diabetic mouse model by integrated transcriptomic and lipidomic analyses, which showed that CSF improved insulin sensitivity while reducing ER stress, oxidative injury, and lipogenesis. Activity-guided screening subsequently identified procyanidin C1 (PCC1) as a potential active constituent. Integration of transcriptomic and Connectivity Map analyses prioritized SERCA2b as a central molecular target. Restoration of SERCA2b-dependent ER Ca^{2+} homeostasis was associated with suppression of the IRE1α-JNK-IRS1 and PERK-eIF2α-ATF4 pathways, thereby improving insulin signaling and redox homeostasis. Molecular docking, molecular dynamics simulations, surface plasmon resonance (SPR), cellular thermal shift assays (CETSA), pharmacological SERCA2b inhibition with thapsigargin, and SERCA2b knockdown in vitro and in vivo collectively supported a direct interaction between PCC1 and SERCA2b and demonstrated the SERCA2b dependence of its metabolic effects. These findings reveal that PCC1 might target SERCA2b to restore ER Ca^{2+} homeostasis, providing a mechanistic basis for developing innovative small-molecule lead compounds against ER stress-associated metabolic disorders.

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GL44: Dietary EGCG Promotes Transgenerational Host Defense Through a Lactate-H3K27ac Axis

Wenqi Huang, Jianbo Xiao, Hui Cao
Universidade de Vigo, Nutrition and Bromatology Group, Department of Analytical and Food Chemistry, Faculty of Sciences, 32004 Ourense, Spain

Parental diet is a key determinant of offspring health and immune function, in part through epigenetic regulation[1,2]. However, the mechanism by which specific dietary bioactive compounds reshape metabolic-epigenetic networks to drive transgenerational adaptive responses remains poorly understood. Here, we found that early-life EGCG exposure increased survival upon *Pseudomonas aeruginosa* or *Staphylococcus aureus* infection and persisted for two subsequent generations in *Drosophila melanogaster*. Mechanistically, EGCG reduced intestinal amino acids, thereby moderately inducing activation of activating transcription factor 4 (ATF4), which in turn enhanced maternal glycolysis and immune adaptation. Tyrosine supplementation abolished the enhanced host defense and metabolic changes. Furthermore, ATF4-induced activation of glycolysis promoted ovarian lactate production, serving as a substrate for increased global H3K27 acetylation in the offspring. Together, these findings suggest that dietary bioactive compounds modulate metabolic and gene regulatory processes, with functional evidence supporting a role for amino acid metabolism and lactate in linking metabolic remodeling to enhanced resistance to infection in the offspring. This work provides mechanistic insight into how diet can shape heritable immune function through metabolic-epigenetic interplay[3].

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GL45: Mechanistic Study on the Effects of Hawthorn Red Pigment Via the cAMP-PKA-CREB Axis on Proliferation, Apoptosis and Autophagy of Non-Small Cell Lung Cancer

Quanhong Gao[1], Wen-teng Yang[1], kun Ranc, Mu-xuan Wang[2]*, Ning-yang Lia*
[1]State Key Laboratory of Marine Food Processing & Safety Control, College of Food Science and Engineering/Sanya Ocean Institute, Ocean University of China, Qingdao, Sanya, 266003/572000, PR China
[2]Key Laboratory of Novel Food Resources Processing, Ministry of Agriculture and Rural Affairs/Institute of Food & Nutrition Science and Technology, Shandong Academy of Agricultural Sciences.
[3]Shandong Institute of Pomology, Taian, China

Lung cancer remains one of the leading causes of cancer incidence and mortality worldwide. Although surgery, chemotherapy and conventional treatments can provide clinical benefit, treatment toxicity, recurrence and metastasis limit long-term outcomes. Hawthorn red pigment (HRP), a polyphenol-rich pigment isolated from hawthorn pulp, has shown antitumor potential, but its direct activity and mechanism in non-small cell lung cancer (NSCLC) remain insufficiently defined. Therefore, cell assays using HRP-treated A549 cells revealed that HRP suppressed cell growth and induced apoptosis. We also demonstrated that the cyclic adenosine monophosphate - protein kinase A - cAMP response element binding protein (cAMP-PKA-CREB) pathway played a regulatory role in the anti-cancer effect of HRP. Its antitumor effects were mediated by activating cAMP-PKA-CREB signaling, and animal xenograft experiments further confirmed that high-dose HRP restrained tumor growth, induced tumor cell apoptosis and reshaped gut microbiota with no evident toxic side effects.

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GL46: Afternoon Shading of Grapevine Regulates Berry Development and Flavor Profile in Cabernet Sauvignon Grapes and Wines

Mengbo Tian[1,2], Ruiling Liu[1], Haiyan Gao[1], Jun Wang[2]*
[1]State Key Laboratory for Quality and Safety of Agro-Products, Zhejiang Key Laboratory of Intelligent Food Logistic and Processing, Key Laboratory of Post-Harvest Fruit Processing, Ministry of Agriculture and Rural Affairs, Institute of Food Science, Zhejiang Academy of Agricultural Sciences, Hangzhou 310021, China
[2]Center for Viticulture and Enology, College of Food Science and Nutritional Engineering, China Agricultural University, Beijing 100083, China

To mitigate the rapid ripening by afternoon high temperature in semi-arid wine regions, grapevine artificial shading was applied in a three-year experiment (2021-2023) in northwest China. The moderate shading (1.5 h, MD) and strong shading (2.5 h, SD) were applied in the afternoon. Climatic parameters were collected, flavonoids and volatiles of grapes and wines were determined by HPLC-MS and GC-MS. Results revealed that photosynthetic assimilation of grapevines was suppressed by 50% during shading, while photosynthesis during exposure and leaf area were enhanced. Shading reduced the berry surface temperature by up to 4 °C and delayed sugar accumulation, resulting in grapes with higher acidity (~1 g/L) and lower Brix (~0.5 °Brix) at harvest. Berry volatiles in MD and SD were 16% and 10% lower than CK at 2021 harvest but were enhanced in the latter two years. Linalool, hexanal, β-damascenone, and 6-methyl-5-hepten-2-one were key light-responsive biomarkers. MD and SD wines had lower flavonols, red hue, and anthocyanin derivates. Specific non-methylated anthocyanins and kaempferol-based flavonols were bioindicators of solar radiation. Shaded wines exhibited elevated levels of terpenoids and norisoprenoids, contributing to improved fruity-floral aromas and sensory scores in 2022 and 2023. Overall, afternoon shading delays grape ripening and regulates grape flavonoid and volatile profiles, thus modifies wine flavor and sensory distribution. This study provides insights into regulating grape and wine quality in semi-arid regions.

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GL47: Molecular and Neurovascular Pathogenic Mechanisms Underlying Focal Cortical Dysplasia-Related Epilepsy

Xinyu Mei[1]*, Yi Liu[3,4], Chuantao Fang[2], Jingjing Guo[1], Jianbo Xiao[3], Dashi Qi[1]*
[1]Center for Clinical Research and Translational Medicine, Yangpu Hospital, School of Medicine, Tongji University, Shanghai 200090, China
[2]Shanghai Tenth People's Hospital, Institute for Infectious Diseases and Vaccine Development, Tongji University School of Medicine, Shanghai 200072, China
[3]Universidade de Vigo, Nutrition and Bromatology Group, Department of Analytical Chemistry and Food Science, Faculty of Science, 32004, Ourense, Spain
[4]Institute of Urban Agriculture, Chinese Academy of Agricultural Sciences, Chengdu 610213, China

Focal cortical dysplasia (FCD) is a major cause of drug-resistant epilepsy characterized by molecular and cellular heterogeneity[1]. Although aberrant mTOR signaling is a hallmark of FCD, it does not fully explain epileptogenesis, highlighting the need to identify complementary pathogenic pathways. Hyperhomocysteinemia has been implicated in epilepsy, yet the mechanisms linking it to epileptogenesis remain largely unknown[2]. N-homocysteinylated Cofilin-1 was detected in epilepsy patients and hyperhomocysteinemic mice[3]. N-homocysteinylation impaired Cofilin-1-mediated actin depolymerization, leading to disrupted actin dynamics, cytoskeletal rigidity, abnormal axonal development, and increased seizure susceptibility[3]. Circulating homocysteine levels positively correlated with N-Hcy–CFL1 abundance in epileptic brain tissues, supporting its clinical relevance[3]. In FCDIIb, single-nucleus transcriptomic analysis of 217,506 nuclei from paired lesion and adjacent cortical tissues revealed extensive remodeling of vascular cell populations, particularly smooth muscle cells and astrocytes[4]. A previously unrecognized vascular smooth muscle cell subtype, termed "Firework cells," migrated from blood vessels into the brain parenchyma and was closely associated with VIM^+ cells[4]. These vascular abnormalities created localized ischemic-hypoxic microenvironments, activated HIF-1α/mTOR/S6 signaling, impaired astrocyte homeostasis, promoted neuronal loss, and increased seizure susceptibility[4]. Collectively, these findings identify metabolic stress-induced neuronal cytoskeletal dysfunction and neurovascular remodeling as pathogenic mechanisms underlying epileptogenesis in FCD, thereby extending the current mTOR-centered understanding of FCD pathogenesis and providing new opportunities for mechanism-based therapeutic intervention in drug-resistant epilepsy.

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GL48: Steam Explosion–Induced Structural Remodeling of Auricularia Auricula Polysaccharides Enhances Anti-Aging Efficacy in Drosophila Melanogaster

Zirong Huang[1,2], Baodong Zheng[1,2]*
[1]College of Food Science, Fujian Agriculture and Forestry University, Fuzhou, 350002, China
[2]Integrated Scientific Research Base of Edible Fungi Processing and Comprehensive Utilization Technology, Ministry of Agriculture and Rural Affairs, Fuzhou, 350002, China

This paper studied the physicochemical properties and bioactivity of *Auricularia auricula* polysaccharides (AAP) before and after steam explosion (SE) pretreatment[1]. AAP consisted mainly of mannose, galactose, and glucose; SE pretreatment shifted monosaccharide proportions and reduced the weight-average molecular weight to 3.37×10^5 Da. Fourier-transform infrared spectroscopy showed SE did not alter the fundamental functional groups of the polysaccharides. Thermal stability was enhanced after SE, as evidenced by scanning electron microscopy, which revealed a transition from a dense architecture to a more open, stratified microstructure with increase surface roughness[2]. Compared with the control (AAP-CK), the SE-treated group (AAP-SE) exhibited enhanced in vitro antioxidant capacity. Dietary supplementation with 0.0312% AAP-SE significantly extended the average lifespan of *Drosophila melanogaster* by 28.44% in females and 22.08% in males. In fruit flies, AAP-SE enhanced antioxidant enzyme activities, increasing superoxide dismutase by 67.32% and glutathione peroxidase by 2.61-fold in males, while reducing malondialdehyde levels by 42.75% in females[3]. Furthermore, fruit flies fed AAP-SE showed improved resistance to hydrogen peroxide-induced oxidative stress and starvation stress, with gender-specific effects. These results suggested that SE pretreatment effectively enhanced the antioxidant and anti-aging activities of AAP, suggesting its potential as a natural lifespan-extending antioxidant[4].

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GL49: Ultrasonic Modified Ovalbumin-fish Oil Emulsion Gel: A Novel Strategy for Replacing Animal Fat

Boyu Chen[1], Ruizi Zhou[1,2], Miaoqi Dai[1], Yuanju He[1], Chao Ai[1,2], Yanan Zhao[1,2], Hui Wang[1,2], Hui Teng[1,2]*, Lei Chen[1,2,3]*
[1]College of Food Science and Technology, Guangdong Ocean University, Guangdong Provincial Key Laboratory of Aquatic Product Processing and Safety, Guangdong Province Engineering Laboratory for Marine Biological Products, Guangdong Provincial Engineering Technology Research Center of Seafood, Key Laboratory of Advanced Processing of Aquatic Product of Guangdong Higher Education Institution, Zhanjiang 524088, China
[2]Shenzhen Institute of Guangdong Ocean University, No. 3 of Binhai 2nd Road, Dapeng New District, Shenzhen, Guangdong Province, 518108, China

Currently, obesity and overweight are prevalent and continuously increasing globally. According to World Health Organization (WHO) data, in 2022, 2.5 billion adults (aged 18 and above) were overweight, with 890 million suffering from obesity[1]. Traditional meat products typically contain high levels of fat, which contribute to desirable sensory attributes including taste, aroma, smooth texture, glossy appearance, and structural integrity[2]. However, excessive consumption of saturated and trans fats has been linked to obesity and related chronic diseases such as hypercholesterolemia, coronary heart disease (CHD), and other cardiovascular disorders[3]. In response to these health concerns, fat substitutes have emerged as a viable strategy to reduce fat content in processed foods while preserving sensory quality. In recent years, emulsion-based systems have attracted increasing research attention due to their structural versatility and compatibility with food matrices. In particular, emulsion gels—solid-like materials formed by structuring emulsions into three-dimensional gel networks—have shown considerable promise as fat mimetics[4]. Numerous studies have explored the application of emulsion gels as fat substitutes in various foods, such as sausages, hamburger meat, and cream cheese. Fish oil, extracted from fatty or deep-sea fish, is rich in omega-3 polyunsaturated fatty acids (PUFAs), particularly eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA), which exhibit anti-inflammatory, lipid-regulating, and cardiovascular benefits[5]. However, fish oil suffers from poor quality stability, poor water solubility, and susceptibility to oxidation, severely limiting its application in food. Ovalbumin (OVA) is the primary protein component in egg whites, rich in disulfide bonds that form a stable gel network during processing.Ultrasound-induced cavitation can disrupt protein structures, break non-covalent bonds, and expose polar groups, significantly impacting functional properties including emulsification (emulsifying activity and emulsion stability)[6]. Based on this, we first modified OVA through ultrasonic treatment, then combined it with fish oil to prepare a conventional emulsion (E) and a high internal phase emulsion (HE). Finally, emulsion gels (EG) and high internal phase emulsion gels (HEG) were prepared via Ca2+ sustained release., which were subsequently used to replace pork back fat in sausages. The study systematically evaluated the effects of varying substitution rates on sausage quality, digestive properties, and flavor profile.

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GL50: Improvement of Sparassis Crispa Polysaccharide Quality by Steam Explosion Technology: Physicochemical, Structural and Functional Properties

Jingru Wu[1,2], Yueyue Qiang[1,2], Haoxuan Peng[1,2], Qiao Guan[1,2], Lei Pan[1,2], Zhiwei Huang[1,2], Zebin Guo[1,2], Jianbo Xiao[3,4], Baodong Zheng[1,2]*, Yafeng Zheng[1,2]*
[1]College of Food Science, Fujian Agriculture and Forestry University, Fuzhou 350002, China
[2]Integrated Scientific Research Base of Edible fungi Processing and Comprehensive Utilization Technology, Ministry of Agriculture and Rural Affairs, Fuzhou 350002, China
[3]Universidade de Vigo, Nutrition and Bromatology Group, Instituto de Agroecoloxía e Alimentación (IAA), Department of Analytical Chemistry and Food Science, Faculty of Science, 32004 Ourense, Spain
[4]Research Group on Food, Nutritional Biochemistry and Health, Universidad Europea del Atlántico, Isabel Torres 21, 39011 Santander, Spain

Steam explosion (SE) is an emerging physical technology that is attracting increasing interest. SE is based on using saturated steam at high temperature and high pressure to infiltrate the tissues of the raw material, thereby saturating it with superheated water. This is followed by instantaneous pressure release that explosively disrupts the raw material structure, facilitating the release of active substances. This study aimed to evaluate the influence of steam explosion (SE) technology on the physicochemical, structural, and functional properties of *Sparassis crispa* polysaccharide (SCP). The results showed that SE could significantly increase the yield of SCP. Additionally, the particle size, molecular weight, and crystallinity of the SCP gradually decrease with the increasing SE pressure. SE changed the molar ratio of monosaccharides in SCP and disrupted its dense structure. However, the major functional groups of SCP were unaffected by SE. Thermogravimetric analysis indicated that the thermal stability of SCP was enhanced by SE. Furthermore, the physiochemical and structural changes induced by SE resulted in improved functional properties. Particularly at 1.2 MPa, SCP had better hydration properties, hypolipidemic, hypoglycemic, and antioxidant activities. Therefore, SE is an effective method to improve the quality and comprehensive utilization rate of edible fungus polysaccharide.

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GL51: Study on Construction of Gel System in Salt-Reduced Surimi Products and Its Saltiness Perception Mechanism

Siqi Yang[1,2], Yi Zhang[1,2], Hongliang Zeng[1,2]
[1]Engineering Research Center of Fujian-Taiwan Special Marine Food Processing and Nutrition, Ministry of Education, Fuzhou, Fujian 350002, China
[2]College of Food Science, Fujian Agriculture and Forestry University, Fuzhou 350002, China

Salt is a critical auxiliary material in surimi products processing, which effectively promotes the solubilization of salt-soluble proteins (myofibrillar proteins, MP) in surimi, enhances the gel strength and water-holding capacity of surimi products, and reduces cooking loss rate. Meanwhile, saltiness is the primary taste among all flavors, which effectively stimulates the flavor presentation characteristics of other flavor substances and exerts a decisive influence on the sensory quality of surimi products. However, traditional surimi products generally have a high salt content (>3 g/100 g, corresponding to a sodium content of 1300 mg/100 g). Long-term excessive salt intake easily increases the risk of chronic diseases such as hypertension. Therefore, developing appropriate processing technologies to achieve the synergistic improvement of taste and quality in salt-reduced surimi products has become an important research direction in marine food processing. Therefore, based on the salt reduction strategy of modifying food matrix structure and achieving sodium heterogeneous distribution, this study utilized the synergistic effect of soy protein isolate (SPI) and gelling polysaccharide (curdlan (Cur) or gellan gum (GL)) to improve the gel properties and flavor quality of salt-reduced surimi products, and developed salt-reduced surimi products with synergistic taste and quality effects. By constructing the MP-SPI-Cur ternary interaction system, this study systematically elucidated the synergistic mechanism of SPI and Cur under salt-reduced conditions and their enhancing effect on the gel properties of salt-reduced surimi. Furthermore, this study investigated the dynamic saltiness perception of this gel system during human oral processing to reveal the molecular mechanism by which SPI and Cur enhance saltiness perception in salt-reduced gels. This study aims to provide a scientific basis for the processing of salt-reduced surimi products in the food industry and a theoretical foundation for research on saltiness perception mechanisms.

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GL53: Soluble Dietary Fiber from *Piper sarmentosum* Roxb. Leaves Modulates Gut Microbiota-derived Cis-11-Eicosenoic Acid to Regulate Lipid Metabolism

Yangyang Wang[1], Jianbo Xiao[2], Hui Wang[1]*, Hui Cao[1,2]
[1]College of Food Science and Technology, Guangdong Ocean University, Guangdong Provincial Key Laboratory of Aquatic Product Processing and Safety, Guangdong Province Engineering Laboratory for Marine Biological Products, Zhanjiang 524088, China
[2]Universidade de Vigo, Nutrition and Bromatology Group, Department of Analytical and Food Chemistry, Faculty of Science, 32004 Ourense, Spain

Obesity represents a critical global health challenge, significantly elevating risks for major chronic diseases. This underscores the urgent necessity to develop innovative prevention and therapeutic interventions. While *Piper sarmentosum* Roxb. has demonstrated antidiabetic and antihypertensive properties, its anti-obesity effects and underlying mechanisms remain largely uncharacterized[1]. This study aimed to evaluate the anti-obesity effects of soluble dietary fiber from *Piper sarmentosum* Roxb. leaves (PSDF) and elucidate its molecular basis. PSDF was characterized as an acidic dietary fiber, predominantly composed of galacturonic acid (55.64%), galactose (21.74%), and arabinose (11.97%), exhibiting a triple-helical conformation and high thermal stability. In diet-induced obese mice, six weeks of PSDF administration significantly ameliorated glucose and lipid metabolic disorders ($p < 0.05$), an effect associated with modulation of gut microbiota[2]. Untargeted metabolomics identified cis-11-eicosenoic acid (GA) as a key metabolite. In a 3T3-L1 single-cell model, GA treatment did not affect adipocyte differentiation. However, in a co-culture model of 3T3-L1 adipocytes and RAW264.7 macrophages, GA significantly downregulated pro-inflammatory cytokines (IL-1β, TNF-α) and SREBF1 expression, while upregulating anti-inflammatory markers (IL-4, IL-10) and fatty acid oxidation genes (CPT1A, PGC-1α). These results initially suggested that GA may exert anti-obesity effects primarily through modulating inflammation-associated lipid metabolism pathways. Fecal microbiota transplantation (FMT) confirmed both GA elevation and anti-adiposity effects were microbiota-dependent[3]. These findings demonstrated PSDF alleviated lipid accumulation by modulating a gut microbiota-adipose axis centered on GA production, thereby improving inflammation-mediated lipid metabolism. This newly elucidated microbiota-GA axis establishes a theoretical basis for developing PSDF-based soluble dietary fibers into microbiota-focused anti-obesity nutraceuticals.

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GL54: Divergent Polyphenol Transformations in *Oenanthe javanica* Induced by Dry-Heat and Moist-Heat Processing as Revealed by UPLC-Q-TOF-MS/MS

Fuying Wang[1,2], Haolin Zhang[1,2], Hui Cao[1,2]*
[1]College of Food Science and Technology, Guangdong Ocean University, Guangdong Provincial Key Laboratory of Aquatic Product Processing and Safety, Guangdong Province Engineering Laboratory for Marine Biological Products, Guangdong Provincial Engineering Technology Research Center of Seafood, Guangdong Provincial Engineering Technology Research Center of Prefabricated Seafood Processing and Quality Control, Zhanjiang 524088, China
[2]Collaborative Innovation Center of Seafood Deep Processing, Dalian Polytechnic University, Dalian 116034, China

Oenanthe javanica is a characteristic aquatic vegetable rich in polyphenols. Thermal processing is the most common preparation method, yet the transformation of polyphenols and their functional responses under different heating environments remain unclear. In this study, microscopic observation, UPLC-MS/MS, and multivariate statistical analysis were combined to investigate the dynamic changes in polyphenols and antioxidant activity of *O. javanica* stems and leaves during dry-heat roasting and moist-heat boiling. Thermal processing disrupted the tissue microstructure, promoting the release of free and partially bound polyphenols. A total of 31 major polyphenols were identified, including flavonoid glycosides, flavonoid aglycones, chlorogenic acid, ferulic acid, caffeic acid, and related phenolic acid derivatives. The leaves contained a greater diversity and abundance of polyphenols than the stems. During dry-heat processing, leaf polyphenols exhibited a sequential pattern of release followed by degradation, while antioxidant activity remained relatively stable. In contrast, moist-heat processing promoted the migration of polyphenols into the cooking water, resulting in reduced antioxidant capacity in the leaves. The antioxidant activity of the cooking water changed synchronously with polyphenol release and degradation. In the stems, most phenolic acids increased during dry-heat treatment, whereas under moist heat they first increased and then declined. Changes in antioxidant activity of both stems and leaves were strongly correlated with alterations in polyphenol composition. Mechanistically, flavonoid glycosides were deglycosylated into aglycones and subsequently transformed into simple phenolic acids, while complex phenolic acids underwent isomerization, ester hydrolysis, and thermal degradation. These findings reveal the medium-dependent transformation of polyphenols and its association with antioxidant activity, providing a scientific basis for improving the functional quality of thermally processed vegetables.

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Master student’s forum

MF1: Study on the Effects of Ginseng Adventitious Root Extract on Immune-Mediated Liver Injury Based on the PI3K/Akt Signaling Pathway

Xinyu Wang, Xin Qi*, Chengbi Cui*
College of Agricultural, Yanbian University, Yanji, Jilin, 133000

Immune-mediated liver injury (ILI) is a common clinical liver disease, and currently, there is a lack of highly effective and low-toxicity intervention methods. Therefore, discovering natural and effective prevention and treatment strategies is of great significance. This study aims to investigate the protective effect of ginseng adventitious root extract (GARE) on ILI based on the PI3K/Akt pathway[1]. First, network pharmacology was used to screen and identify the core target of GARE and the key PI3K/Akt pathway[2]. In vitro, a concanavalin A (ConA)-induced RAW264.7 cell injury model was constructed, and cell viability and the expression of phosphorylated proteins in the PI3K/Akt pathway were detected[3]. In vivo, 48 C57BL/6 mice were randomly divided into a normal group, a model group, low- and high-dose GARE groups (100 and 200 mg/kg), and a positive drug group[4]. After 14 days of intervention by gavage, the model was established, and serum liver function indicators ALT and AST, liver tissue pathology, cell apoptosis, inflammatory factors, and pathway protein expression were detected. The results confirmed that different concentrations of GARE significantly enhanced the viability of damaged cells and downregulated the expression of p-PI3K, p-AKT, and p-mTOR proteins in a dose-dependent manner ($p < 0.01$)[5]. GARE significantly reduced serum ALT and AST levels in mice and alleviated pathological damage to liver tissue in a dose-dependent manner; it significantly inhibited hepatocyte apoptosis, upregulated Bcl-2 protein expression, downregulated Bax and cleaved caspase-3 expression, and significantly inhibited the mRNA levels of inflammatory factors TNF-α, IL-6, IL-18, and IL-1β in liver tissue, while effectively inhibiting the abnormal activation of the PI3K/AKT/mTOR pathway ($p < 0.01$). In conclusion, GARE can exert a significant anti-ILI protective effect by inhibiting the abnormal activation of the PI3K/Akt signaling pathway, suppressing liver inflammation and hepatocyte apoptosis.

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MF2: Screening of the Optimal Hyaluronic Acid Molecular Weight for Fabricating Naringin-Loaded Microneedles with Enhanced Antibacterial Activity and Accelerated Diabetic Wound Healing

Keyue Qiu[1], Yitong Wang[1,2], RuiZi Zhou[1], Lei Chen[1,2]*
[1]College of Food Science and Technology, Guangdong Ocean University, Guangdong Provincial Key Laboratory of Aquatic Product Processing and Safety, Guangdong Province Engineering Laboratory for Marine Biological Products, Guangdong Provincial Engineering Technology Research Center of Seafood, Key Laboratory of Advanced Processing of Aquatic Product of Guangdong Higher Education Institution, Zhanjiang 524088, China
[2]Shenzhen Institute of Guangdong Ocean University, No. 3 of Binhai 2nd Road, Dapeng New District, Shenzhen, Guangdong Province, 518108, China

For diabetic patients, hyperglycemia broadly suppresses immune function and turns wounds concentrations at wound sites provide favorable conditions for bacterial overgrowth and rapid proliferation, which readily triggers local infection and directly hinders wound healing[1]. Conventional treatments deliver limited therapeutic effects, and novel therapies capable of actively regulating the wound microenvironment to facilitate efficient tissue repair remain scarce. Accordingly, the management of diabetic wounds has become one of the major clinical burdens[2]. Naringin (NRG) is a natural flavonoid compound with potent antioxidant and anti-inflammatory properties. However, its poor water solubility and weak transdermal permeability restrict its practical application. Hyaluronic acid (HA) is a natural high-molecular-weight polysaccharide that features excellent water retention, superior biocompatibility, full biodegradability and non-toxicity. Herein, we developed sodium hyaluronate-based microneedle patches loaded with a specific concentration of naringin[3]. These patches possess favorable mechanical strength and biological properties; the microneedles penetrate the epidermal layer to efficiently deliver sodium hyaluronate and naringin that exert anti-inflammatory and antioxidant effects.Nevertheless, differences in the molecular weight of HA significantly alter its physicochemical properties and biological activities, which further determine the fabrication process and therapeutic efficacy of dissolvable microneedles[4]. In this study, naringin (NRG) was used as a model drug. Three types of HA with distinct molecular weights (100-200 kDa, 400-800 kDa, and 800-1500 kDa) were systematically screened to fabricate dissolvable microneedles. The regulatory effects of HA molecular weight on microneedle performance and therapeutic efficiency were comprehensively evaluated in terms of physicochemical characteristics and mechanical properties.The results reveal that microneedles fabricated from 400-800 kDa HA achieve an optimal balance among mechanical strength, skin penetration capacity and drug release rate This formulation not only enables effective skin insertion of microneedles, but also realizes rapid onset and sustained release of NRG[5]. Antibacterial tests demonstrate that microneedlesof this molecular weight exert prominent inhibitory activity against *Escherichia coli* and *Staphylococcus aureus*. Furthermore, the drug-loaded microneedles (HA-NRG-MN) significantly accelerate wound healing in a mouse model of diabetic ulcers[5].

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MF3: Evaluation of Rice Freshness During Storage Based on Flavor Marker Characterization and Vision-Spectroscopy Multimodal Fusion

Shiyun Tang, Zhiyang Peng, Jingwan Ye, Yiming Zhou*, Minglong Wang, Lan Zhang, Renzhi Lv
Faculty of Flavour Fragrance and Cosmetics, Shanghai Institute of Technology, Shanghai 201418, China

Changes in rice quality during storage are characterized by pronounced temporal dynamics and multidimensionality. However, flavor chemistry and rapid nondestructive detection have generally been investigated separately, limiting the simultaneous interpretation of deterioration mechanisms, identification of storage stages, and practical quality monitoring. In this study, japonica rice cultivar "Nanjing 9108" was stored for 40 weeks under ambient conditions with naturally fluctuating temperatures, refrigerated conditions at 5 °C, and frozen conditions at -20 °C, with sampling conducted every two weeks. Volatile compounds, physicochemical indices, microstructure, visual images, and near-infrared spectra were synchronously acquired from the same samples. A unified sample-coding system was used to establish one-to-one correspondence among image, spectral, GC-MS, and physicochemical data, thereby ensuring that all modalities represented an identical storage background and providing a basis for cross-modal association analysis. A total of 58 volatile compounds were detected. The storage process generally exhibited three stages, namely initial accumulation, rapid change, and late-stage transformation, with weeks 12 and 28 identified as important turning points in flavor evolution. Ambient storage accelerated lipid oxidation and volatile-compound conversion, refrigerated storage delayed compound generation, accumulation, and differentiation, whereas several oxidation products showed abnormal accumulation and fluctuation under frozen storage. Sensory validation indicated that 2-acetyl-1-pyrroline was an important contributor to the characteristic rice aroma, while hexanal and nonanal were closely associated with grassy, fatty, and stale odors. Microstructural observations and correlation analysis suggested that loss of membrane integrity promoted lipid hydrolysis and oxidation and represented an important driving factor in flavor deterioration. The single spectral model achieved an accuracy of 84.44% for storage-temperature classification, which increased to 89.10% after attention-based fusion of visual and spectral features. The multi-task model achieved accuracies of 87.24% and 86.20% for storage-duration classification and overall quality grading, respectively, while the LSTM model achieved an accuracy of 88.2% in predicting key volatile markers. The models were further integrated into a visual evaluation prototype that automatically generated storage-status and quality results from image and near-infrared spectral inputs. By defining rice freshness through sensory-validated flavor markers and mechanism-related indicators, using vision-spectroscopy multimodal modeling for rapid and nondestructive identification, and extending the framework to trend prediction through temporal modeling, this study established an integrated evaluation pathway comprising mechanism elucidation, marker confirmation, multimodal perception, and intelligent prediction. The proposed approach may provide methodological support for quality monitoring, deterioration warning, and storage-condition optimization during rice storage.

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MF4: Low-Molecular-Weight Fucoidan Improves Cold Tolerance and Modulates the Gut Microbiota-Short-Chain Fatty Acid-GLP-1 Axis in Mice

Yu Huang[1], Ningyang Li[1]*
[1]College of Food Science and Engineering, Ocean University of China, No. 1299 Sansha Road, Qingdao 266404, Shandong, China

Cold exposure imposes a substantial metabolic burden and may disturb intestinal homeostasis, while food-derived interventions with clearly defined mechanisms remain limited. Fucoidan is a sulfated polysaccharide from brown algae with prebiotic and metabolic regulatory potential. Previous studies have shown that low-molecular-weight fucoidans can be utilized by intestinal microbiota, reshape microbial communities and metabolites, and influence GLP-1-related metabolic signaling[1–3]. This study investigated whether low-molecular-weight fucoidan (LMAF) improves cold tolerance and explored the involvement of the gut microbiota–short-chain fatty acid (SCFA)–glucagon-like peptide-1 (GLP-1) axis. LMAF was prepared by trifluoroacetic acid hydrolysis, ethanol precipitation, and freeze-drying. Monosaccharide analysis showed that fucose was the predominant sugar (39.33 mol%), and molecular-weight analysis identified three major peaks at approximately 1,234, 322, and 181 Da. Male C57BL/6J mice were orally administered LMAF at 50 or 150 mg/kg for 40 days and subsequently exposed to 4 °C for 6 h or −20 °C for 30 min. Rectal temperature, serum GLP-1 and free fatty acids, cecal acetate, and gut microbial composition were assessed. LMAF-treated mice maintained higher rectal temperatures than cold-exposed controls after 4 °C exposure, indicating improved thermoregulatory capacity. Under acute −20 °C exposure, serum GLP-1 was significantly increased by LMAF, while a similar upward trend was observed at 4 °C. LMAF treatment was also associated with higher serum free fatty acid and cecal acetate levels, together with an increased relative abundance of Akkermansia and several SCFA-associated taxa. These findings suggest that LMAF may enhance cold tolerance by reshaping the gut microbiota, promoting acetate production and GLP-1 secretion, and facilitating lipid mobilization to support adaptive thermogenesis. This study provides preliminary evidence for developing LMAF as a marine-derived functional ingredient for protection against cold stress.

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MF5: Sichuan TCM Formulae Inhibit ACE2-Dependent Coronavirus Entry by Targeting the JAK/STAT3 Pathway to Downregulate ACE2

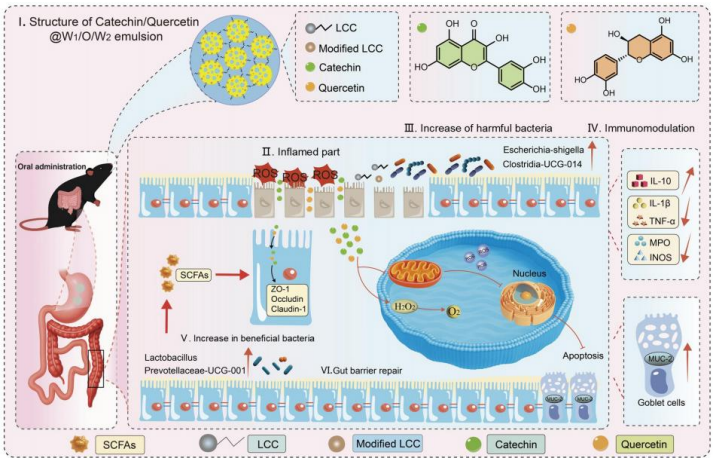
Wenjia Ni[1], Hanyue Lei[1], Yan Zhao[2], Jie Yuan[1], Hang Deng[1], Junda Zhou[2], Conglian Tan[3], Jimin Li[4], Xiaoyu Hu[4], Jinlin Guo[3], Xinhe Huang[2]*, Xu Jia[1]*
[1]Chengdu Qingbaijiang District Hospital of Traditional Chinese Medicine, Key Laboratory of Non-coding RNA and Drug Discovery at Chengdu Medical College of Sichuan Province, Chengdu Medical College, Chengdu 610500, Sichuan, China
[2]Life Science and Engineering, Southwest Jiaotong University, Chengdu, China, 610031
[3]Department of Infectious Diseases, Affiliated Hospital of Chengdu University of Traditional Chinese Medicine, Chengdu 610072, Sichuan Province, China
[4]Key Laboratory of Systematic Research of Distinctive Chinese Medicine Resources in Southwest China, Chengdu University of Traditional Chinese Medicine, Chengdu, China

Background: ACE2-dependent coronaviruses, such as SARS-CoV, SARS-CoV-2, and HCoV-NL63, pose continuous global health threats due to high genetic variability and cross-species adaptability. While single-target antivirals face limitations, multi-component Traditional Chinese Medicine (TCM) formulae offer a promising alternative for holistic viral management and cytokine storm mitigation. Objectives: This study aims to elucidate the core regulatory mechanisms and broad-spectrum antiviral potential of three prominent Sichuan hospital formulae—Ganlu Disinfection Powder (NO.1), Huopu Xialing Decoction (NO.2), and Huopu Xialing Improved Decoction (NO.3)—against ACE2-utilizing coronaviruses.
Methods: High-performance liquid chromatography (HPLC) was first utilized to establish chromatographic fingerprints and identify major bioactive compounds (e.g., Stigmasterol, Linarin, Fortunellin), ensuring batch-to-batch chemical consistency. Subsequently, ACE2-dependent pseudovirus models were constructed to evaluate the viral entry inhibition elicited by drug-containing serum. Network pharmacology and molecular docking were deployed to predict active compounds and upstream targets, followed by molecular validation and CRISPR/Cas9 knockout experiments to resolve the precise downstream pathways.
Results and Conclusions: The three Sichuan TCM formulae significantly suppressed ACE2 expression and blocked pseudovirus entry into host cells through multi-target and multi-pathway regulation. Mechanistically, STAT3 was identified as the central hub regulator. Medicated serum components effectively targeted the JAK/STAT3 signaling pathway, down-regulating ACE2 expression to achieve broad-spectrum inhibition against coronavirus invasion. These findings provide novel mechanistic insights into the therapeutic value of TCM formulae and offer potent candidates for countering current and future emerging coronavirus outbreaks.

MF6: Lignin–Carbohydrate Complex-mediated Oil–Water Interface Regulation for Targeted Polyphenol Delivery and Colitis Therapy

Linli Zhu[1], Xinyu Zhang[1], Gaohui Huang[1], Jianbo Xiao[3], Qian Wu[1,2]*, Haiyan Fu[2]*
[1]Hubei Key Laboratory of Industrial Microbiology, Hubei University of Technology, Wuhan, Hubei, 430068, China
[2]The Modernization Engineering Technology Research Center of Ethnic Minority Medicine of Hubei Province, School of Pharmaceutical Sciences, South-Central Minzu University, Wuhan, 430074, China
[3]Faculty of Sciences, Department of Analytical and Food Chemistry, Universidade de Vigo, Nutrition and Bromatology Group, Ourense, 32448, Spain

Polyphenols have potential for ulcerative colitis treatment but are limited by low oral bioavailability. Here, a colon-targeted $W_1/O/W_2$ double-emulsion system was developed using an engineered lignin–carbohydrate complex (LCC) as a dual-functional emulsifier[1]. Native LCC stabilized the O/W interface, while laccase-mediated isoeugenol grafting increased its lipophilicity for W/O stabilization[2]. The system enabled stable co-encapsulation of polyphenols with different polarities and pH-responsive release under colonic conditions. In a dextran sulfate sodium-induced colitis model, LCC promoted short-chain fatty acid-producing bacteria, while released polyphenols improved intestinal barrier function, together facilitating colonic mucosal repair[3]. This study demonstrates a sustainable biomass-derived platform for colon-targeted delivery, microbiota modulation, and ulcerative colitis therapy.



Acknowledgements
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MF7: Phase Transition Effects of a Beet Pectin-Ovalbumin Complex Emulsion-Gel Enhance Astaxanthin Bioavailability

Jingteng Deng[1], Zilin Chen[1], Hui Teng[1], Lei Chen[1]*, Chao Ai[1]*
[1]College of Food Science and Technology, Guangdong Ocean University, Guangdong Provincial Key Laboratory of Aquatic Product Processing and Safety, Guangdong Province Engineering Laboratory for Marine Biological Products, Guangdong Provincial Engineering Technology Research Center of Seafood, Guangdong Provincial Engineering Technology Research Center of Prefabricated Seafood Processing and Quality Control, Zhanjiang 524088, China

In this study, suger beet pectin (SBP) and ovalbumin (OVA) were assembled into a binary complex via electrostatic complexation. Based on their interfacial properties, a continuous-phase gel emulsion was prepared, which enhanced the bioavailability of astaxanthin (AST). At the optimal complex ratio (1:1), the droplet size of the oil-in-water emulsion with a 1.5% complex concentration was 641.1 nm. The addition of calcium ions to induce a continuous-phase gel emulsion improved emulsion stability. After 14 days of storage, the droplet size of the gel emulsion increased only to 997.6 nm, and the AST retention rate (80.4%) was significantly higher than that of free AST (26.1%). After 5 hours of UV irradiation, the AST retention rate in the gel emulsion (77.1%) was also significantly higher than that of free AST (25.2%). In an in vitro simulation of gastrointestinal digestion, the bioavailability of AST in the gel emulsion reached 48.3%, whereas that of free astaxanthin was only 17.0%. These results indicate that OVA-SBP possesses excellent emulsifying properties. The formation of a calcium-induced emulsion-gel provides protection for AST during storage and UV irradiation, and enhances AST bioavailability during digestion, highlighting the potential of the beet pectin-ovomucoid complex as a food-grade emulsifier and astaxanthin delivery system.

Acknowledgments
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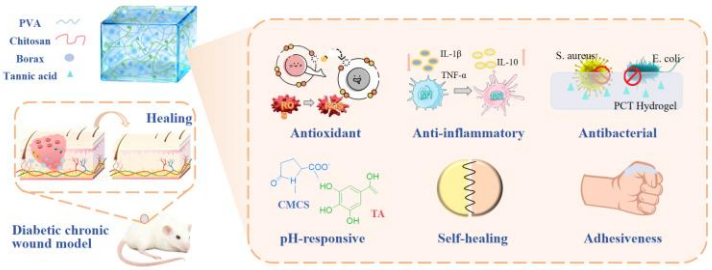
MF8: Mechanism Study of Dynamic Hydrogels Based on Tannic Acid Functional Regulation for Chronic Wound Repair in Diabetes

Gaohui Huang[1], Yuyan Zhang[1], Jianbo Xiao[3], Qian Wu[1,2]*, Haiyan Fu[2]*
[1]Hubei Key Laboratory of Industrial Microbiology, Hubei University of Technology, Wuhan, Hubei, 430068, China
[2]The Modernization Engineering Technology Research Center of Ethnic Minority Medicine of Hubei Province, School of Pharmaceutical Sciences, South-Central Minzu University, Wuhan, 430074, China
[3]Faculty of Sciences, Department of Analytical and Food Chemistry, Universidade de Vigo, Nutrition and Bromatology Group, Ourense, 32448, Spain

Diabetic chronic wounds are characterized by persistent inflammation, oxidative stress, and impaired angiogenesis under a hyperglycemic microenvironment, leading to delayed wound healing. Conventional wound dressings mainly provide passive protection and fail to regulate the complex pathological microenvironment[1]. Therefore, developing intelligent wound dressings with favorable mechanical properties and bioactivity is of great importance. In this study, a multiple dynamically crosslinked hydrogel was fabricated using polyvinyl alcohol (PVA), carboxymethyl chitosan (CMCS), borax, and the natural polyphenol tannic acid (TA)[2]. This hydrogel was systematically characterized, and its therapeutic efficacy and mechanisms were evaluated in a diabetic wound model. The dynamic crosslinking network markedly enhanced the hydrogel's structural stability, self-healing ability, tissue adhesion, and environmental responsiveness. The incorporation of TA further strengthened its antioxidant and antibacterial properties, effectively relieving wound oxidative stress and inflammation. In vivo, the hydrogel significantly accelerated wound closure, re-epithelialization, collagen deposition, and angiogenesis, thereby facilitating diabetic wound repair. This study offers a promising strategy for designing multifunctional dynamic hydrogels and highlights their potential as advanced dressings for diabetic chronic wounds.



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MF9: Research Progress on Extraction, Structural Characterization, and Bioactivities of Cereal β-Glucan

Haojun Lin, Junyi Yin*
State Key Laboratory of Food Science and Resources, China-Canada Joint Laboratory of Food Science and Technology (Nanchang), Key Laboratory of Bioactive Polysaccharides of Jiangxi Province; Nanchang University, Nanchang 330047, China

Cereal β-glucan, a linear polysaccharide predominantly found in oats and barley, consists of mixed-linked β-(1→3) and β-(1→4)-D-glucose units. Due to its excellent water solubility, high viscosity, and gel-forming ability, it has been widely utilized as a thickener, stabilizer, and emulsifier in food and pharmaceutical industries. Numerous studies have confirmed its physiological functions, including cholesterol-lowering, glycemic regulation, and gut health improvement. However, these bioactivities are closely correlated with its molecular weight and other structural features. We systematically summarize recent advances in the extraction, purification, structural characterization, and bioactivities of cereal β-glucan. Dry extraction methods, such as grinding and sieving preserve native structure but suffer from low yields. Wet extraction includes hot water, alkaline, and enzyme-assisted extraction, with ultrasound-assisted and microwave-assisted techniques often employed to improve yields. Purification is critical for obtaining high-purity β-glucan, focusing on the removal of starch, proteins, and pigments from crude extracts. Conventional approaches include enzymatic hydrolysis and dialysis, while emerging natural flocculants such as chitosan have shown effectiveness in removing protein and ash impurities. Further purification can be achieved by ethanol precipitation and DEAE-cellulose column. Structural characterization relies on the integration of multiple analytical techniques, including molecular weight analysis, methylation analysis, and NMR spectroscopy for DP3/DP4 ratio determination. Extraction temperature, pH, and ionic strength have been shown to influence the molecular weight of β-glucan. The cholesterol-lowering and hypoglycemic effects of cereal β-glucan have been recognized by the FDA and EFSA. Its bioactivity is strongly molecular weight-dependent, high-Mw β-glucan (>1000 kDa) primarily acts by increasing intestinal chyme viscosity and delaying glucose absorption, whereas low-Mw fragments (<300 kDa) may exert prebiotic effects via gut microbiota fermentation and enhanced antioxidant activity. Nevertheless, the dynamic structural evolution of β-glucan during extraction and processing, as well as its structure-activity relationship, remains poorly understood and requires further investigation.

MF10: Exploring BCRP-Mediated Molecular Transport Mechanisms of Intestinal Anthocyanins Absorption

Nuo Wang[1], Xiujun Li[1], Yue Li[1], Bin Li[1], Jinlong Tian[1]*
[1]College of Food Science, Shenyang Agricultural University, Shenyang, 110866, China

Anthocyanins (ACNs) are bioactive flavonoids with extensive health benefits, yet their low bioavailability severely limits functional applications. While prior studies focus on uptake transporters (e.g., SGLT1, GLUT2), the role of efflux transporters in ACNs excretion remains unclear. This study systematically investigated the BCRP (breast cancer resistance protein)-mediated efflux mechanism of ACNs using integrated in vitro and in vivo models[1,2].

Inhibition of BCRP by Ko143 increased intestinal ACNs absorption by 18.4% and systemic exposure by 21% in everted intestinal sac and pharmacokinetic assays. Spectroscopic analyses (UV-Vis, CD, 3D fluorescence) revealed that ACNs binding induced subtle conformational changes in BCRP, primarily through hydrogen bonding and electrostatic interactions. Isothermal titration calorimetry confirmed spontaneous binding with enthalpy-driven thermodynamics. Molecular docking and dynamics simulations demonstrated that ACNs occupy the BCRP transmembrane channel, while Ko143 competitively binds key residues (ASN-436, PHE-439), reducing binding energy to -27.82 kcal/mol and destabilizing the ACNs-BCRP complex[3,4].

This study provides the first molecular-level evidence that BCRP acts as a critical efflux transporter limiting ACNs bioavailability. The identified competitive inhibition strategy offers a novel approach to enhance ACNs absorption, supporting precision nutrition and functional food development[5,6].

Acknowledgments
This work was supported by the Natural Science Foundation of China (32202074 and 32572634).

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MF11: Study on the Anti-fatigue Effects of Ginseng Polysaccharides and Their Crude Extracts

Chaojun Li, Yan Zhu, Yanyan Pan, Meng Liao, Jia Li, Xiangrui Zhang, Shuai Liu, Jielun Hu, Mingyong Xie*
[1]State Key Laboratory of Food Science and Resources, Nanchang University, Nanchang, China
[2]China-Canada Joint Lab of Food Science and Technology, Nanchang University, Nanchang, China
[3]Key Laboratory of Bioactive Polysaccharides of Jiangxi Province, Nanchang University, Nanchang, China

Fatigue can induce various diseases and poses a serious threat to health, whereas commonly used clinical anti-fatigue drugs are associated with significant adverse effects. Naturally derived polysaccharides have attracted considerable attention due to their safety, efficacy, and multiple biological activities. Ginseng polysaccharide, as one of the important active constituents of ginseng, possesses anti-fatigue potential; however, a systematic comparison of its anti-fatigue effects with those of the crude extract is still lacking. In this study, a fatigue mouse model (male C57BL/6J) was established to compare the anti-fatigue effects of ginseng polysaccharide (GPS) and ginseng crude extract (GCE). The results demonstrated that, compared with the model control group, both low-dose GPS and low-dose GCE prolonged EST in mice, albeit with limited efficacy. The high-dose GPS group significantly prolonged exhaustive swimming time (EST) by 19.48%, concurrently reduced serum lactate (LD) and blood urea nitrogen (BUN) levels by 23.16% and 19.48%, respectively, and increased liver glycogen (LG) and muscle glycogen (MG) reserves by 11.86% and 41.34%, respectively. In comparison with the high-dose GPS group, the high-dose GCE group produced a more pronounced prolongation of EST (53.68%), greater decreases in LD and BUN (42.93% and 53.68%, respectively), and larger increments in LG and MG reserves (55.52% and 19.89%, respectively). In conclusion, under the present experimental conditions, both GPS and GCE effectively alleviated fatigue in mice in a dose-dependent manner, with the high-dose GCE showing superior overall efficacy to high-dose GPS. This study not only provides a theoretical foundation for the development and utilization of ginseng resources and expands the source pool of anti-fatigue products, but also offers novel perspectives for fatigue intervention strategies based on polysaccharides derived from edible medicinal substances.

MF12: Cloning and Functional Analysis of Two Pectin Methylesterases from Gonggan (*Citrus reticulata* Blanco var. Gonggan)

Deng Chunnong[1,2], Wanshan Huang[1,2], Zhuang Jiamiao[1,2], Lui Huifan[1,2], Wang Qin[1,2], Xiao Gengsheng[2], XieXi[1,2]*
[1]Zhongkai University of Agriculture and Engineering, Guangzhou, 510070
[2]Key Laboratory of Green Processing and Intelligent Manufacturing of Lingnan Specialty Food of Ministry and Rural Affairs, Guangdong Provincial Key Laboratory of Lingnan Specialty Food Science and Technology, College of Light Industry and Food Technology Guangzhou, 510070

Gonggan (*Citrus reticulata* Blanco var. Gonggan) is a widely cultivated citrus fruit in south China with potential for producing cloudy juices. However, pectin methylesterase (PME) is the primary enzyme responsible for cloud loss in fruit juices by catalyzing pectin demethylation. To elucidate PME function in Gonggan, two PME genes, GgPME3 and GgPME6, were identified and cloned. The recombinant GgPME3 and GgPME6 exhibited activities of 0.15 and 0.12 nkat/mg, respectively. Enzymatic activity increased with increasing substrate concentration, with Km and Vmax values of 2.21 mg/mL and 0.15 nkat/mg for GgPME3, and 2.37 mg/mL and 0.12 nkat/mg for GgPME6, respectively. GgPME3 and GgPME6 exhibited optimal activity at pH 6.0 and retained more than 80% of their enzymatic activity across a temperature range of 25–65 °C, exhibiting a low temperature sensitivity. Following heat treatment at 100 ℃, the residual activities of GgPME3 and GgPME6 were 71.47% and 76.97% relative to control, respectively. The presence of 10 mM Na^+, 20 mM Na^+ and 20 mM K^+ significantly enhanced GgPME activity, whereas Ca^{2+}, Mg^{2+}, Zn^{2+}, and Cu^{2+} exhibited an inhibitory effect. qRT-PCR analysis revealed that GgPME6 expression was highest at the yellow fruit stage, while GgPME3 expression peaked at the yellow-green stage. Both genes showed maximal expression in the albedo tissue. These results provide a theoretical basis and experimental support for optimizing Gonggan cloudy juice processing.

MF13: Effects of *Astragalus* Polysaccharides on Loperamide Hydrochloride-induced Functional Constipation in Mice

Yanyan Pan, Yan Zhu, Chaojun Li, Meng Liao, Dechang Xu, Xiangrui Zhang, Shuai Liu, Jielun Hu, Mingyong Xie*
[1]State Key Laboratory of Food Science and Resources, Nanchang University, Nanchang, China
[2]China-Canada Joint Lab of Food Science and Technology, Nanchang University, Nanchang, China
[3]Key Laboratory of Bioactive Polysaccharides of Jiangxi Province, Nanchang University, Nanchang, China

Functional constipation affects approximately 15% of the global population. *Astragalus membranaceus* is used clinically for constipation, but its active constituents remain unclear. This study prepared crude *Astragalus* extract (ACE) and purified its polysaccharide fraction (APS), then compared their effects in male BALB/c mice with loperamide-induced constipation by assessing defecation parameters, gastrointestinal (GI) transit, colonic histology, and 16S rRNA sequencing. ACE slightly outperformed APS in promoting GI transit (86%) and improving crypt depth (21.05%), whereas APS more significantly increased fecal weight (187%). Microbiota analysis showed that both treatments modulated diversity and composition, but APS restored the microbial structure closer to the normal control, with marked increases in beneficial taxa, including Bacteroidetes (26.66%), *Parabacteroides* (40.26%), and Lactobacillaceae (223%), while reducing Oscillibacter (28.15%) and the Firmicutes/Bacteroidetes (F/B) ratio (30.82%), indicating a superior capacity to restore intestinal ecological homeostasis. Collectively, this study demonstrates for the first time that APS is the core active component in ACE for constipation relief, acting primarily through restoration of gut homeostasis rather than simple prokinetic action. Based on this differential efficacy, we propose tailored processing strategies for distinct therapeutic goals, facilitating simplified *Astragalus* processing and efficient resource utilization. This result also underscore the critical importance of component fractionation in evaluating natural product efficacy.

MF14: Metabolic Engineering Strategies for Efficient Squalene Production in Yeast: A Review

Zifu Wang, Jiaqi Hu*, Junyi Yin*
State Key Laboratory of Food Science and Resources, China-Canada Joint Laboratory of Food Science and Technology (Nanchang), Key Laboratory of Bioactive Polysaccharides of Jiangxi Province; Nanchang University, Nanchang 330047, China

Squalene, a naturally occurring polyunsaturated triterpene hydrocarbon, possesses potent antioxidant, moisturizing, and oxygen-carrying functions, rendering it an irreplaceable in vaccine adjuvants, functional foods, and high-end chemicals[1]. However, conventional sourcing from shark liver oil and plant materials faces severe bottlenecks, including resource scarcity, ecological unsustainability, and inconsistent product purity, which urgently calls for alternative production platforms. Yeast-based biosynthesis via the endogenous mevalonate pathway has emerged as a promising and sustainable route for scalable squalene production. This review systematically summarizes recent advances in metabolic engineering strategies aimed at enhancing squalene titers in yeast, with a focus on three core engineering strategies: (i) pulling carbon flux by hyper-expressing rate-limiting enzymes, employing fusion protein strategies, and engineering substrate channeling to boost precursor supply[2-3]; (ii) implementing precise dynamic regulation of the competing squalene epoxidase branch through promoter replacement and degron-based protein degradation systems[4]; and (iii) significantly expanding intracellular storage capacity by overexpression of lipid droplet structural proteins[5]. Furthermore, the distinct physiological and metabolic characteristics of the two widely adopted chassis yeasts, *Saccharomyces cerevisiae* and *Yarrowia lipolytica*, are critically compared to guide strain selection and process optimization. By integrating these complementary strategies, this review provides a systematic framework for the rational design and construction of high-performance yeast cell factories, facilitating the transition from laboratory studies to industrial-scale fermentation and purification, thereby supporting the green and sustainable manufacturing of squalene.

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MF15: Microbial Biosynthesis of Squalene: Host Selection, Metabolic Engineering and Bioprocess Optimization

Chi Zhang, Junyi Yin*, Jiaqi Hu*
State Key Laboratory of Food Science and Resources, China-Canada Joint Laboratory of Food Science and Technology (Nanchang), Key Laboratory of Bioactive Polysaccharides of Jiangxi Province; Nanchang University, Nanchang 330047, China

Squalene, a high-value acyclic triterpenoid, is widely utilized across the food, nutraceutical, cosmetic and pharmaceutical industries. Traditional production from shark liver oil and plant oils faces mounting constraints, including ecological concerns, supply fluctuation and intricate purification steps, thereby driving the pursuit of microbial fermentation as an attractive sustainable alternative. This review summarizes recent advances in microbial squalene biosynthesis with emphasis on host strain selection, metabolic regulation and bioprocess engineering. The mevalonate pathway converts acetyl-CoA to farnesyl pyrophosphate and subsequently to squalene, but productivity is curtailed by inadequate precursor provisioning, restricted NADPH regeneration, catalytic efficiency of key enzymes, and competition from downstream sterol formation. Among the evaluated hosts, oleaginous yeasts such as *Yarrowia lipolytica* are promising due to their robust lipid metabolism, high intrinsic acetyl-CoA flux and ample lipid droplet compartments for product sequestration, whereas *Saccharomyces cerevisiae* offers mature genetic tools and proven industrial robustness. Emerging evidence indicates that maximal yields rely on a combinatorial engineering framework encompassing: overexpression of HMG-CoA reductase and squalene synthase, reinforcement of cofactor regeneration, attenuating squalene epoxidation, expanding lipid droplets capacity and subcellular pathway redistribution across cytoplasm, peroxisomes, mitochondria or endoplasmic reticulum. Furthermore, systematic fermentation parameters optimization and fed-batch strategies further improve final titer and productivity. Collectively, microbial squalene production is transitioning from single-pathway manipulation to integrated cell-factory design, establishing a robust and sustainable platform for the commercial production of food- and medicine-oriented hydrophobic terpenoids.

MF16: Comparative Study of the Flavor Profile of Raw and Fried *Ziziphi Spinosae Semen*

Zijun Xue, Falin Sun, Nuo Wang, Xiaolin Yu, Weitao Han, Jin Li, Bin Li, Jinlong Tian*
College of Food Science, Shenyang Agricultural University, Shenyang, 110866, China

Ziziphi Spinosae Semen (ZSS) is widely used as a medicinal and edible resource and frying is a traditional processing method that markedly affects its flavor quality[1,2]. However, the dynamic flavor evolution of ZSS during frying remains insufficiently understood, particularly from an integrated perspective linking chemical composition, sensory attributes and neural perception. This study investigated frying-induced flavor changes in ZSS using electronic nose, electronic tongue, HS-SPME-GC-MS, GC-IMS and EEG analyses. This study investigated stir-frying-induced flavor changes in ZSS at seven processing durations: 0, 5, 10, 15, 20, 25 and 30 min, coded as F0, F5, F10, F15, F20, F25 and F30, respectively, where F0 represents raw ZSS. Frying reduced bitterness and astringency while enhancing sweetness, umami, richness and thermally derived aroma characteristics. Volatile analysis revealed a shift from aldehyde- and ketone-associated raw, fatty and oxidized notes toward alcohol-, ester-, furan- and heterocyclic compound-enriched sweet, fruity, roasted and nutty characteristics. These changes were mainly associated with lipid oxidation, Maillard-type reactions, Strecker degradation, caramelization, esterification and secondary thermal transformations[3,4]. GC-IMS fingerprinting further showed that F20-F25 favored the accumulation of characteristic volatile markers, whereas F30 exhibited weakened volatile signals, suggesting possible volatile loss or over-frying. EEG analysis demonstrated that frying-induced flavor changes were reflected in human neural responses, especially in frontal and temporal regions[5,6], however, the strongest EEG response at F30 should be interpreted as higher neural salience rather than the highest flavor quality. This study fills the gap in understanding the time-dependent flavor evolution of fried ZSS and establishes a chemical-sensory-neurophysiological framework for evaluating flavor changes during processing.

Acknowledgments
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MF17: Ligand Engineering Combined with Thermodynamic Regulation to Construct Water-Dispersible CsPbCl3 Nanocrystals for HBCD Detection

Jingyu Feng, Yi Liu, Shuo Wang*, Haiyan Fu*
The Modernization Engineering Technology Research Center of Ethnic Minority Medicine of Hubei Province, School of Pharmaceutical Sciences, South-Central Minzu University, Wuhan 430074, China

Hexabromocyclododecane (HBCD) is a typical persistent organic pollutant (POPs) with high environmental persistence[1], bioaccumulation and biotoxicity, which has been listed in the Stockholm Convention, making its accurate and configuration-selective detection highly desirable for environmental monitoring[2]. Herein, water-dispersible CsPbCl3 perovskite nanocrystals (NCs) were synthesized via a ligand-assisted reprecipitation method. The effects of chloroalkanoic acid ligand chain length on the fabrication and performance of CsPbCl3 NCs were systematically investigated, and thermodynamic investigation was conducted to optimize the synthetic strategy for high-performance perovskite with excellent photoluminescence and photocatalytic activity[3]. The optimized CsPbCl3 NCs can efficiently trigger photocatalytic degradation and fast anion exchange (FAE) toward HBCD, producing distinct fluorescence color variation and emission peak shift that can be used for quantitative detection of HBCD. Combined with machine learning analysis, the proposed platform achieves high-precision discrimination of different HBCD isomeric configurations. Validated in various complex real samples, this sensing method exhibits excellent stability and anti-interference ability. It is well applicable to biological, environmental, and food sample analysis, providing a novel and reliable technique for POPs monitoring and isomer identification in practical complex systems.

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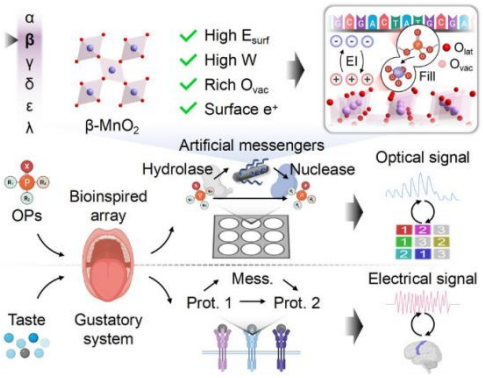
MF18: Crystal Phase-Driven MnO2-DNA as Editable Artificial Messengers Enabling a Bioinspired Array for High-Resolution Biosensing

Yi Liu, Jingyu Feng, Shuo Wang*, Haiyan Fu*
The Modernization Engineering Technology Research Center of Ethnic Minority Medicine of Hubei Province, School of Pharmaceutical Sciences, South-Central Minzu University, Wuhan 430074, China

High-precision identification of structurally similar compounds serves as a core technological foundation in research fields such as chemistry, biology, and medicine[1]. However, the current recognition mechanisms for structurally similar compounds using multi-channel array sensors exhibit homogenization and low sensitivity, making it difficult to achieve integrated qualitative-quantitative high-resolution biosensing[2]. This study proposes a high-resolution biosensor array constructed from a complex of β-phase MnO2 nanomaterials and single-stranded DNA (ssDNA) for detecting structurally similar organophosphorus compounds[3]. By leveraging the adsorption and desorption properties of MnO2 in different crystalline phases toward ssDNA, combined with a nuclease cascade reaction, a multi-channel sensor array was successfully developed. This array enables high-resolution detection of 19 organophosphorus compounds through digital encoding and machine learning algorithms. Experimental results demonstrated that the target compounds (e.g., chlorpyrifos) significantly enhance fluorescence signal output in the cascade reaction through interaction with the enzyme system, and the array exhibits strong selectivity and interference resistance. Studies demonstrate that this MnO2-based multi-enzyme array provides a novel application paradigm for high-resolution biosensing, with significant potential in environmental monitoring and food safety detection.



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MF19: Food-Sourced *Bacillus amyloliquefaciens* NC-1 for Deltamethrin Degradation in Whole-Corn Silage

Jiang liu[1], Qi Wen[1], Jie Tang[1,2]*, Xuan Yu[1,2]*
[1]College of Food and Bioengineering, Xihua University, Chengdu, Sichuan, China
[2]Enterprise External Supervisor, Feed Biotechnology Laboratory

Pyrethroid pesticide residues commonly contaminate environments and foods, and microbial degradation is an efficient strategy[1] for their harmless remediation. A highly deltamethrin-degrading strain NC-1 was isolated from Pixian broad bean paste and identified as *Bacillus amyloliquefaciens*. The strain exhibited favorable biosafety and probiotic characteristics with no hemolytic activity or harmful decarboxylase activity, high sensitivity to common antibiotics, and excellent aggregation ability, surface hydrophobicity, antibacterial activity and stress resistance. Based on response surface methodology, the optimal degradation conditions were determined as pH 6.1, 27.5 ℃ and an initial deltamethrin concentration of 29.7 mg/L, under which the degradation rate reached 84.2% within 72 h. Strain NC-1 also displayed broad-spectrum degradation capacity against various pyrethroid pesticides. A total of 12 metabolic intermediates were identified by GC-MS, and the degradation pathway was clarified: deltamethrin was completely mineralized through ester hydrolysis, redox reactions and aromatic ring cleavage. Genomic sequencing and RT-qPCR analysis verified abundant functional genes related to pesticide degradation, and 21 key degradation genes were significantly upregulated, revealing the molecular mechanism underlying its degradation performance. Practical silage fermentation experiments confirmed that strain NC-1 effectively removed deltamethrin residues with a degradation rate of 52.3%, which was significantly higher than that of the natural degradation group. In addition, NC-1 inoculation optimized the microbial community structure and improved the fermentation quality of pesticide-contaminated silage[2]. This study provides a promising microbial resource and theoretical basis for the bioremediation of pyrethroid-contaminated feed and safe silage fermentation.

Acknowledgments
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MF20: The Mechanism and Application of Cypermethrin Degradation by *L. bacillus* VF-2

Wanting Wang[1], Hu Zhou[1], Jie Tang[1,2]*, Xuan Yu[1,2]*
[1]College of Food and Bioengineering, Xihua University, Chengdu, Sichuan, China
[2]Enterprise External Supervisor, Feed Biotechnology Laboratory

Deltamethrin (β-CY) residues and its highly toxic metabolite 3-phenoxybenzoic acid (3-PBA) cause severe soil and agricultural product pollution, threatening ecological and food safety[0]. Currently, few studies have explored pyrethroid biodegradation by *Lysinibacillus*, restricting the bioremediation of pyrethroid contamination. This study systematically investigated the pyrethroid-degrading performance, molecular mechanism and application potential of a novel functional strain. Strain VF-2, identified as *Lysinibacillus pakistanensis*, was isolated from long-term pyrethroid-contaminated farmland soil[154]. Under optimized conditions (pH 6.94, 5.5% inoculum, 40.84 mg/L substrate), it degraded 81.66% of 50 mg/L β-CY. GC-MS analysis revealed 11 intermediates and a degradation pathway involving ester and diphenyl ether cleavage as well as benzene ring opening, with efficient mineralization of toxic 3-PBA. Genomic and RT-qPCR analyses confirmed key esterase genes est2566 and est3341 were significantly upregulated under β-CY stress. Soil inoculation with VF-2 increased β-CY and 3-PBA degradation efficiencies by 3.60-fold and 6.84-fold, respectively[0]. The heterologously expressed Est3341 enzyme achieved 98.68% degradation of 100 mg/L β-CY within 36 h, with wide temperature and pH adaptability, and could remove various pyrethroid residues from tea leaves[0]. This study first verifies the pyrethroid-degrading capacity of *Lysinibacillus pakistanensis*, providing valuable microbial and enzyme resources for pesticide residue bioremediation in soil and agricultural products.

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MF21: Nutritional Strategy of Medicinal and Edible Polysaccharides for Functional Dyspepsia Intervention via Gut Microbiota Remodeling

Chuanbo Cui[1], Xiaojun Huang[1]
[1]State Key Laboratory of Food Science and Resource, Nanchang University, 235 Nanjing East Road, Nanchang 330047, China

Functional dyspepsia (FD) affects 7%-10% of adults, traditionally attributed to motility disorders and visceral hypersensitivity. Recent studies reveal that duodenal barrier damage and local immune activation, via vagus-mediated central sensory reshaping, constitute the core pathology. Gut dysbiosis and its metabolites (lipopolysaccharides, lactate) are critical triggers. Animal multi- omics show that dysbiosis upregulates TLR2/4-NF-κB, with AEA correlating with symptoms, while lactate inhibits motility via GPR81-mediated interference with 5-HT and ghrelin. These findings support the interventional potential of dietary polysaccharides. Medicinal and edible polysaccharides, due to multi- target effects, low toxicity, and colonic fermentability, are ideal agents. Fucoidan modulates 5-HT and restores microbial balance to alleviate hypersensitivity; laminarin normalizes mechanotransduction via PIEZO2-EPAC1 and readjusts Bacteroidetes/Firmicutes; *Elsholtzia* polysaccharides activate PI3K/Akt/cGMP-PKG to reduce inflammation. Moreover, they promote Bifidobacterium, increase butyrate, and upregulate occludin/ZO-1 to repair the barrier. FD involves a disordered "microbiota-immune-neural" axis, and these polysaccharides offer a safe nutritional strategy by remodeling microecology and restoring barrier integrity. Future work should integrate fecal metabolic profiling for precision studies on polysaccharide types and dosages, facilitating functional food development and new clinical approaches for FD.

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MF22: Recent Advances in Research on the Mechanisms by Which Plant Polysaccharides Alleviate Functional Constipation

Xiao Jiang[1]，Xiaojun Huang[1]
[1]State Key Laboratory of Food Science and Resource, Nanchang University, 235 Nanjing East Road, Nanchang 330047, China

Functional constipation (FC) is a common functional gastrointestinal disorder with a global prevalence of 10%-15%[1], which significantly impairs patients' quality of life and imposes a heavy socio-economic burden. Current clinical treatments primarily consist of osmotic laxatives, prokinetic agents and secretagogues; however, long-term use is associated with issues such as drug dependence, electrolyte imbalances and diminished efficacy. Due to their natural origin, multiple bioactive properties and good safety profile, plant polysaccharides have demonstrated unique advantages in alleviating functional constipation and have become a research focus in recent years. This paper employs a three-axis analytical framework-'polysaccharide structure, gut microbiota and host function '-to systematically review the molecular mechanisms by which plant polysaccharides alleviate constipation through multiple pathways, including the regulation of gut microbiota[2], neurotransmitter and hormone levels[3], the repair of the intestinal mucosal barrier[4], and the modulation of aquaporins[5] and short-chain fatty acid metabolism[6] . Research indicates that the laxative activity of plant polysaccharides follows a complementary pattern of 'high-molecular-weight physical swelling-low-molecular-weight fermentative metabolism', with the core mechanism involving short-chain fatty acids-metabolic products of the gut microbiota—acting as a central signalling hub that integrates multiple pathways, including neural, hormonal, barrier, immune and fluid metabolism, to achieve multi-target synergistic regulation. This paper also discusses current research gaps in this field, including the lack of systematic integration of multi- pathway synergistic mechanisms, insufficient cross-comparisons between different polysaccharides, and a dearth of clinical translation studies, whilst outlining future research directions based on multi-omics technologies and precision-targeted delivery.

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MF23: Research Progress on the Mechanism of Natural Polysaccharides in Preventing Alcohol-Induced Liver Injury

Yuxuan Yang[1], Xiaojun Huang[1]
[1]State Key Laboratory of Food Science and Resource, Nanchang University, 235 Nanjing East Road, Nanchang 330047, China

Alcoholic liver disease (ALD) is the most prevalent type of chronic liver disease worldwide.The pathogenesis of ALD includes hepatic steatosis, oxidative stress, acetaldehyde-mediated toxicity and cytokine and chemokine-induced inflammation[1,2]. Many natural polysaccharides from bio-resources hold advantages of multi-functions, high efficiency, non toxicity or low side effect, and have strong potentials in protection against alcoholic liver damages[3]. They mitigate alcohol-induced hepatic steatosis, suppress pro-inflammatory cytokine expression, preserve antioxidant enzyme activity, and prevent pathological lipid accumulation in hepatocytes. Moreover, natural polysaccharides modulate intestinal homeostasis by regulating the expression of tight junction proteins, promoting beneficial microbial metabolite production (e.g., short-chain fatty acids), and restoring gut microbiota composition. These intestinal effects contribute to attenuation of systemic and hepatic inflammation via the gut-liver axis[4,5]. At the hepatic level, natural polysaccharides exert therapeutic actions through coordinated regulation of inflammatory signaling, redox balance, and lipid metabolism pathways[4]. The pathogenesis of alcoholic liver injury, as well as natural polysaccharides used to prevent or treat alcoholic liver disease and their underlying mechanisms are reviewed in this report, in order to provide reference for prevention and treatment of alcoholic liver disease and the development of functional liver-protecting foods.

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MF24: RSM-MLP-Based Optimization of Water Tempering and Processing Quality Control Mechanism for Germ-Retained Rice

Jiatong Li[1], Xiaoyi Jiang[1]*, Yong Fang[1]
[1]College of Food Science and Engineering, Nanjing University of Finance and Economics/Collaborative Innovation Center for Modern Grain Circulation and Safety, Nanjing, 210023, China

Germ-retained rice holds high nutritional value and development potential as it retains the germ and part of the aleurone layer[1]. However, during processing, it is prone to poor milling performance including high broken rice rate and structural damage, which restrict its quality improvement and industrial application[2]. Water tempering is a pre-milling moisture adjustment step, which critically affects the mechanical properties of rice kernels and thus directly influences subsequent milling behavior[3]. To optimize this process, this study employs response surface methodology (RSM) to optimize the tempering conditions and milling parameters, and integrates a multi-layer perceptron (MLP) model to predict and analyze the process response.

The main factors investigated are water addition, equilibrium time, equilibrium temperature, and milling time, with germ retention rate and broken rice rate as response variables. Regression models are established to analyze the effects of individual parameters and their interactions on the processing performance of germ-retained rice. RSM is effective in describing the response characteristics of process factors and determining a suitable processing window[4]. On this basis, MLP model is further constructed to perform nonlinear fitting of the tempering and milling process, and the predictive accuracy and generalization ability of the model are evaluated to verify the optimal process conditions[5]. Results show that RSM and MLP produce very close optimal solutions, and the relative error of the RSM-based optimization is smaller. Both models are able to describe the process response well, indicating that the optimization results are reliable and consistent.

Under the optimal conditions, the moisture migration process and its influence on processing quality are further investigated to reveal the underlying mechanism. Low-field nuclear magnetic resonance (LF-NMR) is used to analyze the water distribution in rice kernels, MRI is applied to visualize moisture migration, and scanning electron microscopy (SEM) is used to observe the cross-sectional microstructure of rice kernels. In addition, the changes in bran retention under different water addition levels and milling degrees were examined. Results show that water tempering promotes moisture redistribution within rice kernels, altered the internal microstructure and mechanical properties, and thus improves milling adaptability. Consequently, the broken rice rate decreases while germ retention is maintained. These findings indicate that water tempering improves processing performance by regulating internal water distribution and kernel mechanical properties, providing a mechanistic basis for the quality control of germ-retained rice.

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MF25: Soybean Hull-derived ITOC/LAE Complexes for HIPPE Stabilization

Junwei Yin[1], Ziqian Li[1]*, Yong Fang[1]*
[1]College of Food Science and Engineering, Nanjing University of Finance and Economics/Collaborative Innovation Center for Modern Grain Circulation and Safety, Nanjing, 210023, China

High internal phase Pickering emulsions (Φinternal > 0.74) conventionally require synthetic surfactants at concentrations exceeding 5 wt%, raising cytotoxicity and clean-label concerns[3]. Plant-derived cellulose nanofibers present a sustainable alternative, but native or mechanically fibrillated celluloses exhibit limited surface activity, necessitating high concentrations or additional modification[3]. Among various modification routes, complexation with food-grade cationic surfactants like lauroyl arginate ethyl ester (LAE) offers a facile way to render cellulose surfaces amphiphilic. However, existing systems predominantly rely on wood pulp feedstocks[4]. Herein, we employ insoluble TEMPO-oxidized cellulose (ITOC) derived from soybean hull, an agricultural byproduct rich in insoluble dietary fiber[5], as Pickering stabilizers for oil-in-water HIPPEs. These ITOC possess abundant carboxyl groups (1.6 mmol/g) introduced via selective oxidation, enabling strong electrostatic complexation with cationic LAE. We systematically investigate the role of mass ratio (ITOC to LAE) and complex concentration (from 0.1 wt% to) in modulating interfacial coverage, droplet morphology, and bulk network formation, revealing a critical concentration threshold for effective stabilization. In this study, ITOC/LAE complexes were characterized by ζ-potential, TEM, WCA, and FTIR. Complexation shifted wettability from hydrophilic to amphiphilic at an optimized mass ratio of 17, confirming suitability for Pickering stabilization. CLSM showed that increasing complex concentration enhanced interfacial particle coverage and reduced emulsion droplet size, however, at 0.5 wt%, excessive fiber aggregation impaired homogenization, leading to droplet coarsening. Meanwhile, all emulsions exhibited solid-like behavior (G' > G''), and stability tests confirmed strong resistance to creaming and coalescence, with EI exceeding 90% at higher concentrations. These results reveal a concentration-dependent interfacial adsorption mechanism and establish ITOC/LAE complexes as low-concentration, food-grade HIPPE stabilizers, valorizing soybean hull waste.

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MF26: From Peel Waste to Functional Ingredient: Green pH-driven Self-assembly of Tilapia Protein-Chondroitin Sulfate Nanoparticles for Enhancing the Stability and Bioavailability of Betanin

An Luo[1], Qiaoli Zhao[1]*, Xuan Zhang[1], Zhuo Wang[1], Rui Li[1], Saiyi Zhong[1,2]*
[1]College of Food Science and Technology, Guangdong Ocean University, Guangdong Provincial Key Laboratory of Aquatic Product Processing and Safety, Guangdong Province Engineering Laboratory for Marine Biological Products, Guangdong Provincial Engineering Technology Research Center of Seafood, Guangdong Provincial Science and Technology Innovation Center for Subtropical Fruit and Vegetable Processing, Zhanjiang 524088, China
[2]Shenzhen Research Institute, Guangdong Ocean University, Shenzhen 518108, China

Red-fleshed dragon fruit is a characteristic tropical fruit, but its peel, which accounts for 20-30% of the fruit mass, is commonly discarded by landfilling or incineration, causing resource loss, environmental pressure and disposal costs. The dragon fruit peel is rich in betanin, a water-soluble natural pigment with antioxidant and anti-inflammatory, and can function as both a colorant and a nutritional fortifier. However, betanin is readily degraded by heat, pH, oxygen and light, resulting in poor stability and low bioaccessibility. To overcome this limitation, we developed betanin-loaded tilapia protein isolate-chondroitin sulfate nanoparticles (TPI-CS/Bt) using a green pH-driven self-assembly strategy. Results indicate that at an optimal CS concentration of 2 mg/mL, the nanoparticles showed a particle size of 567.26 nm, a zeta potential of -35.93 mV, an encapsulation efficiency of 81.43% and a loading capacity of 11.63 μg/mg. Spectroscopic analyses (UV–vis, fluorescence, circular dichroism and FT-IR) revealed that betanin was incorporated primarily through hydrogen bonding and hydrophobic interactions. Compared with free betanin, TPI-CS/Bt improved thermal and ultraviolet stability and increased bioaccessibility by 2.44-fold, from 18.31% to 44.66%. In vitro gastrointestinal digestion experiments demonstrated that the release profiles of betanin showed reduced premature gastric release and fitted the Logistic model, while Ritger–Peppas kinetics indicated Fickian diffusion as the dominant release mechanism. This work offers a sustainable and efficient delivery platform that simultaneously valorizes dragon fruit peel waste and boosts betanin stability and bioavailability, opening a new avenue for the high-value utilization of fruit processing by-products in functional food applications.

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MF27: Identification and Antifungal Mechanism of Phytoalexins in Anoectochilus Roxburghii

Wenting Tan[1,2], Yuxiao Jiang[1,2], Ying Zheng[1,2]*
[1]State Key Laboratory for Development and Utilization of Forest Food Resources, Zhejiang A&F University, Hangzhou 311300, China
[2]She Herbal Medicine Industry Innovation Center of Jingning She Autonomous County, Lishui 323500, China

Phytoalexins derived from divergent plant species present prominent variations in structural profiles and bioactivities, executing anti-pathogenic functions through suppressing spore germination, restraining mycelial development and impairing pathogen membrane integrity[1]. Stem rot disease induced by *Fusarium oxysporum* severely restrains the growth and development of *Anoectochilus roxburghii*, and even causes plant withering and mortality, deteriorating its quality and yield[2,3]. Discovery of its anti-pathogenic metabolites and clarification of their inhibitory pathways are vital to establish eco-friendly disease management strategies for this medicinal herb[4]. This study integrated metabolomics, transcriptomics and molecular biology to explore defensive metabolites in *A. roxburghii* against *F. oxysporum*. Metabolomics analysis revealed that *F. oxysporum* infection markedly activated the phenylpropanoid pathway in *A. roxburghii* and boosted the biosynthesis of defensive metabolites. Among them, Batatasin III and Coelonin were sharply upregulated, with Batatasin III exhibiting superior antifungal activity. In vitro assays verified that Batatasin III could effectively suppress fungal mycelial growth. Transcriptome data revealed Batatasin III widely repressed *F. oxysporum* genes related to redox, transport and cell homeostasis, with ferric reductase gene FRD4 as the core target. Overexpression of FRD4 promoted fungal growth and virulence by disturbing iron redox balance, while Batatasin III markedly repressed FRD4 expression and alleviated disease severity. In summary, Batatasin III serves as an inducible phytoalexin to suppress the virulence of *F. oxysporum* via disrupting iron redox homeostasis. This research clarifies that the phytoalexin Batatasin III from *A. roxburghii* disturbs fungal iron homeostasis via targeting FRD4, which supplies theoretical and practical references for green disease management and natural fungicide exploitation of this medicinal herb.

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MF28: Sequential Physical Field Pretreatment Modulates Tilapia Soup Quality: A Multi-omics Investigation of Processing Order to Flavor and Nutrition

Jiaxuan Huang[1], Qiaoli Zhao[1]*, Di Huang[1], Zhuo Wang[1,2], Ziru Dai[3], Saiyi Zhong[1,2]*
[1]College of Food Science and Technology, Guangdong Ocean University, Zhanjiang 524088, China
[2]Shenzhen Research Institute, Guangdong Ocean University, Shenzhen, 518108, China
[3] College of Food Engineering, Beibu Gulf University, Qinzhou, 535011, China

Traditional tilapia soup production faces critical bottlenecks: low soluble solids release from fish tissue into broth, insufficient nutrient leaching, and severe flavor loss. Although individual physical treatments enhance soup quality, the sequential effects of distinct physical fields remain poorly characterized. This study investigated the effects of two physical field processing sequences (colloid milling followed by ultrasonication, CMUFS, and ultrasonication followed by colloid milling, UCMFS) on the microstructure, nutritional composition, flavor profile, and overall quality of tilapia soup, using untargeted metabolomics, volatilomics, electronic sensory technology, and correlation network analysis. Results showed that the CMUFS group produced smaller droplets (D4,3=16.51 μm) and a more stable suspension, yet exhibited lower total hydrolyzed amino acid content (284.9 mg/100 mL) and a poorer amino acid score (13.4). This was attributed to initial shear-induced protein aggregation that could not be fully disrupted by subsequent ultrasonication, entrapping nutrients within dense matrices. Conversely, UCMFS achieved a higher amino acid score (24.9, 86% improvement) and richer flavor richness (electronic tongue richness value of 0.663), despite larger droplets (D4,3=28.77 μm) and reduced stability. The sequence of ultrasonication followed by colloid milling avoids shear-induced protein aggregation, achieves thorough dispersion of the material, and reduces damage to the protein conformation caused by the shearing, enhancing substrate availability for Maillard reactions and lipid oxidation pathways. Metabolomics analysis identified 15 differential metabolites involved in lipid and amino acid metabolism, confirming UCMFS improves both nutritional value and flavor quality. These findings provide a theoretical basis for sequence-guided quality regulation of aquatic soup production.

MF29: Onchidium Struma Polysaccharides Ameliorate Type 2 Diabetes via Gut Microbiota Modulation

Ying Gao[1], Xiaodong Ge[1], Ligen Chen[1,2]*, Wei Xu[1,2]*, Rong Shao[1,2]
[1]School of Marine and Bioengineering, Yancheng Institute of Technology, Yancheng 224051, China
[2]Jiangsu Key Laboratory of Biochemistry and Biotechnology of Marine Wetland, Yancheng Institute of Technology, Yancheng 224051, China

Onchidium struma polysaccharides (OsPs) are natural biologically active compounds, and our previous work showed that they can inhibit the activity of α-glucosidase in vitro, showing potential hypoglycemic activity. However, the effects of OsPs on type 2 diabetes mellitus (T2DM) in vivo remain unknown. It is estimated that diabetes affects over 415 million adults worldwide and is projected to rise to over 640 million by 2040, with T2DM accounting for approximately 90% of cases, establishing it as a global health burden[1]. Consequently, the prevention and treatment of obesity and related metabolic complications are subjects undergoing intense research[2]. Thus, the anti-diabetic activity of OsPs was evaluated in the present study in diabetic mice. The results showed that OsPs can significantly ameliorate the features of T2DM in mice by improving the levels of fasting blood glucose (FBG), oral glucose tolerance test (OGTT), and pro-inflammatory factors, and ameliorating insulin resistance. Furthermore, OsPs can significantly improve biochemical indicators, decrease the contents of total cholesterol (TC) and triglyceride (TG), and reduce lipid accumulation in the liver. The possible mechanism of the prevention and treatment of T2DM by OsPs may involve the phosphoinositide 3-kinase (PI3K)/protein kinase B (AKT-1) signaling pathway. The possible mechanism of the prevention and treatment of T2DM by OsPs may involve the PI3K/AKT-1 signaling pathway[3]. OsPs can regulate the dysbiosis of gut microbiota and reverse the abundance of Lactobacillus in mice with T2DM. Moreover, OsPs significantly increased the concentration of short-chain fatty acids (SCFAs) in mice with T2DM. Recent evidence has presented the important role of gut microbiota in the development and treatment of T2DM, suggesting modulation of microbiota is a novel therapeutic opportunity[4]. Our results indicate that OsPs can be used as a novel food supplement for the prevention and treatment of T2DM, and dietary polysaccharides are expected to serve as potential sources of prebiotics through modulating the gut microbiota.

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MF30: Supernatant of Water Extraction–Ethanol Precipitation of Chaga Mushroom Improves Hyperglycemia in Type 2 Diabetes Mellitus and Is Accompanied by Changes in Gut Microbiota Composition

Yang Yang[1], Xiaodong Ge[2,3], Wei Xu[2,3], Rong Shao[1,2,3]*
[1]School of Chemistry & Chemical Engineering, Yancheng Institute of Technology, Yancheng 224051, China
[2]College of Marine and Bioengineering, Yancheng Institute of Technology, Yancheng 224051, China
[3]Jiangsu Key Laboratory for Exploration and Utilization of Marine Wetland Biological Resources,Yancheng Institute of Technology, Yancheng 224051, China

Type 2 diabetes mellitus (T2DM) is a chronic metabolic disorder characterized by insulin resistance and inadequate insulin secretion[1,2]. Prolonged hyperglycemia is associated with disruption of gut microbiota (GM) homeostasis[3-5]. Although bioactive compounds in Chaga mushroom, such as polysaccharides, have hypoglycemic effects, research on its polysaccharide preparation by-product, the supernatant of water extraction–ethanol precipitation of Chaga mushroom (SWEPC), remains limited. In this study, we investigated the effects of SWEPC on GM composition and its therapeutic potential in alleviating hyperglycemia in T2DM mice. After four weeks of SWEPC intervention (300 mg/kg/day), T2DM mice exhibited significant improvements: fasting blood glucose (FBG) decreased by 52.29% ($p < 0.001$); the area under the curve of oral glucose tolerance decreased by 37.68% ($p < 0.001$); glycated serum protein decreased by 65.36% ($p < 0.001$); the insulin resistance index decreased by 44.42% ($p < 0.001$); and the insulin sensitivity index increased by 90.24% ($p < 0.001$). Spearman's correlation analysis revealed that Anaeroplasma, Anaerotruncus, and *Ruminococcus* were associated with serum low-density lipoprotein cholesterol ($r = 0.75$), FBG ($r = -0.81$), and body weight ($r = -0.65$), respectively, suggesting their potential involvement in T2DM-related metabolic traits and warranting further investigation. Overall, SWEPC ameliorated hyperglycemic manifestations in T2DM mice, which was accompanied by changes in the GM community.

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MF31: Construction and Stability Evaluation of an All-Food-Grade Naringenin Nanodelivery System

Weiyi Chen, Pan Wei, Ruixue Sun*
College of Food and Health, College of Modern Grain Industry, Zhejiang A&F University, Hangzhou 311300, Zhejiang, China

Naringenin has poor aqueous solubility and limited environmental stability and is susceptible to degradation during gastrointestinal digestion, thereby restricting its oral delivery and effective utilization. In this study, a food-grade nanodelivery system was constructed by antisolvent self-assembly using *Polygonatum* polysaccharides (PSP) as the carrier matrix, and nanoparticle formation was regulated by adjusting the aqueous-to-ethanol phase volume ratio. As the aqueous-to-ethanol ratio increased, the mean particle size and polydispersity index of the nanoparticles gradually decreased, while a high encapsulation efficiency was maintained. At the optimal ratio of 7:1, the resulting PSP–naringenin nanoparticles (PSP–NAR NPs) exhibited an encapsulation efficiency of 94%, a mean particle size of approximately 250 nm, and a polydispersity index of 0.15. The nanoparticles displayed a nearly spherical morphology and a distinct core–shell structure. Hydrogen bonding, electrostatic interactions, and hydrophobic interactions were identified as the main driving forces for nanoparticle assembly, and encapsulation markedly reduced the crystallinity of naringenin. PSP–NAR NPs also exhibited good short-term stability under light exposure and thermal treatment at 45–75 °C. Their DPPH radical-scavenging rate was approximately 64%, higher than those of free naringenin and the physical mixture, which were approximately 19% and 50%, respectively. During simulated intestinal digestion, PSP–NAR NPs exhibited a slower and more sustained release profile than free naringenin. Their release kinetics were best fitted by the Higuchi model, indicating that the release process was mainly controlled by diffusion. These results demonstrate that adjusting the aqueous-to-ethanol ratio can effectively regulate the formation of PSP–NAR NPs and provide a basis for improving the sustained release of naringenin during intestinal digestion.

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MF32: Optimal Harvest Time in Three *Torreya grandis* Cultivars at Six Growth Stages: Integrating Metabolome and Transcriptome to Maximize Health Benefits

Zehua Chen[1]*, Zuying Zhang[1,2], Lili Song[1, 2], Fei Gao[1,2], Han Tao[1,2]
[1]State Key Laboratory for Development and Utilization of Forest Food Resources, Zhejiang A&F University, 311300 Hangzhou, China
[2]Zhejiang Key Laboratory for Non-wood Forest and Quality Control and Utilization of Its Products, Zhejiang A&F University, 311300 Hangzhou, China

Torreya grandis (*T. grandis*) is a highly valued multipurpose tree in southern China, utilized for food, medicine, oil, timber, and ornamentation[1]. It is characterized by high flavonoid accumulation, a class of secondary metabolites with strong antioxidant properties[2,3]. Although previous studies have reported significant cultivar differences in flavonoid levels[4], the temporal accumulation patterns of these compounds and other metabolites during the pivotal growing season (May to September) remain uninvestigated systematically. Three representative cultivars of *T. grandis* were selected: 'Xifei' (the predominant cultivar with the largest cultivation area), 'Xiangyafei' (a high-priced cultivar highly favored by the market), and 'Shishengfei' (widely utilized as a grafting rootstock for its strong resistance)[5]. Sampled at six growth stages, they were subjected to integrated metabolomic and transcriptomic analyses, along with measurements of antioxidant capacity and antioxidant enzymes. The results showed that total metabolite content peaked in May and gradually declined to the lowest level in September[6]. Despite this general trend, specific compounds exhibited distinct temporal dynamics: sakuranetin and hesperidin accumulated markedly in September, while quercetin-3-galactoside and vanillin showed cultivar-dependent accumulation and were completely undetectable in 'Shishengfei'. Additionally, DPPH radical scavenging activity and the enzymatic activities of SOD, CAT, and POD indicated stage-specific antioxidant defense status, reflecting adaptive physiological adjustments. Joint analysis of key genes and metabolic pathways in phenylpropanoid and flavonoid biosynthesis further elucidated the regulatory networks underlying health-promoting components. This study establishes seasonal metabolite profiles for *T. grandis* and provides a scientific basis for optimizing harvest schedules to maximize health-promoting components.

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MF33: Mechanism of Efficient (−)-Epigallocatechin Biosynthesis Catalyzed by Torreya grandis ANR (TgANR) and Its Protein Engineering Modification

Suwan Li[1], Fei Gao[1,2], Wenjing Jiang[1,3], Miaomiao Chen[1,2], Kexin Liu[1,2], Liang Wei[1,2], Han Tao[1,2]*, Lili Song[1,2]*
[1]State Key Laboratory for Development and Utilization of Forest Food Resources, Zhejiang A&F University, Hangzhou, 311300, China
[2]Zhejiang Key Laboratory of Non-wood Forest Products Quality Regulation and Processing Utilization, Zhejiang A&F University, Hangzhou 311300, China
[3]State Key Laboratory of Crop Genetics & Germplasm Enhancement and Utilization, Nanjing Agricultural University, Zhongshan Biological Breeding Laboratory, Nanjing 210095, China

(−)-Epigallocatechin (EGC), a cis-configured non-ester-type catechin, is one of the six major monomeric catechins in plants, alongside (−)-epigallocatechin gallate (EGCG), (−)-epicatechin gallate (ECG), (+)-gallocatechin (GC) (−)-epicatechin (EC), and (+)-catechin (C)[1,2]. The biosynthesis of EGC initiates from phenylalanine, which is converted to cinnamic acid and further transformed through a sequential enzymatic cascade. The terminal and rate-influencing step involve the reduction of delphinidin to EGC, is catalyzed by anthocyanidin reductase (ANR). Consequently, ANR serves as the key enzyme responsible for EGC synthesis. (-)-Epigallocatechin has multiple bioactivities, ANR catalyzes its biosynthesis, with unclear structure and mechanism restricting enzyme modification. Here, we first screened ANRs from 21 plant species and identified *Torreya grandis* ANR (TgANR) as the most efficient candidate based on molecular docking and in vitro assays. Through integrated alanine scanning and computational prediction, we constructed a combinatorial mutant N15S/F106E/P182S, which exhibited a 3.88-fold higher EGC synthesis activity than the wild-type enzyme. The interaction mechanism between TgANR and the substrate delphinidin as well as the structure-activity relationship in the catalytic production of EGC were studied on the basis of protein engineering modification, thus clarifying the catalytic mechanism of TgANR. Furthermore, transient overexpression of the mutant gene in *T. grandis* kernels significantly increased EGC accumulation. This study not only elucidates the structure activity relationship of TgANR but also provides an efficient enzyme variant and a protein engineering framework for boosting EGC biosynthesis in plants.

Acknowledgments
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MF34: Effects of *Premna microphylla* Turcz on the Textural Quality of Noodles and Underlying Mechanisms

Lanlan Shan
College of Food and Health, Zhejiang Agriculture and Forestry University, No. 666 Wusu Road, Linan District, 311300, Hangzhou, Zhejiang Province, China

Leaves of *Premna microphylla* Turcz contain significant amounts of pectin, fiber, protein, flavonoids, and polyphenolic substances, showcasing antioxidative and anti-inflammatory activities1,2. The pectin in *Premna microphylla* Turcz, predominantly low-methoxyl pectin, possesses gelation properties regulated by calcium ions, making it a potential natural material for food gelling agents or thickeners3,4. Despite its rich availability in China, *Premna microphylla* Turcz has not been fully exploited or utilized efficiently. This study attempted to develop novel nutritious noodles by incorporating *Premna microphylla* Turcz into wheat flour. However, research on its application in noodle products and its impact on gluten network structure remains scarce. Therefore, we systematically investigated the effects of *Premna microphylla* Turcz on textural properties of raw and cooked noodles. First, rheological analysis of raw dough demonstrated that with an increase in *Premna microphylla* Turcz addition, the solid-like properties of the dough were enhanced, while its extensibility was reduced and its rheological mechanical properties were weakened. This macroscopic deterioration was attributed to the disruption of gluten network continuity, a reduction in glutenin macropolymer content, and alterations in protein secondary structure (a decrease in α-helices, an increase in β-sheets, and an increase in random coils)5. Second, studies on the cooking quality of cooked noodles showed that as the addition level of *Premna microphylla* Turcz increased, cooking time, water absorption, and cooking loss rate increased, while cohesiveness, chewiness, and elasticity decreased, and hardness increased, which collectively indicated the deterioration of cooking quality6. This study revealed the mechanism of action of *Premna microphylla* Turcz on gluten network structure at multiple scales, providing a theoretical basis and practical reference for the high-value utilization of *Premna microphylla* Turcz resources and the development of functional noodles.

Acknowledgement
The authors gratefully acknowledge the financial support from Zhejiang Agriculture and Forestry University Scientific Research Development Fund Talent Launch Project (2024LFR006 and 2020FR078).

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MF35: Deep Learning-Based Study of the Antihypertensive Efficacy of Food-derived Protein Peptides Produced by Multi-enzyme Synergistic Hydrolysis

Shilong Cheng[1], Shuai Jiang[1]*, Ling Jiang[1,2]*
[1]College of Food Science and Light Industry, Nanjing Tech University, Nanjing 211816, China
[2]State Key Laboratory of Materials-Oriented Chemical Engineering, Nanjing Tech University, Nanjing 211816, China

Hypertension is a major global health concern and an important risk factor for cardiovascular and cerebrovascular diseases. Food-derived antihypertensive peptides have attracted increasing attention because of their potential efficacy and favorable safety profiles. However, conventional enzymatic hydrolysis strategies are generally limited by complex enzyme combinations and low efficiency in the production and identification of bioactive peptides. In this study, deep learning and large language models were applied to optimize multi-enzyme hydrolysis for the discovery of antihypertensive peptides from walnut and whey proteins. The optimized walnut protein hydrolysate W1 and whey protein hydrolysate MC5 exhibited angiotensin-converting enzyme (ACE) inhibition rates of 77.96% and 89.08%, respectively, and retained strong inhibitory activity following simulated gastrointestinal digestion. Both hydrolysates also showed considerable antioxidant activity and significantly reduced systolic and diastolic blood pressure in spontaneously hypertensive rats. Mechanistically, their antihypertensive effects were associated with regulation of the renin–angiotensin system, attenuation of oxidative stress and inflammatory responses, and improvement of vascular endothelial function. Molecular docking further identified VIRGNARL, PSYQPTPSL, PQYSNAPQL, LPEW, LKPTPEGDL, LNYW, and LLL as potential ACE-inhibitory peptides. These findings demonstrate that deep learning-guided multi-enzyme hydrolysis provides an effective strategy for the targeted production and efficient discovery of food-derived antihypertensive peptides.

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This research was funded by the Major Science and Technology Projects of the Xinjiang Uygur Autonomous Region (grant No. 2022A02004), the National Natural Science Foundation of China (grant No. 32302060), the China Postdoctoral Science Foundation (grant Nos. GZC20231118, 2024T170411, and 2024M761426), and the Jiangsu Province Excellent Postdoctoral Program (grant No. 2023ZB620).

MF36: Patchouli Alcohol Isolated from Pogostemonis Herba Ameliorates Sleep Deprivation-Induced Cognitive Dysfunction in Mice Through Modulation of the Brain-gut Axis

Yongxian Li[1], Huosheng Liang[1], Zhangye Chen[1], Guangyang Chen[1], Guodong Zheng[1]*, Chuwen Li[1]*
[1]Guangzhou Municipal and Guangdong Provincial Key Laboratory of Molecular Target & Clinical Pharmacology, the NMPAand State Key Laboratory of Respiratory Disease, School of Pharmaceutical Sciences, Guangzhou 511436, China

Chronic sleep deprivation (SD), a highly prevalent public health risk factor in modern societies, induces persistent impairments in spatial learning and memory, thereby posing a substantial threat to population-wide cognitive health. The "microbiota-gut-brain axis" theory has recently emerged as a novel research framework for dissecting the pathological mechanisms underlying SD-associated cognitive deficits. While gut microbiota dysbiosis and central neuroinflammation have been validated as two core drivers of this pathological process, the complete molecular cascade mediating their inter-organ crosstalk remains uncharacterized, and targeted therapeutic agents that concurrently exert peripheral barrier restoration and central neuroprotection are still severely lacking. Grounded in the systemic regulatory logic of the microbiota-gut-brain axis, the present study systematically dissects the mechanism by which patchoulol (PA), a natural multi-target bioactive molecule, ameliorates SD-induced cognitive impairment. We identify for the first time that the core feature of PA's intervention efficacy lies in the deep synergy between peripheral defense and central repair, achieving dual-targeted regulation of SD-associated cognitive deficits via a unique "brain-gut co-regulation" paradigm.
At the peripheral level, PA exhibits remarkable intestinal barrier-remodeling activity: it not only effectively reverses SD-induced structural dysbiosis of the gut microbiota and restores the dysregulated microbial abundance and composition, but also reconstructs the intestinal epithelial physical barrier by upregulating the expression of tight junction proteins ZO-1, Occludin and Claudin-5, while concurrently fortifying the intestinal mucosal chemical barrier. This dual barrier-restoration effect markedly attenuates SD-mediated elevation of intestinal permeability, thereby fundamentally blocking the inter-organ translocation of gut-derived pro-inflammatory toxins into the circulatory system and central nervous system, and interrupting the pathological pathway for peripheral inflammation to propagate into the brain. At the central level, PA selectively inhibits aberrant overactivation of the NLRP3 inflammasome in the hippocampus, reduces the release of pro-inflammatory cytokines, and effectively ameliorates the SD-disrupted central neuroinflammatory microenvironment. Integrated multi-omics analyses combining metagenomics, transcriptomics and proteomics demonstrate that PA specifically upregulates the expression of the integrin receptor ITGB1 in the hippocampus, which subsequently reactivates the downstream MAPK (p-ERK/ERK) kinase cascade suppressed under SD conditions, ultimately restoring the expression of SNAP25, reversing hippocampal synaptic plasticity deficits, and rescuing impaired learning and memory functions.
Collectively, the present study defines the unique "brain-gut co-regulation" mechanism of PA: peripherally, it blocks the propagation of inflammatory mediators by restoring the intestinal mucosal barrier, while centrally, it rescues normal synaptic transmission by activating the "ITGB1-MAPK-SNAP25" signaling axis. These findings not only provide a novel natural-origin neuroprotective candidate for the clinical prevention and treatment of SD-related cognitive impairments, but also deliver innovative insights and robust experimental evidence to support the research field of integrated traditional Chinese and Western medicine for central cognitive regulation.

MF37: Sea Cucumber Peptides Alleviate Hyperuricemic Nephropathy via HIF-1α/NF-κB/STAT3-SIRT1/p300 Axis-Mediated Metabolic and Epigenetic Modulation

Peiting Lv[1,2], Shuzhen Cheng[1,2]* and Ming Du[1,2,3]*
[1]State Key Laboratory of Marine Food Processing & Safety Control, School of Food Science and Technology, Dalian Polytechnic University, Dalian, 116034, China
[2]National Engineering Research Center of Seafood, School of Food Science and Technology, Dalian Polytechnic University, Dalian 116034, China
[3]College of Food Science and Engineering, Dalian Ocean University, Dalian 116023, China

Hyperuricemic nephropathy (HN) is a progressive kidney disease resulting from impaired urate metabolism, with limited effective therapies from natural sources. Sea cucumber peptide (SCP) have shown metabolic regulatory potential in chronic diseases, but their efficacy in HN and underlying mechanisms remain unclear. This study investigated SCP's effects using hyperuricemic mouse models and HK-2 cells. Interestingly, SCP did not inhibit xanthine oxidase activity, yet significantly reduced serum uric acid (UA) levels, improved renal function, and attenuated pathological damage in mice. Mechanistically, SCP reversed HN-induced metabolic reprogramming by downregulating key glycolytic enzymes (HK2, PFKFB3, LDHA), reducing lactate accumulation, and enhancing ATP production. Multi-omics analyses revealed that SCP optimized glycolysis-TCA cycle flux. Crucially, SCP restored lactylation homeostasis via the SIRT1/p300 axis, suppressing global protein and histone lactylation. Concurrently, SCP inhibited the HIF-1α/NF-κB/STAT3 pathway, decoupling metabolic-inflammatory signaling. These findings demonstrate that SCP alleviate HN through multi-targeted regulation of urate metabolism, metabolic reprogramming, and lactylation, offering a novel strategy for functional food development.

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MF38: Dietary Polysaccharide in the Control of Gut Microbiota-related TMAO: Mechanisms, Structure-Activity Relationships, and Food Applications

YuPing Song, Fangwei Liu, Junyi Yin*
State Key Laboratory of Food Science and Resources, China-Canada Joint Laboratory of Food Science and Technology (Nanchang), Key Laboratory of Bioactive Polysaccharides of Jiangxi Province, Nanchang University, Nanchang, Jiangxi Province, 330047, China

Trimethylamine N-oxide (TMAO), a gut microbiota-related metabolite induced by high sugar and fat diet, is associated with the risk of chronic diseases, including cardiovascular disease, chronic kidney disease, and diabetes. Natural inhibitors have attracted extensive attention, but existing research remains focuse predominantly on polyphenolic compounds, whereas dietary polysaccharides have not been systematically explored. This review elaborates on the formation pathways of TMAO in food systems, representative biomarkers, and their dietary relevance, and then integrates the current research on the anti-TMAO mechanisms, structure-activity relationships, and food applications of dietary polysaccharides. Current evidence indicates that polysaccharides can inhibit TMAO production and transformation through multiple mechanisms, including modulation of gut microbiota composition and function, suppression of intestinal TMA lyase activity, restoration of intestinal barrier function, as well as regulation of short-chain fatty acid and bile acid metabolism. Among dietary polysaccharides, arabinoxylan and *Butyriboletus roseoflavus* polysaccharide have provided the most direct evidence for TMAO inhibition, whereas polysaccharides such as lentinan, *Lycium barbarum* polysaccharide, and *Poria cocos* polysaccharide are currently supported primarily by preliminary, indirect, or presumptive evidence. Nevertheless, limited studies in food systems have suggested that these polysaccharides possess considerable engineering value, because certain dietary polysaccharides can not only suppress TMAO accumulation but also improve food texture, stability, and sensory quality. Overall, dietary polysaccharides represent an ideal multifunctional ingredient category for the development of foods that inhibit gut-derived harmful metabolites. However, their practical application still necessitates more standardized evaluation systems, clearer process-structure-activity relationship models, and predictive models that can more accurately simulate real dietary intake scenarios.

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MF39: Antifungal Effects of Violet LED Light on *Penicillium expansum* and the Underlying Mechanisms

Ning Ding[1], Haiyan Lin[1], Ruiyu Zhu[1]*
[1]School of Biological and Chemical Engineering, Zhejiang University of Science and Technology, Hangzhou, 310023, China

Accumulating evidence indicates that the antifungal activity of visible LED light is wavelength-dependent. However, little is known about the antifungal effects of violet light. In this study, we evaluated the inhibitory effect of violet LED irradiation on *Penicillium expansum* and investigated its underlying mechanisms. Exposure to violet LED light (80 μmol·m^{-2}·s^{-1}) delayed spore germination by 6 h, reduced colony diameter by 77% following 7 days of continuous irradiation, and completely suppressed sporulation. This treatment also disrupted cell membrane integrity, induced DNA damage, and downregulated the expression of genes involved in key developmental pathways. Notably, even a 6-h violet light exposure followed by dark incubation still resulted in significant inhibition of spore germination, growth, and sporulation, indicating a sustained inhibitory effect. After removal of the light source, *P. expansum* continued to exhibit severe DNA damage, and the transcription of DNA damage recognition and repair genes was only transiently upregulated before being markedly suppressed. Thus, violet LED light not only triggers DNA damage but also compromises the fungal DNA repair capacity, thereby effectively inhibiting the growth and development of *P. expansum*. These findings advance our understanding of the antifungal mechanisms of visible LED light.

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MF40: Construction and Optimization of a Cell Factory for Synthesis of Dendrobium catenatum Glucomannan

Chuyun Guan[1], Shuqi Zhang[1], Jingjing Liu[1], Peng Jin[2], Jinping Si[1]
[1] National Key Laboratory for Development and Utilization of Forest Food Resources, Zhejiang A&F University, Hangzhou 311300, China
[2] College of Agricultural and Food Sciences, Zhejiang A&F University, Hangzhou 311300, China

Glucomannan, as the principal bioactive polysaccharide of *Dendrobium catenatum*, is currently sourced almost exclusively via plant extraction, an approach inherently limited by low yield, long growth periods, and poor batch-to-batch consistency[1]. Hence, developing a green, efficient, and stable biosynthetic approach represents a promising direction to address these challenges[2]. In this study, we reconstituted the glucomannan biosynthetic pathway in *Escherichia coli* C41(DE3) by introducing the key synthase gene Csl A/D from *D. catenatum*. To further optimize the pathway, we co-expressed galU and manC to enhance the supply of the precursors UDP-glucose and GDP-mannose, resulting in a 23.63% increase in glucomannan production. Through comparative screening of strains harboring different Csls genes, we identified strain D03 as the highest producer, achieving a titer of 0.287 g/L. Subsequent fermentation medium optimization elevated the production of strain D03 to 0.341 g/L. Collectively, our findings demonstrate the feasibility of employing microbial cell factories for natural product biosynthesis and lay a foundation for future investigations into the gene–structure–function relationships of *D. catenatum* glucomannan.

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MF41: Multi-Strain Fermentation of Whole Grains: Structural Remodeling, Flavor Modulation, and Development of Low-GI Functional Bakery Products

Jinchen Li, Yiming Zhou*, Minglong Wang, Lan Zhang, Renzhi Lv
Faculty of Flavour Fragrance and Cosmetics, Shanghai Institute of Technology, Shanghai, 201418, China

Whole grains are rich in dietary fiber, resistant starch, and polyphenols, which have been shown to reduce the risk of type 2 diabetes and cardiovascular diseases, as well as to improve gut microbiota composition. However, traditional whole grain products often suffer from coarse texture, poor palatability, and unsatisfactory processing properties due to the use of single and conventional processing methods, thus failing to meet the dual consumer demands for both palatable taste and nutritional quality. Lactic acid bacteria fermentation offers an innovative solution to these challenges. Nevertheless, the complex molecular mechanisms underlying the interactions between lactic acid bacteria and whole grain substrates during fermentation remain insufficiently elucidated, which limits the full exploitation of their potential advantages.

In this study, we systematically investigated the effects of fermentation with *Lactiplantibacillus plantarum* on the multiscale structure of coarse grain flours (tartary buckwheat, highland barley, and oat), as well as its subsequent impacts on dough processing performance, bread quality, and starch digestibility. Our results demonstrated that fermentation simultaneously improved the processing properties and nutritional functionality of coarse grain flours by remodeling starch crystalline structures and inducing a conformational transition of protein secondary structures from random coils to thermodynamically stable β-sheets. On this basis, we further employed a multi-strain synergistic fermentation strategy and isolated five lactic acid bacteria strains with outstanding acid- and ester-producing capacities. Through integrated volatile flavor compound analysis and metabolomic profiling, pyruvate, acetyl-CoA, valine, leucine, and isoleucine were identified as key nodes in the flavor metabolic network, enabling the establishment of a precision quality regulation model. Additionally, lactic acid bacteria fermentation was found to achieve simultaneous degradation of acrylamide and endogenous gluten allergens generated during processing.

Breads prepared with the fermented coarse grain flours exhibited significantly increased specific volume and retarded staling rates. In vitro digestion assays further revealed that the estimated glycemic index (eGI) of these breads was reduced to 52.03–55.17, meeting the criteria for low-GI foods. Collectively, this study systematically established a core technological system for whole grain fermented foods encompassing structural modification, flavor regulation, and safety hazard mitigation. Our findings provide a robust scientific foundation for the development of high-value-added functional whole grain products and facilitate the sustainable advancement of the whole grain industry toward health-oriented and quality-enhanced directions.

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MF42: Antiviral Effect and Mechanism of Geraniin Against Enterovirus 71

Chengyin Feng[1], Qian Zhang[1,2], Tian Chen[1]*
[1]School of Basic Medical Sciences, Chengdu Medical College, Chengdu, China
[2]Department of Nursing, The Second People's Hospital of Xindu District, Chengdu, China

Enterovirus 71 (EV71) is a major pathogen causing severe hand, foot, and mouth disease, yet no effective therapeutic agents are available[1,2]. Traditional Chinese medicines show antiviral potential, but their complex compositions limit clinical use. Computer-aided virtual screening offers an efficient approach to discover active compounds. We aimed to identify Chinese herbal monomers inhibiting EV71 3C protease via virtual screening and elucidate their antiviral mechanisms. Monomers from TCM Database@Taiwan were docked against EV71 3C protease using AutoDock Vina. Geraniin, a top-ranking candidate, was selected for in vitro evaluation in Vero cells. Cytotoxicity and anti-EV71 efficacy were assessed via CPE, MTT, and plaque reduction assays. Time-of-addition and virucidal assays determined stage-specific effects. Viral adsorption, penetration, and mRNA expression of EV71 proteins (3C, 2A, 3D, VP1) were analyzed using RT-qPCR. Geraniin exhibited low cytotoxicity (TC50 = 245 μmol/L) and significantly inhibited EV71 replication (IC50 = 9.43 μmol/L, SI = 25.87). Time-course analyses revealed that geraniin exerts its most potent effect during early viral infection stages, demonstrating both prophylactic and direct virucidal activities. Mechanistically, geraniin inhibited viral adsorption and penetration, while significantly downregulating the mRNA expression of essential viral proteins 3C, 2A, 3D, and VP1. Geraniin exhibits significant anti-EV71 activity by targeting the 3C protease. It potently blocks early-stage viral replication by inhibiting adsorption, penetration, and viral gene expression, highlighting its potential as a natural anti-EV71 therapeutic candidate[3].

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MF43: Evaluation of Rice Freshness During Storage Based on Flavor Marker Characterization and Vision-Spectroscopy Multimodal Fusion

Shiyun Tang, Zhiyang Peng, Jingwan Ye, Yiming Zhou*, Minglong Wang, Lan Zhang, Renzhi Lv
Faculty of Flavour Fragrance and Cosmetics, Shanghai Institute of Technology, Shanghai 201418, China

Changes in rice quality during storage are characterized by pronounced temporal dynamics and multidimensionality. However, flavor chemistry and rapid nondestructive detection have generally been investigated separately, limiting the simultaneous interpretation of deterioration mechanisms, identification of storage stages, and practical quality monitoring. In this study, japonica rice cultivar "Nanjing 9108" was stored for 40 weeks under ambient conditions with naturally fluctuating temperatures, refrigerated conditions at 5 °C, and frozen conditions at -20 °C, with sampling conducted every two weeks. Volatile compounds, physicochemical indices, microstructure, visual images, and near-infrared spectra were synchronously acquired from the same samples. A unified sample-coding system was used to establish one-to-one correspondence among image, spectral, GC-MS, and physicochemical data, thereby ensuring that all modalities represented an identical storage background and providing a basis for cross-modal association analysis. A total of 58 volatile compounds were detected. The storage process generally exhibited three stages, namely initial accumulation, rapid change, and late-stage transformation, with weeks 12 and 28 identified as important turning points in flavor evolution. Ambient storage accelerated lipid oxidation and volatile-compound conversion, refrigerated storage delayed compound generation, accumulation, and differentiation, whereas several oxidation products showed abnormal accumulation and fluctuation under frozen storage. Sensory validation indicated that 2-acetyl-1-pyrroline was an important contributor to the characteristic rice aroma, while hexanal and nonanal were closely associated with grassy, fatty, and stale odors. Microstructural observations and correlation analysis suggested that loss of membrane integrity promoted lipid hydrolysis and oxidation and represented an important driving factor in flavor deterioration. The single spectral model achieved an accuracy of 84.44% for storage-temperature classification, which increased to 89.10% after attention-based fusion of visual and spectral features. The multi-task model achieved accuracies of 87.24% and 86.20% for storage-duration classification and overall quality grading, respectively, while the LSTM model achieved an accuracy of 88.2% in predicting key volatile markers. The models were further integrated into a visual evaluation prototype that automatically generated storage-status and quality results from image and near-infrared spectral inputs. By defining rice freshness through sensory-validated flavor markers and mechanism-related indicators, using vision-spectroscopy multimodal modeling for rapid and nondestructive identification, and extending the framework to trend prediction through temporal modeling, this study established an integrated evaluation pathway comprising mechanism elucidation, marker confirmation, multimodal perception, and intelligent prediction. The proposed approach may provide methodological support for quality monitoring, deterioration warning, and storage-condition optimization during rice storage.

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MF44: Fermentation of Celery (*Apium graveolens L.*) with *Lactobacillus plantarum* NCU116: Impact on Physicochemical Properties, Free Amino Acids, and Volatile Aroma Compounds

Yuhao Li, Weiwei He, Yuxin He, Shuai Liu, Xiaoyi Hu, Shuigen Bian, Xiaoxiao Song, Junyi Yin, Shaoping Nie, Mingyong Xie*
State Key Laboratory of Food Science and Resources, China-Canada Joint Laboratory of Food Science and Technology (Nanchang), Key Laboratory of Bioactive Polysaccharides of Jiangxi Province, Nanchang University, Nanchang, 330047, China

Lactic acid bacteria (LAB) fermentation has been demonstrated to enhance the flavor and nutritional composition of vegetables. In this study, the physicochemical properties, amino acids and aroma compounds of celery were systematically analyzed during the *Lactobacillus plantarum* NCU116 (*L. plantarum* NCU116) fermentation. Significant changes in its physicochemical properties were observed predominantly within the first 24 h. Then, the total amino acid in the celery significantly decreased from 4.52 to 3.73 mg/L. The content of total sugar and reducing sugar decreased steadily by 85.33% and 82.61% respectively. In addition, a total of 65 volatile compounds, including 5 alcohols, 29 terpenoids, 3 aldehydes, 2 acids, 3 ketones, 4 alkenes, and 13 esters, were identified. Fermentation progress significantly increased the diversity and content of alcohols, aldehydes and alkanes. Further analysis revealed that 18 key aroma compounds (ROAV > 1), including trans-2-octen-1-ol, copaene, terpinen-4-ol, and linalool, significantly contributed to the fruity and woody aroma profile of fermented celery and conferred the fruity and woody aromas. Moreover, the result of sensory evaluation demonstrated that the increase in the concentration of the above compounds during fermentation contributes to the sensory characteristics. The study indicated that fermentation is a promising approach to improve the flavor of celery.

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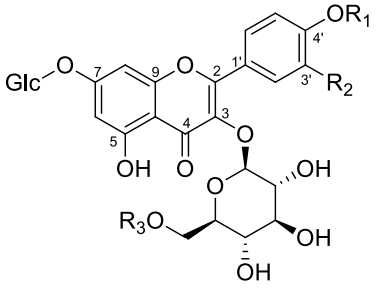
Poster Presentation

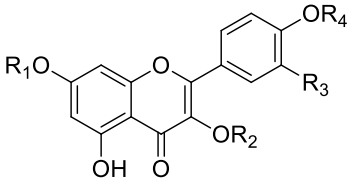
P1: Flavonol Glucosides from the Leaves of a Korean Endemic and Edible Garlic, *Allium ulleungense*

Ji-Sun Lee[1], So-Ri Son[2], and Dae Sik Jang[1]
Department of Fundamental Pharmaceutical Sciences, Graduate School, Kyung Hee University, 26, Kyungheedae-ro, Dongdaemun-gu, Seoul, 02447, Korea

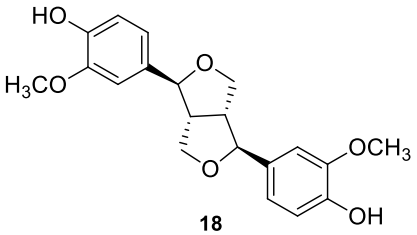
Allium ulleungense (Ulleungdo wild garlic; Myeongyi namul) is an endemic species native to Ulleung Island, South Korea, where it has traditionally been consumed as a popular edible wild herb. Despite its culinary value and unique ecological characteristics, research on its chemical constituents remains limited. Therefore, this study aimed to isolate and structurally elucidate secondary metabolites from the 70% ethanol extract of the aerial parts of *A. ulleungense*. As a result, seventeen flavonoids (1–17) were predominantly isolated, along with one lignan (18), and two phenylpropanoids (19 and 20). Notably, four of these compounds were identified as previously unreported flavonol glucosides, named myeongyiflavonols A–D (1–4). The chemical structures of the isolated compounds were elucidated using spectroscopic analysis, including nuclear magnetic resonance (NMR) and mass spectrometry (MS), and confirmed by comparison with published data. These findings are expected to support as an foundation for developing natural products derived from Korean plants.



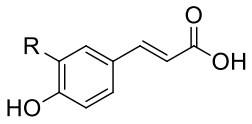
1 R_1 = Glc, R_2 = H, R_3 = (*E*)-caffeoyl
2 R_1 = Glc, R_2 = OH, R_3 = (*E*)-caffeoyl
3 R_1 = R_2 = H, R_3 = (*E*)-caffeoyl
4 R_1 = H, R_2 = OH, R_3 = (*E*)-*p*-coumaroyl
5 R_1 = Glc, R_3 = (*E*)-*p*-coumaroyl, R_3 = H
6 R_1 = R_2 = H, R_3 = (*E*)-feruloyl
7 R_1 = Glc, R_3 = (*E*)-feruloyl, R_2 = OH
8 R_1 = Glc, R_3 = (*E*)-feruloyl, R_3 = H



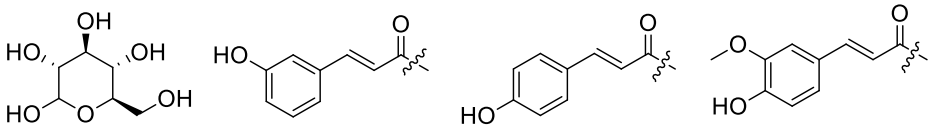
9 R_1 = R_3 = H, R_2 = R_4 = Glc
10 R_1 = H, R_3 = OH, R_2 = R_4 = Glc
11 R_1 = R_2 = R_4 = Glc, R_3 = H
12 R_1 = R_2 = R_4 = Glc, R_3 = OH
13 R_1 = R_2 = R_3 = R_4 = H
14 R_1 = R_4 = H, R_2 = R_3 = OH
15 R_1 = R_3 = R_4 = H, R_2 = Glc
16 R_1 = R_4 = H, R_2 = Glc, R_3 = OH
17 R_1 = R_2 = Glc, R_3 = R_4 = H



18



19 R = H
20 R = OCH_3



Glc: D-glucose (*E*)-caffeoyl (*E*)-*p*-coumaoyl (*E*)-feruloyl

P2: *Agrimonia pilosa-Eclipta prostrata* Herb Pair Mitigates Abnormal Uterine Bleeding Through the PI3K/Akt1/mTOR Axis: A Combined Study of Network Pharmacology and Experimental Validation

Chuanqi Huang[1], Li Yin[2], Rakotoniaina Andriatsiresena[3], Qingfeng Ruan[1], Fen Zhang[2], Xiaoxuan Zeng[1], Wenxuan Chen[3], Guilin Chen[3]*
[1]Department of Pharmacy, Wuhan Hospital of Traditional Chinese and Western Medicine, Wuhan 430030, China
[2]Shiyan Hospital of Integrated Traditional and Western Medicine, Shiyan 442001, China
[3]State Key Laboratory of Plant Diversity and Specialty Crops, Wuhan Botanical Garden, Chinese Academy of Sciences, 430074 Wuhan, China

Abnormal uterine bleeding (AUB) remains a challenging gynecological condition with limited safe therapeutic options available in clinical practice[1]. Conventional hormonal and hemostatic treatments are often accompanied by obvious side effects and high recurrence rates, making it necessary to explore alternative natural therapeutic strategies[2,3]. The herb pair of *Agrimonia pilosa* and *Eclipta prostrata* (AE) has long been used in traditional Chinese medicine for hemostasis and endometrial repair; nevertheless, its active components, core targets and molecular mechanisms underlying AUB treatment remain poorly clarified[4]. In this study, network pharmacology and molecular docking were integrated to screen bioactive ingredients, predict potential therapeutic targets, and enrich critical signaling pathways. A mifepristone-misoprostol-induced AUB rat model was established for in vivo validation. Uterine bleeding volume, coagulation function, endometrial histopathology, serum reproductive hormones, inflammatory cytokines, endometrial apoptosis and pathway-related protein expression were comprehensively evaluated. A total of 16 bioactive ingredients and 196 intersection targets associated with AE and AUB were identified. Functional enrichment indicated the PI3K/Akt1/mTOR pathway as the core regulatory mechanism[5]. Molecular docking verified that the key active components of AE exhibited strong binding affinity to core targets AKT1, PIK3CA and PIK3R1. In vivo results demonstrated that AE markedly reduced uterine bleeding volume, recovered coagulation dysfunction, alleviated endometrial pathological injury, normalized hormone secretion, suppressed inflammatory overactivation, and inhibited excessive endometrial apoptosis. Meanwhile, AE significantly down-regulated the elevated expression of PI3K, Akt1, mTOR, MMP-9 and TNF-α, while up-regulating VEGF expression in endometrial tissues. In conclusion, these protective effects are closely associated with suppressing the PI3K/Akt1/mTOR signaling pathway. This study provides novel mechanistic insights and experimental evidence for the clinical application and further development of AE herb pair.

Acknowledgments
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P3: Exploring BCRP-Mediated Molecular Transport Mechanisms of Intestinal Anthocyanins Absorption

Nuo Wang[1], Xiujun Li[1], Yue Li[1], Bin Li[1], Jinlong Tian[1]*
[1]College of Food Science, Shenyang Agricultural University, Shenyang, 110866, China

Anthocyanins (ACNs) are important nutritional compounds in foods, but their low bioavailability limits their application. Current research mainly focuses on enhancing intestinal absorption, while studies on how efflux transporters excrete anthocyanins back into the intestinal lumen are scarce[1,2]. Based on an efflux-oriented perspective, this study explored the mechanism of anthocyanins efflux using both in vitro and in vivo models[3,4]. Inhibition of breast cancer resistance protein (BCRP) increased intestinal absorption by 18.4% and systemic exposure by 21%. Spectroscopic, thermodynamic, and molecular simulation analyses revealed that anthocyanins are actively pumped back into the intestinal lumen via the BCRP efflux channel, and the inhibitor reduced binding energy to -27.82 kcal/mol by occupying key residues (ASN-436, PHE-439), thereby decreasing anthocyanins efflux.
This study provides the first molecular-level evidence that BCRP restricts intestinal absorption of anthocyanins, offering a new strategy to enhance their bioavailability by regulating efflux pathways[5,6].

Acknowledgments
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P4: Antidiabetic Effects and Underlying Mechanisms of Melia Azedarach Based on an Integrated Multilevel Approach

Minxia Fan[1,2], Guangwan Hu[1,2,3], Guilin Chen[1,2,3]*
[1]State Key Laboratory of Plant Diversity and Specialty Crops, Wuhan Botanical Garden, Chinese Academy of Sciences, Wuhan, 430074, China
[2]University of Chinese Academy of Sciences, Beijing, 100049, China
[3]Sino-Africa Joint Research Center, Chinese Academy of Sciences, Wuhan, 430074, China
[4]Hubei Jiangxia Laboratory, Wuhan, 430200, China

Melia azedarach is a fast-growing medicinal plant with diverse therapeutic potential, and has been traditionally used for its hypoglycemic properties, although current research has largely been confined to in vitro enzyme inhibition assays using crude extracts[1-3]. To comprehensively evaluate its antidiabetic potential, this study employed an integrated approach combining in vitro, cellular, and in vivo experiments. The crude extract exhibited potent dual inhibition of α-glucosidase and protein tyrosine phosphatase 1B (PTP1B) ($P < 0.05$). In insulin-resistant HepG2 cells, treatment with the ethyl acetate fraction (EA, 5 μg/mL) markedly stimulated glucose uptake ($P < 0.01$) and reduced PTP1B protein levels, an effect comparable to that observed with metformin ($P > 0.05$). In STZ-induced diabetic mice, oral administration of the EA fraction (300 and 600 mg/kg) for four weeks yielded notable improvements in body weight, glucose tolerance, and serum insulin, alongside favorable modulation of lipid profiles, including TC, TG, LDL-C, and HDL-C ($P < 0.05$). Moreover, EA treatment conferred hepatoprotection, as indicated by decreased ALT and AST activities ($P < 0.01$), suppressed inflammatory responses via downregulation of IL-6, IL-1β, and TNF-α ($P < 0.05$), and mitigated oxidative stress through elevated SOD activity and reduced MDA levels. Histological examination further confirmed the amelioration of diabetes-induced hepatic and renal injury, consistent with the observed suppression of PTP1B overexpression in liver tissues. Collectively, these findings demonstrate that the EA fraction of *M. azedarach* exerts robust antidiabetic effects through multifaceted mechanisms involving PTP1B modulation, reversal of insulin resistance, and anti-inflammatory and antioxidant activities, thereby providing pharmacological validation for its ethnomedicinal use and highlighting its therapeutic promise for diabetes management.

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P5: Improvement of *Sparassis crispa* Polysaccharide Quality by Steam Explosion Technology: Physicochemical, Structural and Functional Properties

Jingru Wu[1,2], Yueyue Qiang[1,2], Haoxuan Peng[1,2], Qiao Guan[1,2], Lei Pan[1,2], Zhiwei Huang[1,2], Zebin Guo [1,2], Jianbo Xiao[3,4], Baodong Zheng[1,2]*, Yafeng Zheng[1,2]*
[1]College of Food Science, Fujian Agriculture and Forestry University, Fuzhou 350002, China
[2]Integrated Scientific Research Base of Edible fungi Processing and Comprehensive Utilization Technology, Ministry of Agriculture and Rural Affairs, Fuzhou 350002, China
[3]Universidade de Vigo, Nutrition and Bromatology Group, Instituto de Agroecoloxía e Alimentación (IAA), Department of Analytical Chemistry and Food Science, Faculty of Science, 32004 Ourense, Spain
[4]Research Group on Food, Nutritional Biochemistry and Health, Universidad Europea del Atlántico, Isabel Torres 21, 39011 Santander, Spain

Steam explosion (SE) is an emerging physical technology that is attracting increasing interest. SE is based on using saturated steam at high temperature and high pressure to infiltrate the tissues of the raw material, thereby saturating it with superheated water. This is followed by instantaneous pressure release that explosively disrupts the raw material structure, facilitating the release of active substances. This study aimed to evaluate the influence of steam explosion (SE) technology on the physicochemical, structural, and functional properties of *Sparassis crispa* polysaccharide (SCP). The results showed that SE could significantly increase the yield of SCP. Additionally, the particle size, molecular weight, and crystallinity of the SCP gradually decrease with the increasing SE pressure. SE changed the molar ratio of monosaccharides in SCP and disrupted its dense structure. However, the major functional groups of SCP were unaffected by SE. Thermogravimetric analysis indicated that the thermal stability of SCP was enhanced by SE. Furthermore, the physiochemical and structural changes induced by SE resulted in improved functional properties. Particularly at 1.2 MPa, SCP had better hydration properties, hypolipidemic, hypoglycemic, and antioxidant activities. Therefore, SE is an effective method to improve the quality and comprehensive utilization rate of edible fungus polysaccharide.

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P6: Food-Sourced *Bacillus amyloliquefaciens* NC-1 for Deltamethrin Degradation in Whole-Corn Silage

Jiang liu[1], Qi Wen[1], Jie Tang[1,2]*, Xuan Yu[1,2]*
[1]College of Food and Bioengineering, Xihua University, Chengdu, Sichuan, China
[2]Enterprise External Supervisor, Feed Biotechnology Laboratory

Pyrethroid pesticide residues commonly contaminate environments and foods, and microbial degradation is an efficient strategy[1] for their harmless remediation. A highly deltamethrin-degrading strain NC-1 was isolated from Pixian broad bean paste and identified as *Bacillus amyloliquefaciens*. The strain exhibited favorable biosafety and probiotic characteristics with no hemolytic activity or harmful decarboxylase activity, high sensitivity to common antibiotics, and excellent aggregation ability, surface hydrophobicity, antibacterial activity and stress resistance. Based on response surface methodology, the optimal degradation conditions were determined as pH 6.1, 27.5 ℃ and an initial deltamethrin concentration of 29.7 mg/L, under which the degradation rate reached 84.2% within 72 h. Strain NC-1 also displayed broad-spectrum degradation capacity against various pyrethroid pesticides. A total of 12 metabolic intermediates were identified by GC-MS, and the degradation pathway was clarified: deltamethrin was completely mineralized through ester hydrolysis, redox reactions and aromatic ring cleavage. Genomic sequencing and RT-qPCR analysis verified abundant functional genes related to pesticide degradation, and 21 key degradation genes were significantly upregulated, revealing the molecular mechanism underlying its degradation performance. Practical silage fermentation experiments confirmed that strain NC-1 effectively removed deltamethrin residues with a degradation rate of 52.3%, which was significantly higher than that of the natural degradation group. In addition, NC-1 inoculation optimized the microbial community structure and improved the fermentation quality of pesticide-contaminated silage[2]. This study provides a promising microbial resource and theoretical basis for the bioremediation of pyrethroid-contaminated feed and safe silage fermentation.

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P7: From Thailand's National Tree to Global Quality: An Integrated Analytical Platform for Quality Assessment of *Cassia fistula L. pulp*

Jiranuch Mingmuang*, Lalita Ramsak, Nawarat Chadchen, Sakwichai Onthong, and Santakit Ninudomsak
Medicinal Plant Research Institute, Department of Medical Sciences, Ministry of Public Health, Nonthaburi, 11000, Thailand

Cassia fistula L., Thailand's national tree, is an important medicinal plant traditionally used as a natural laxative. Its pulp contains anthraquinone derivatives, particularly rhein, which can serve as a chemical marker for quality assessment. This study aimed to establish an integrated analytical platform for the quality assessment of *C. fistula* pulp by combining UPLC-PDA determination of rhein with UV-Vis spectrophotometric determination of total anthraquinones expressed as rhein. Sixteen pulp samples collected from different regions of Thailand were analyzed. Sample extraction was optimized using methanol with sonication for 15 min. The UPLC-PDA method employed an Acquity UPLC BEH C_{18} column with gradient elution using 0.1% phosphoric acid in water and acetonitrile, with detection at 430 nm. Both UPLC-PDA and UV-Vis methods were validated in accordance with the Eurachem 2026 guidelines for specificity, linearity, accuracy, precision, LOD, and LOQ. The developed UPLC-PDA method provided selective detection of rhein at a retention time of 2.676 min without co-eluting interference. Both methods showed good linearity over the range of 0.01–0.06 mg/mL, with $R^2 > 0.999$. Accuracy and precision met the acceptance criteria, with recoveries between 95% and 105% and RSD values below 3%. Rhein content determined by UPLC-PDA ranged from 0.07–0.23% w/w in raw materials and 0.11–0.50% w/w in water extracts. Total anthraquinones, expressed as rhein, determined by UV-Vis spectrophotometry, ranged from 0.15–0.73% w/w in raw materials and 0.30–1.09% w/w in water extracts. This integrated platform provides complementary analytical tools: UPLC-PDA offers specific quantification of rhein, whereas UV-Vis enables rapid estimation of total anthraquinones. The approach supports routine quality control of *C. fistula* pulp and may contribute to future standardization of Thai herbal medicines for global quality assurance.

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P8: Lonicera Caerulea Iridoids Ameliorate Hyperuricemia and Kidney Injury in Mice by Modulating Urate Transport and Nrf2/ROS/NLRP3-Related Signaling

Zeyang Bao[1,2], Weijie Wu[1], Huizhi Chen[1], Ruiling Liu[1], Xiangjun Fang[1], Yan Xu[3], Hangjun Chen[1], Mohamed A. Farag[4], Jianming Zhang[1], Ming Yin[1], Lishu Wang[5], Chaoyi Shen[1]*, Jianbo Xiao[2]*, Haiyan Gao[1]*

[1]Zhejiang Key Laboratory of Intelligent Food Logistic and Processing, Key Laboratory of Post-Harvest Fruit Processing, Ministry of Agriculture and Rural Affairs, Key laboratory of post-harvest preservation and processing of fruits and vegetables, China National Light Industry, Institute of Food Science, Zhejiang Academy of Agricultural Sciences, Hangzhou 310021, China

[2]Nutrition and Bromatology Group, Department of Analytical Chemistry and Food Science, Faculty of Science, University of Vigo, E32004 Ourense, Spain

[3]School of Food and Pharmacy, Zhejiang Ocean University, Zhoushan, 316022, China

[4]Pharmacognosy Department, College of Pharmacy, Cairo University, Kasr El Aini St., Cairo P.B. 11562, Egypt

[5]Department of Hematology and Hematopoietic Cell Transplantation, Comprehensive Cancer Center, City of Hope National Medical Center, Duarte, California, USA

Hyperuricemia is a metabolic disorder caused by an imbalance between uric acid production and excretion. Persistent elevation of serum uric acid can induce renal tubular oxidative stress and inflammation, ultimately leading to kidney injury. This study investigated the effects of *Lonicera caerulea* iridoids (LCI) on uric acid metabolism and renal injury in hyperuricemic mice. Amouse model of hyperuricemia was established using potassium oxonate combined with adenine. Serum and urinary uric acid levels, renal function, kidney histopathology, urate transporter expression, and oxidative stress- and inflammation-related markers were assessed. LCI reduced serum uric acid, promoted urinary uric acid excretion, and alleviated renal dysfunction and histopathological injury. These effects were accompanied by downregulation of the urate reabsorption transporters URAT1 and GLUT9 and upregulation of the urate secretion transporters OAT1 and ABCG2. Moreover, LCI enhanced the Nrf2-related antioxidant response, reduced reactive oxygen species production, and suppressed NLRP3 inflammasome activation and inflammatory cytokine expression. This research reveals that LCI may ameliorate hyperuricemia and associated renal injury by regulating renal urate transport and attenuating oxidative and inflammatory damage. These findings provide experimental support for the development of LCI as a functional food ingredient for the auxiliary regulation of serum uric acid.

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P9: Processing-Induced Chemical Signatures and Antidiabetic-related α-Glucosidase Inhibitory Potential of Camellia Ptilophylla

Zhipeng Kan[1], Ting Zhao[2], Jiayi Guo[2], Hangjun Chen[3], Ying Gao[1]*, Junfeng Yin[1]*
[1]Tea Research Institute Chinese Academy of Agricultural Sciences, National Key Laboratory for Tea Plant Germplasm Innovation and Resource Utilization, Hangzhou 310008, China
[2]College of Horticulture, Fujian Agriculture and Forestry University, Fuzhou 350002, China
[3]Food Science Institute of Zhejiang Academy of Agricultural Sciences, Hangzhou 310021, China

Postprandial hyperglycemia is closely associated with metabolic disorders, and food-derived α-glucosidase inhibitors have attracted increasing attention for modulating carbohydrate digestion[1]. Tea processing profoundly reshapes chemical composition and bioactivity[2], yet the processing-dependent functional chemistry of underutilized *Camellia* resources remains insufficiently understood. *Camellia ptilophylla*, a naturally caffeine-free tea resource, possesses distinctive alkaloid and polyphenol profiles [3], but its processing-induced chemical signatures and α-glucosidase inhibitory potential have not been systematically characterized. In this study, fresh leaves of *C. ptilophylla* and *Camellia sinensis* were processed under standardized conditions into green, white and black teas, followed by untargeted metabolomics, targeted chemical validation, and α-glucosidase inhibition assays. Multivariate analysis revealed characteristic metabolic features of *C. ptilophylla*, mainly involving non-epicatechins, purine alkaloids, amino acid derivatives, and flavonol glycosides. Among the processed products, *C. ptilophylla* green tea exhibited the strongest α-glucosidase inhibitory activity, indicating that green tea processing favored the formation or retention of activity-associated constituents. Chemical profiling identified gallocatechin gallate (GCG), catechin and salicylic acid as processing-responsive markers associated with activity variation. Functional validation using PVPP-mediated depletion and GCG add-back assays demonstrated that GCG was the principal direct contributor to the inhibitory activity of *C. ptilophylla* green tea, whereas catechin and theobromine showed much weaker inhibitory effects. Enzyme kinetic analysis further revealed that GCG inhibited α-glucosidase through a noncompetitive mode, suggesting suppression of catalytic efficiency rather than direct competition with the substrate. These findings demonstrate that the antidiabetic-related α-glucosidase inhibitory potential of *C. ptilophylla* is mainly associated with processing-induced GCG accumulation and its noncompetitive inhibition of α-glucosidase, providing a chemical and functional basis for the value-added utilization of this distinctive tea resource.

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P10: Advances in the Extraction, Purification, and Lipid-lowering Mechanisms of Lotus Leaf Alkaloids

Yuntao Lin[1,2], Wenxuan Chen[2], Bohan Zhang[2,3], Kefan Zhao[2], Minxia Fan[2], Guangwan Hu[2]*, Guilin Chen[2]*
[1]College of Biological & Pharmaceutical Sciences, China Three Gorges University, Yichang 443002, China
[2]State Key Laboratory of Plant Diversity and Specialty Crops, Wuhan Botanical Garden, Chinese Academy of Sciences, Wuhan 430074, China
[3]School of Life and Health Sciences, Hubei University of Technology, Wuhan 430068, China

Lotus leaf alkaloids are the primary bioactive compounds found in *Nelumbo nucifera* Gaertn., possessing significant functions in regulating glucose and lipid metabolism, alongside antioxidant and anti-inflammatory activities[1]. This review summarized the recent advances in the extraction, purification, and comprehensive analytical technologies of these natural alkaloids. Regarding the extraction processes, we critically compared the traditional solvent methods with ultrasound-assisted extraction, macroporous resin adsorption, and high-speed countercurrent chromatography (HSCCC) for enhancing purity and isolating monomers[2]. Concurrently, this study evaluated the chemical profiling methods based on HPLC fingerprinting, UPLC-Q-TOF-MS, and GNPS molecular networking, highlighting the crucial role of high-throughput analysis in expanding their known chemical space[3]. Furthermore, we systematically outlined the diverse molecular mechanisms underlying the lipid-lowering and anti-obesity effects of lotus leaf alkaloids. These mechanisms encompass inhibiting exogenous lipid absorption, modulating adipocyte differentiation and lipolysis, ameliorating hepatic lipid metabolism to prevent non-alcoholic fatty liver disease (NAFLD), regulating gut microbiota, and controlling energy metabolism via central nervous and receptor-mediated networks[4]. Finally, current challenges and future perspectives regarding advanced extraction methodologies and clinical translation are discussed, aiming to provide a theoretical reference for the in-depth development and high-value utilization of these botanical resources.

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P11: Thermal Degradation Mechanism of Myricetin in Palmitic Acid

Shengxiong Chen[1], Fan Zhang[1], Randolph R.J. Arroo[2], Jesus Simal-Gandara[1], Hui Cao[1], Jianbo Xiao[1,3]*
[1]Universidade de Vigo, Nutrition and Bromatology Group, Department of Analytical Chemistry and Food Science, Instituto de Agroecoloxía eAlimentación (lAA)-CITEXVI, 36310 Vigo, Spain
[2]De Montfort University - Leicester School of Pharmacy, The Gateway, Leicester LE1 9BH, UK
[3]Research Group on Food, Nutritional Biochemistry and Health, Universidad Europea del Atlántico, Isabel Torres 21, 39011 Santander, Spain

Dietary polyphenols are susceptible to degradation during high-temperature cooking, yet their transformation behavior in lipid-rich frying systems remains poorly understood. The thermal stability and degradation of myricetin in a simplified palmitic acid model under frying-relevant conditions was investigated. Myricetin degraded rapidly at 180°C but remained relatively stable at 120°C. UPLC–QTOF–MS/MS, supported by density functional theory calculations, suggested that myricetin transformation is temperature-dependent but primarily governed by lipid oxidation–derived radical and carbonyl chemistry. Vitamin C markedly delayed myricetin degradation by suppressing radical initiation and limiting o-quinone–centered downstream reactions. These findings highlight lipid oxidation as a key determinant of polyphenol stability during frying and clarify the protective role of antioxidants in lipid-rich thermal processing systems.

P12: Screening of Easy-to-Cook Barley Varieties and Quality Evaluation of Blended Barley Rice

Peng Lianxin[1]*, Lü Wenwen[1], Liu Ting[1], Ren Jing[1]
[1]Key Laboratory of Millet Processing, Ministry of Agriculture and Rural Affairs, College of Food and Biological Engineering, Chengdu University

Currently, the high prevalence of chronic diseases such as diabetes, obesity, and cardiovascular disease is linked to low intake of whole grains among the population[1], The "Healthy China 2030" Outline states that, at the national level, a balanced diet should be vigorously promoted, and the proportion of whole grains in the population's diet should be increased. While ensuring adequate intake of staple grains, the shortfall in whole grain consumption should be addressed by incorporating them into staple food combinations. The "Chinese Dietary Guidelines (2022)" recommend a daily intake of 50–150 g of whole grains and legumes for adults, However, 80.3% of adults consume less than 50 g per day. Studies have shown that insufficient intake of whole grains and mixed grains is closely linked to the onset of chronic diseases such as obesity and dyslipidemia[2]. Currently, there are few varieties of mixed-grain rice blends on the market. Most consist of combinations of several pure whole grains, resulting in a coarse and hard texture that is poorly accepted by consumers. Furthermore, these blends lack a theoretical basis and have low nutritional value[3], making them suitable primarily for individuals with chronic diseases. The blended rice in this study retains a high proportion of white rice to ensure the overall palatability of the cooked rice. It incorporates a proprietary barley variety blended with white rice, along with bitter and sweet buckwheat, as well as black, white, and red quinoa. As a result, the final product-barley-blended rice-not only receives favorable sensory evaluations but also infuses the nutritional benefits of whole grains into daily staple foods, making whole grains a staple for all populations. It supplements dietary fiber, enhances nutritional content and the levels of bioactive compounds, improves gut health, and lowers blood lipid levels[4]. This study evaluated 14 varieties of barley. Based on their steaming and gelatinization characteristics as well as sensory and textural properties, four varieties with consistently good performance were initially screened. Further evaluation of microstructure, starch thermal properties, and nutritional value led to the final selection of variety Q2. Through a mixed-feed design, the optimal formulation was determined to be 70% rice, 7.5% barley, 6% bitter buckwheat, The optimal formulation was determined through a mixture design, consisting of 70% rice, 7.5% barley, 6% bitter buckwheat, 6% sweet buckwheat, 3.5% white quinoa, 3.5% black quinoa, and 3.5% red quinoa. The nutritional quality and functional properties of this formulation were evaluated in comparison to a rice control.

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P13: *Atractylodes macrocephala* Polysaccharides 1 Ameliorate Ulcerative Colitis by Regulating Gut Microbiota and IL-17RA Signaling Pathway

Mingjiang Mao[1], Qingling Meng[1], Chenhuan Shentu[1], Shijie Dai[1], Na Zhu[1], Chengxin Hu[1], Yangsheng Wu[1], Xiaofeng Yuan[1]*
[1]School of Life Sciences, Zhejiang Chinese Medical University, Hangzhou, Zhejiang 310053, China

Ulcerative colitis (UC) is a chronic, relapsing inflammatory condition primarily affecting the colon and rectum, and its development is closely associated with dysregulation of the gut microbiota[1]. While natural polysaccharides are increasingly utilized for UC prevention, the therapeutic potential of *Atractylodes macrocephala* polysaccharides 1 (AMP 1) remains underexplored[2,3]. In this study, AMP 1 was successfully isolated and purified to investigate its effects on dextran sodium sulfate (DSS)-induced UC in mice. The results demonstrate that AMP 1 mitigates UC symptoms, repairs intestinal barrier damage, and reduces inflammatory cytokine release in a dose-dependent manner. Notably, AMP 1 was ineffective in UC mice treated with antibiotics; however, fecal microbiota transplantation (FMT) from AMP 1-treated mice to antibiotic-pretreated mice restored its therapeutic effects. Transcriptome analysis and further validations suggest that AMP 1 exerts its protective effects by downregulating the IL-17RA signaling pathway[4]. Furthermore, IL-17RA gene inhibition using Brodalumab enhanced AMP 1's protective capacity. These findings collectively indicate that AMP 1 alleviates UC injury in a microbiota dependent manner via the suppression of IL-17RA signaling, highlighting its promise as a potential microbiota-targeted functional food for UC management.

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P14: Steam Explosion–Induced Structural Remodeling of Auricularia Auricula Polysaccharides Enhances Anti-Aging Efficacy in Drosophila Melanogaster

Zirong Huang[1,2], Baodong Zheng[1,2]*
[1]College of Food Science, Fujian Agriculture and Forestry University, Fuzhou, 350002, China
[2]Integrated Scientific Research Base of Edible Fungi Processing and Comprehensive Utilization Technology, Ministry of Agriculture and Rural Affairs, Fuzhou, 350002, China

This paper studied the physicochemical properties and bioactivity of *Auricularia auricula* polysaccharides (AAP) before and after steam explosion (SE) pretreatment[1]. AAP consisted mainly of mannose, galactose, and glucose; SE pretreatment shifted monosaccharide proportions and reduced the weight-average molecular weight to 3.37×10^5 Da. Fourier-transform infrared spectroscopy showed SE did not alter the fundamental functional groups of the polysaccharides. Thermal stability was enhanced after SE, as evidenced by scanning electron microscopy, which revealed a transition from a dense architecture to a more open, stratified microstructure with increase surface roughness[2]. Compared with the control (AAP-CK), the SE-treated group (AAP-SE) exhibited enhanced in vitro antioxidant capacity. Dietary supplementation with 0.0312% AAP-SE significantly extended the average lifespan of *Drosophila melanogaster* by 28.44% in females and 22.08% in males. In fruit flies, AAP-SE enhanced antioxidant enzyme activities, increasing superoxide dismutase by 67.32% and glutathione peroxidase by 2.61-fold in males, while reducing malondialdehyde levels by 42.75% in females[3]. Furthermore, fruit flies fed AAP-SE showed improved resistance to hydrogen peroxide-induced oxidative stress and starvation stress, with gender-specific effects. These results suggested that SE pretreatment effectively enhanced the antioxidant and anti-aging activities of AAP, suggesting its potential as a natural lifespan-extending antioxidant[4].

Acknowledgements
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P15: The Effect of Fermented Olives on the Anti-inflammatory Activities Exerted by LPS-Stimulated RAW264.7 Macrophages

Francesca Giampieri
Department of Clinical Sciences, Polytechnic University of Marche, Ancona Italy

Even if olive by-products have been considered a major environmental issue for many years, in the last decades, numerous studies have deeply described their antioxidant, anti-inflammatory, immunomodulatory, analgesic, antimicrobial, antihypertensive, anticancer, antihyperglycemic activities[1]. The fermentation of olives significantly affects their byproducts, especially wastewater and sansa, not only by changing their chemical composition, but also by reducing their environmental toxicity, thus offering opportunities for nutrient recovery[2]. Therefore, it is essential to understand the impact that some processing methods, usually used in production such as fermentation, may exert on olives. This work aims to evaluate the effect of fermented olive (Carolea variety) on LPS-stimulated RAW264.7 macrophages. Total phenolic and flavonoids contents, as well as total antioxidant capacity and radical scavenging activity were determined. Viability test was assessed treating macrophages with a wide range (25 to 5000 μg/mL) of fermented extracts. Then, the effect of the extract on extracellular NO production was evaluated, together with the protein and genes expressions of several inflammatory markers. In addition, eIF2α levels was measured as well. Finally, cellular metabolism was examined by analyzing phosphorylated AMPK (p-AMPK), PGC-1α expression and mitochondrial respiration. The results demonstrated a modest content of total polyphenols and flavonoids, as well as high antioxidant and scavenging activity. On the other hand, cell viability was not affected after 24 h treatment with fermented extracts. In LPS-activated macrophages, the extract at 250 and 500 μg/mL significantly attenuated pro-inflammatory mediators, such as extracellular NO production, iNOS, COX-2, TNF-α, and IL-6, while increased IL-10 production. Fermented extract also improved cell metabolism, through the activation of AMPK-related pathways, and enhanced mitochondria functionality, through the increase of maximal oxygen consumption and spare respiratory capacity. The above findings indicate that fermentation displayed low cytotoxicity in macrophages, reduced the effect of LPS on NO generation, and modulated several keys signaling pathways, which are intricately involved in the inflammatory response. These results may suggest that fermented olives can be effectively targeted for preventive benefits.

Acknowledgements
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P16: Sour Jujube Seed: A Review of Active Components from Traditional Use to Modern Innovations

Zijun Xue[1], Nuo Wang[1], Xiaolin Yu[1], Weitao Han[1], Rodrigo Quintana[2], Baoru Yang[3], Ying Zhou[3], Sergey S. Makarov[4], Anton I. Chudetsky[4], Jinlong Tian[1]*
[1] College of Food Science, Shenyang Agricultural University, Shenyang, 110866, China
[2]Agricultural Research Institute INIA Chile, National institute of agricultural research, Fidel Oteíza 1956, floors 11,12 and 15 Providencia, Santiago, Chile
[3]Food Sciences, Department of Life Technologies, University of Turku, Turku, Finland
[4]Russian State Agrarian University, Moscow Timiryazev Agricultural Academy

Sour jujube seed (Ziziphi Spinosae Semen, ZSS) is a significant medicinal and edible resource in China, known for its diverse biological activities, particularly in enhancing sleep quality, alleviating anxiety, and providing antioxidant benefits[1]. Extensive research has demonstrated that sour jujube seed is abundant in bioactive compounds, including saponins, flavonoids, polysaccharides, and fatty acids[2]. Most current reviews on sour jujube seeds focus on the pharmacological activities and applications of one or two of its main components. This review further supplements the utilization of active components of sour jujube seed in the past and present, as well as the comparison among different extraction techniques, providing suggestions for the industrial production of sour jujube seed products. The traditional consumption methods have limitations in terms of palatability and extraction efficiency[3]. Although modern extraction techniques have significantly improved the release and retention of active components, they have limitations in terms of environmental friendliness and usage cost[4]. Therefore, large-scale clinical trials and the development of new and sustainable combined extraction methods are needed to fill the existing deficiencies. This review provides new ideas for the development of new extraction technologies for sour jujube seed and offers theoretical guidance for future research in this field.

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P17: The Mechanism and Application of Cypermethrin Degradation by *L. bacillus* VF-2

Wanting Wang[1], Hu Zhou[1], Jie Tang[1,2]*, Xuan Yu[1,2]*
[1]College of Food and Bioengineering, Xihua University, Chengdu, Sichuan, China
[2]Enterprise External Supervisor, Feed Biotechnology Laboratory

Deltamethrin (β-CY) residues and its highly toxic metabolite 3-phenoxybenzoic acid (3-PBA) cause severe soil and agricultural product pollution, threatening ecological and food safety[0]. Currently, few studies have explored pyrethroid biodegradation by *Lysinibacillus*, restricting the bioremediation of pyrethroid contamination. This study systematically investigated the pyrethroid-degrading performance, molecular mechanism and application potential of a novel functional strain. Strain VF-2, identified as *Lysinibacillus pakistanensis*, was isolated from long-term pyrethroid-contaminated farmland soil[154]. Under optimized conditions (pH 6.94, 5.5% inoculum, 40.84 mg/L substrate), it degraded 81.66% of 50 mg/L β-CY. GC-MS analysis revealed 11 intermediates and a degradation pathway involving ester and diphenyl ether cleavage as well as benzene ring opening, with efficient mineralization of toxic 3-PBA. Genomic and RT-qPCR analyses confirmed key esterase genes est2566 and est3341 were significantly upregulated under β-CY stress. Soil inoculation with VF-2 increased β-CY and 3-PBA degradation efficiencies by 3.60-fold and 6.84-fold, respectively[0]. The heterologously expressed Est3341 enzyme achieved 98.68% degradation of 100 mg/L β-CY within 36 h, with wide temperature and pH adaptability, and could remove various pyrethroid residues from tea leaves[0]. This study first verifies the pyrethroid-degrading capacity of *Lysinibacillus pakistanensis*, providing valuable microbial and enzyme resources for pesticide residue bioremediation in soil and agricultural products.

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P18: Minor Polar Secondary Metabolites from the Fresh Ginseng (*Panax ginseng*) Roots

Soo Bin Chung[1], Seo Yeon Kim[1], Dae Sik Jang[1]
[1]Department of Biomedical and Pharmaceutical Sciences, Graduate School, Kyung Hee University, Kyungheedae-ro, Dongdaemun-gu, Seoul, 02447, Republic of Korea

The root of *Panax ginseng* C.A. Meyer (Araliaceae) has been widely used as a traditional herbal medicine in China, Japan and Korea. However, research on *P. ginseng* has been concentrated on ginsenosides, whereas other constituents remain relatively underexplored. In this study, we focused on the isolation and structure elucidation of minor polar secondary metabolites from the fresh ginseng roots. The aqueous fraction from the 70% acetone extract of the fresh ginseng roots was subjected to repeated chromatography, leading to the isolation and characterization of one new phenolic glycoside (1), two new alkylglycosides (2 and 3), and one new isoquinoline alkaloid (4), along with 12 known compounds, 5-O-coumaroylquinic acid (5), 5-O-caffeoylquinic acid (6), threo-1-(4-hydroxy-3-methoxyphenyl)propan-7,8-diol (7), grasshopper ketone (8), maltol 6′-O-β-D-apiofuranosyl-β-D-glucopyranoside (9), ginsenoside Rd (10), ginsenoside Rc (11), L-tryptophan (12), L-indole-3-lactic acid (13), adenine (14), tyramine (15) and thymine (16).

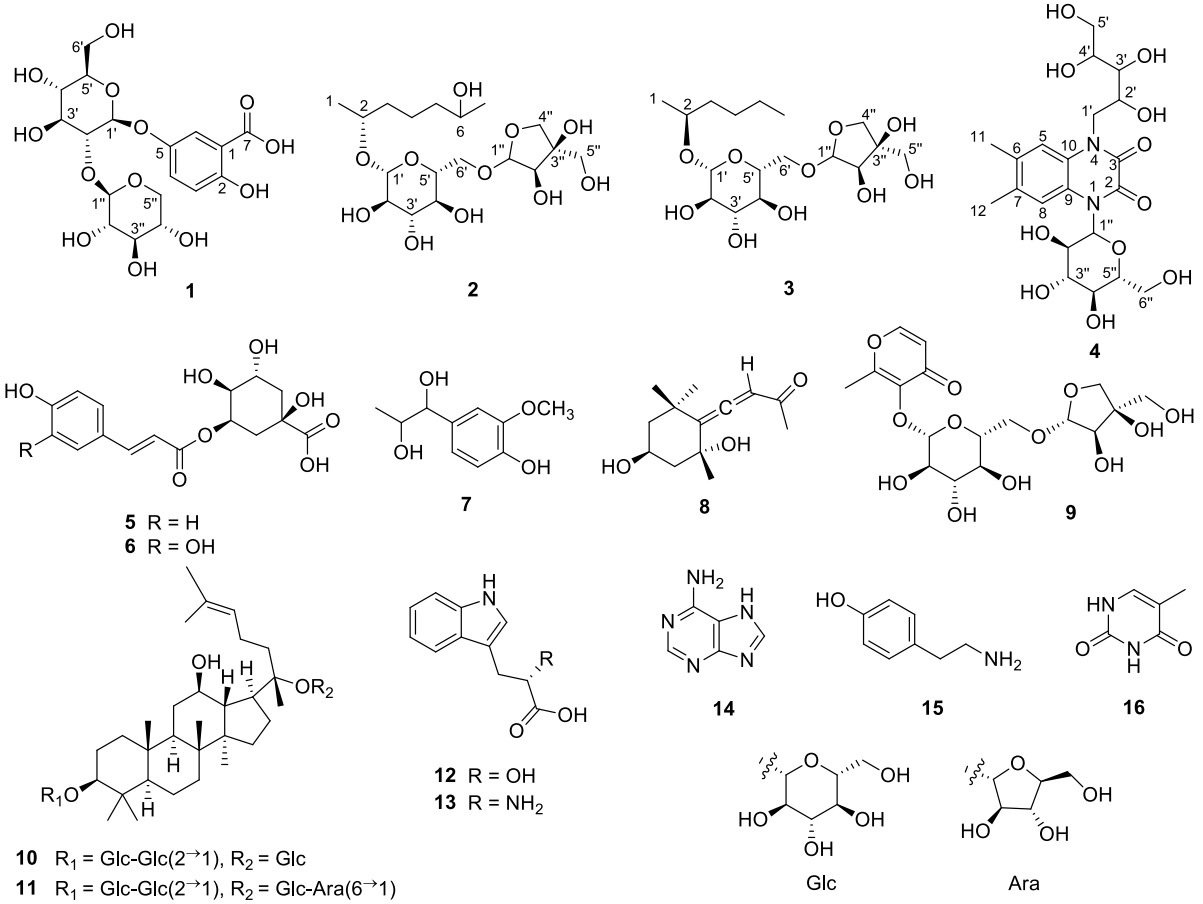

Fig. 1. Structures of the isolated compounds from the fresh ginseng roots.

P19: Research Progress on Chemical Components, Biological Activities and Pharmacology of *Warburgia* Engl. plants

Wenxuan Chen[1], Yuntao Lin[1,2], Bohan Zhang[1,3], Maureen Gacheri Nyongesa[1], Minxia Fan[1], Guangwan Hu[1,4]*, Guilin Chen[1,4]*
[1]State Key Laboratory of Plant Diversity and Specialty Crops, Wuhan Botanical Garden, Chinese Academy of Sciences, Wuhan 430074, China
[2]College of Biological & Pharmaceutical Sciences, China Three Gorges University, Yichang 443002, China
[3]School of Life and Health Sciences, Hubei University of Technology, Wuhan 430068, China
[4]State Key Laboratory for Quality Ensurance and Sustainable Use of Dao-di Herbs, Beijing 100700, China

The genus *Warburgia* (family Canellaceae) is a unique woody medicinal plant group native to the tropical and subtropical regions of Africa. Owing to its remarkable curative effects in folk medicine, it represents a promising and distinctive natural drug resource in African traditional medical systems. Its roots, bark, leaves and fruits are commonly used for the traditional prevention and treatment of respiratory infections, malaria, gastrointestinal disorders, rheumatism and a variety of infectious diseases[1,2]. This work systematically reviews the latest research progress on the phytochemistry, biological activities and pharmacological mechanisms of *Warburgia* plants, aiming to clarify their material basis and pharmacological mechanisms and promote their modern development and translational application. To date, over 100 chemical constituents have been isolated and identified from this genus[3], mainly covering sesquiterpenoids, flavonoids and glycosides, fatty acids and polyols, and volatile oils. Among them, Drimane-type sesquiterpene dialdehydes (e.g., warburganal, polygodial and mukaadial) are the characteristic components of *Warburgia* plants and serve as the core material basis for their pharmacological activities. Modern pharmacological studies have verified that extracts and single compounds isolated from this genus exhibit broad-spectrum biological activities, including antibacterial, antimalarial, insecticidal, antioxidant, anti-inflammatory and anti-proliferative properties[3]. These findings scientifically validate the traditional medicinal applications of *Warburgia* plants. In-depth mechanistic investigations have elucidated the underlying action mechanisms of the active components from *Warburgia* plants. These active components target and regulate key functional enzymes such as NAT, COX and LOX[4], and modulate the core AMPK/AKT signalling pathway[5]. By regulating multiple targets and pathways to induce oxidative stress and DNA damage, these components exert a variety of pharmacological effects, including anti-tuberculosis, anti-tumor, anti-diabetic and immunomodulatory activities. Toxicological studies have confirmed that *Warburgia* plants possess favorable overall safety. However, certain extracts may pose potential risks in specific cell models and combined medication contexts[6]. Overall, *Warburgia* plants have unique resource superiorities and broad prospects for new drug research and development. Nevertheless, further studies are necessary to achieve a more systematic understanding of their chemical components, further explore the in-depth pharmacological mechanisms, and facilitate the sustainable utilization of *Warburgia* plant resources.

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P20: HPTLC-ESI/MS/MS Profiling of Phenolic Bioactive Compounds in the Ethanolic Extract of Supercritical Carbon Dioxide Marigold Residue

Visarut Kiatamornvong[1], Thongchai Koobkokkruad[2], Vesna Glavnik[3], Irena Vovk[3]*, Wanchai De-Eknamkul[1]*
[1]Department of Pharmacognosy and Pharmaceutical botany, Faculty of Pharmaceutical Sciences, Chulalongkorn University, Bangkok, Thailand
[2]National Nanotechnology Center, National Science and Technology Development Agency (NSTDA), Pathumthani, Thailand
[3]Laboratory of Food Chemistry, National Institute of Chemistry, Ljubljana, Slovenia

This study investigated the comprehensive utilization of marigold (*Tagetes erecta* L.) flowers by evaluating the phytochemical profile of the byproduct remaining after supercritical carbon dioxide (SC-CO_2) extraction. To recover the remaining polar bioactive compounds, the exhausted SC-CO_2 marigold residue was subjected to subsequent ultrasonic extraction using 70% ethanol. Phytochemical analysis revealed a distinct separation of bioactive phenolics and flavonoids, whereas the primary SC-CO_2 extraction yielded lipophilic carotenoids (such as α-terthienyl and lutein esters). To facilitate the analysis of this complex mixture, an HPTLC-ESI/MS/MS interface was utilized, allowing for direct and rapid mass spectrometric analysis of targeted bands from the TLC plate. The subsequent ethanolic extraction of the residue successfully recovered highly polar compounds. The residue extract contained significant amounts of phenolic acids, specifically gallic acid, syringic acid, and protocatechuic acid, alongside flavonoid glycosides such as kaempferol hexoside, quercetagetin-7-O-glucoside, and etc. Ultimately, this sequential extraction method provides an effective, zero-waste strategy to fully valorize marigold biomass for potential applications in the pharmaceutical and nutraceutical industries.

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P21: LTP-Dependent Mechanisms of Active Fraction of *Coreopsis tinctoria* in Ameliorating Learning and Memory Impairments

Hongyu Li[1], Guangxin Yuan[1]*
[1]School of Pharmacy, Beihua University, 132013 Jilin, China

Learning and memory impairment is a common clinical symptom caused by pathological diseases or physiological changes, in which the learning and memory impairment caused by aging is more common[1]. In this study, ethyl acetate (EACC) and n-butanol (NBAC) fractions of *Coreopsis tinctoria* were identified as neuroprotective agents through solvent-based screening in a D-galactose-induced (30 $mg \cdot mL^{-1}$) PC12 cell model. UPLC-MS analysis revealed 39 and 26 active components in EACC and NBAC respectively, with network pharmacology identifying 74 and 63 learning/memory-related targets, including 13 (EACC) and 9 (NBAC) targets in long-term potentiation (LTP) pathway. In D-galactose-induced (100 $mg \cdot kg^{-1} \cdot d^{-1}$) cognitive impairment mice[5-7], both EACC (400 $mg \cdot kg^{-1} \cdot d^{-1}$) and NBAC (500 $mg \cdot kg^{-1} \cdot d^{-1}$) significantly improved Morris water maze performance ($P<0.01$, $P<0.05$), and upregulated the ratio of NR2A/NR1, p-αCaMKII/αCaMKII and p-GluR1/GluR1 in the hippocampus ($P<0.01$, $P<0.05$). However, these effects were reversed by co-administration of the NR2A inhibitor PEAQX (5 $mg \cdot kg^{-1} \cdot d^{-1}$). It confirms that both EACC and NBAC ameliorate cognitive deficits by promoting NR2A expression, activating the phosphorylation process of αCaMKII and GluR1, and regulating the activation of LTP pathway mediated by NMDAR.

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P22: Antifungal Mechanism against *Botrytis cinerea*, Microencapsulation, and Application in Postharvest Blueberry of Citral

Dong Yang[1]， Huizhi Chen[1], Weijie Wu[1]， Hangjun Chen[1], Lishu Wang[2], Maratab Ali[1], Ruilin Liu[1], Chaoyi Shen[1], Hailong Yang[3]*, Xiangjun Fang[1]*,Haiyan Gao[1]*
[1]Zhejiang Key Laboratory of Intelligent Food Logistic and Processing, Key laboratory of post-harvest handling of fruits, Ministry of Agriculture and Rural Affairs, Key Laboratory of Postharvest Preservation and Processing of Vegetables (Co-construction by Ministry and Province), Key laboratory of postharvest preservation and processing of fruits and vegetables, China National Light Industry, Food Science Institute, Zhejiang Academy of Agricultural Sciences, Hangzhou 310021, China
[2]Department of Hematology and Hematopoietic Cell Transplantation, Comprehensive Cancer Center, City of Hope National Medical Center, Duarte, California, USA
[3]Wenzhou university college of life and environmental science, Wenzhou, China

Postharvest blueberry decay is largely associated with infection by *Botrytis cinerea*. This study examined citral as an antifungal agent against this pathogen. Citral effectively restricted mycelial growth of *B. cinerea*, with an MIC value of 0.5 μL/mL. Mechanistic analyses showed that citral compromised fungal membrane and cell wall integrity, induced oxidative stress, disrupted mitochondrial function, and suppressed ATP-related energy metabolism. To extend its antifungal efficacy, citral was encapsulated in TEOS/OTES hybrid silica microcapsules using a sol-gel method. The T3O1 formulation exhibited favorable morphology, high encapsulation performance, and sustained release, reaching a cumulative release of 65.16 % over 30 days. In addition, citral-loaded microcapsules (Citral-MC) were evaluated for the postharvest preservation of blueberries. citral-MC treatment reduced visible decay, water loss, firmness loss, membrane damage, and the depletion of nutritional and bioactive compounds, while maintaining antioxidant enzyme activities and suppressing PPO activity. Citral-MC also maintained higher antioxidant enzyme activities than free citral and the untreated control. These findings suggest citral can act as an effective natural antifungal agent against blueberry gray mold, and TEOS/OTES microencapsulation can extend its effect in postharvest blueberry preservation.

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P23: Environment-Driven Differences in Chemical Composition and Bioactivity of Polygonati Rhizoma from Distinct Geographic Populations

Yu Qing[1,2,3], Kefan Zhao[1,2,3], Guilin Chen[1,2,3,4], Minxia Fan[1,3,4]*, Guangwan Hu[1,2,3,4]*
[1]State Key Laboratory of Plant Diversity and Specialty Crops, Wuhan Botanical Garden, Chinese Academy of Sciences, Wuhan 430074, China
[2]University of Chinese Academy of Sciences, Beijing 100049, China
[3]Sino-Africa Joint Research Center, Chinese Academy of Sciences, Wuhan 430074, China
[4]Hubei Jiangxia Laboratory, Wuhan 430200, China

Polygonati Rhizoma, a medicinal and edible plant of the genus *Polygonatum* in the family Asparagaceae, exhibits chemical composition and bioactivity that are jointly regulated by genetic inheritance and environmental conditions[1-3]. However, the quantitative contribution of environmental factors to the chemical and bioactive variation among geographically distinct populations remains unclear. In this study, 30 samples representing 9 germplasm resources from across China were subjected to UPLC-Orbitrap-MS/MS-based untargeted metabolomics, integrated with multivariate statistical analysis and geographic–environmental association analysis, to systematically elucidate the drivers of geographic metabolic differentiation and their links to bioactivity. A total of 1,406 metabolites were identified, of which secondary metabolites accounted for over 70%. Principal component analysis (PCA) and orthogonal partial least squares discriminant analysis (OPLS-DA) revealed pronounced provenance-dependent clustering of metabolic profiles, with metabolic convergence observed among geographically proximate populations even across distinct species, whereas distant populations of the same species exhibited marked divergence. Based on the extreme geographic gradient spanning from the Tibetan Plateau to the Guangxi hills, altitude and mean annual temperature emerged as the dominant environmental drivers shaping the metabolomic geographic differentiation of Polygonati Rhizoma, with their effects partially overriding the genetic background of germplasms under extreme ecological gradients. Flavonoids, organic acids, and alkaloids were identified as environmentally responsive candidate chemical markers. In vitro bioactivity assays demonstrated significant inter-population variations in antioxidant (DPPH/ABTS radical-scavenging), xanthine oxidase (XOD) inhibitory, and cyclooxygenase-2 (COX-2) inhibitory activities, which closely paralleled the accumulation patterns of signature metabolites. This study elucidates, from a metabolomic perspective, the driving role of environmental factors in the geographic differentiation of chemical composition in Polygonati Rhizoma and its association with bioactivity, providing a scientific basis for superior germplasm selection, origin traceability, and ecologically oriented cultivation zoning of this plant.

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P24: Formula Optimization and Quality Analysis of Population-Adapted Tartary Buckwheat Pancake Premix Powder

Lai Shiya[1], Zhao Wenyi[1], Lv Wenwen[1], Peng Lianxin[1]*
[1]College of Food and Bioengineering, Chengdu University, Chengdu, China

Modern sedentary lifestyles and refined dietary patterns have increased the incidence of chronic metabolic diseases such as obesity and hyperlipidemia, and insufficient coarse grain consumption has become a prevalent nutritional problem among Chinese residents. In accordance with the initiatives outlined in the Healthy China 2030 Program and the Chinese Dietary Guidelines (2022) to promote coarse grain supplementation and dietary structure improvement, the development of population-specific coarse grain staple food products is of great practical significance for optimizing public nutritional status. Tartary buckwheat (*Fagopyrum tataricum*) is a typical medicinal and edible coarse grain abundant in flavonoids, polyphenols, and other bioactive components. Core flavonoid compounds, including rutin and quercetin, are widely distributed in its tissues and grains, endowing tartary buckwheat with excellent nutritional properties. Nevertheless, the inherent rough texture limits its sensory acceptability. Furthermore, most commercially available pancake premix powders adopt universal formulas without targeted optimization for the physiological characteristics and dietary requirements of children and adults, resulting in poor population applicability[8]. In this study, child-oriented and adult-oriented tartary buckwheat pancake premix powders were prepared. Single-factor experiments, Plackett–Burman screening design, and Box–Behnken response surface methodology were comprehensively employed to optimize the formulas of the two products. The basic nutritional composition, total flavonoid content, total phenolic content, and in vitro antioxidant capacities (DPPH and ABTS assays) of the optimized samples were determined and comparatively evaluated. The results indicated that the established response surface model exhibited favorable fitting efficiency and high experimental reliability. Significant differences in nutritional quality and bioactive component accumulation were observed between the two differentiated formulas. The adult-formulated premix powder contained higher levels of bioactive substances and possessed superior antioxidant capacity, which satisfies the nutritional supplementation and metabolic regulation demands of adult populations. In comparison, the child-formulated premix powder exhibited a mild, low-fat, and nutritionally balanced composition with better palatability, which is more suitable for the physiological development and dietary habits of children. This study established a population-differentiated formula system for tartary buckwheat pancake premix powder, achieving refined nutritional optimization of coarse grain staple food. The results provide a theoretical basis and technical support for the development and industrial promotion of personalized coarse grain prefabricated food products.

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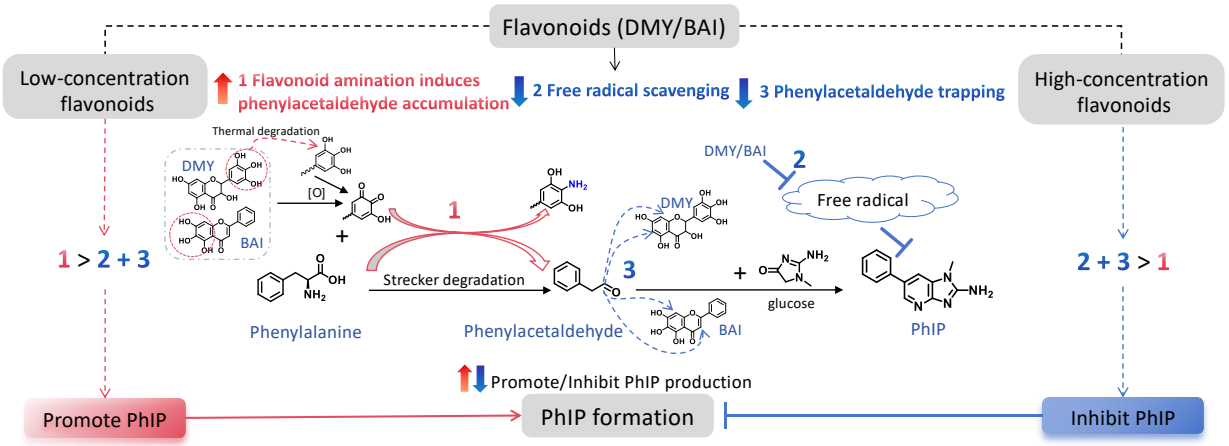
P25: Bidirectional Regulation of Heterocyclic Amines by Flavonoids: Insights from Flavonoid Amination Using Dihydromyricetin and Baicalein

Haolin Zhang[1]*, Jingjing Zhang[1]
[1]College of Food Science and Technology, Guangdong Ocean University, Guangdong Provincial Key Laboratory of Aquatic Product Processing and Safety, Zhanjiang 524088, China

Heterocyclic amines (HCAs) are carcinogenic contaminants formed during thermal processing of meat, and the traditionally recognized inhibitory effects of flavonoids remain controversial due to occasional promotion[1]. This study investigated the concentration-dependent regulation of 2-amino-1-methyl-6-phenylimidazo [4,5-b] pyridine (PhIP) by dihydromyricetin (DMY) and baicalein (BAI) in chemical model systems. Both flavonoids exhibited distinct bidirectional effects: at low concentrations (DMY 125-250 μM, BAI 125-1000 μM), PhIP levels increased to nearly 210% and 300% of control, respectively, whereas at high concentrations (≥ 2000 μM), they were suppressed to < 50% (DMY) and < 20% (BAI). Mechanistic studies revealed that promotion may arise from amination-related reactions of flavonoid thermal degradation products, which generate phenylacetaldehyde, a key PhIP precursor, via Strecker-type pathways. In contrast, inhibition may be driven by potent free-radical scavenging and direct trapping of phenylacetaldehyde through formation of mono- and di-adducts (e.g., 1PA-DMY, 2PA-DMY, and 2PA-BAI)[2]. The net outcome appears to be governed by a dynamic balance between these opposing processes, with the critical turning point determined by flavonoid concentration and structural features (pyrogallol moieties). Notably, heating is the primary stage for amination-promoted phenylacetaldehyde accumulation, as parent flavonoids degrade rapidly into smaller quinone-capable derivatives that sustain aldehyde release. This work provides a mechanistic explanation for the contradictory promotional and inhibitory effects of flavonoids, laying a foundation for optimizing dosage in real meat matrices to effectively mitigate HCA formation without compromising food quality.



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P26: Plant-Derived Antibiotic Adjuvants for Combating Antimicrobial Resistance: Mechanisms, Developmental Progress, and Clinical Translation

Armel J. Seukep[1]*, Minxia Fan[2], Helene G. Mbuntcha[3], Arnaud F. Kouam[1], Cromwel T. Zemnou[4], Francis D. Tatsinkou Bomba[1], Elisabeth Z. Menkem[1], Satiyat D. Sarker[5], V. Kuete[3], Guo Mingquan[6]
[1]Department of Biomedical Sciences, Univeristy of Buea, P.O Box 63, Buea, Cameroon
[2]State Key Laboratory of Plant Diversity and Specialty Crops, Wuhan Botanical Garden, Chinese Academy of Sciences, Wuhan 430074, China
[3]Department of Biochemistry, University of Dschang, P.O Box 67, Dschang, Cameroon
[4]Engineering School BIOMEDTECH, EUROMED University of Fès, Fès, Morocco
[5]Centre for Natural Products Discovery, School of Pharmacy and Biomolecular Sciences, Liverpool John Moores University, Liverpool, L3 3AF, United Kingdom
[6]Laboratory of Advanced Theranostic Materials and Technology, Ningbo Institute of Materials Technology and Engineering, Chinese Academy of Sciences, Ningbo, P. R. China

The accelerating global burden of antimicrobial resistance (AMR) is progressively eroding the effectiveness of existing antibiotics, while the development of new antibacterial agents remains insufficient to address this growing threat[1]. Consequently, antibiotic adjuvants have emerged as a promising strategy for restoring antibiotic efficacy and extending the therapeutic lifespan of current drugs[2,3]. Among these, plant-derived natural products constitute a rich source of structurally diverse resistance-modifying agents capable of targeting multiple bacterial defense mechanisms[4]. This systematic review provides a comprehensive synthesis of validated plant-derived antibiotic adjuvants with demonstrated potential to reverse multidrug resistance. Unlike previous reviews that primarily catalogue synergistic natural products, this review integrates mechanistic evidence, developmental progress, and translational readiness to identify the most clinically promising candidates. We examine the molecular mechanisms through which phytochemicals, including flavonoids, alkaloids, terpenoids, phenolics, and coumarins, enhance antibiotic activity, focusing on inhibition of β-lactamases and other resistance enzymes, suppression of multidrug efflux pumps, disruption of biofilms, interference with quorum sensing, modulation of membrane permeability, and attenuation of bacterial virulence. The review further evaluates contemporary discovery approaches, including high-throughput screening, computational drug discovery, molecular modelling, and artificial intelligence-assisted methodologies. In addition, it maps the antibiotic classes and priority multidrug-resistant pathogens most frequently targeted by plant-derived adjuvants and critically assesses the developmental trajectory of leading candidates, from in vitro and preclinical validation to clinical evaluation. Finally, major barriers to clinical translation are discussed, providing a framework for prioritizing plant-derived antibiotic adjuvants as future resistance-breaking therapies against AMR.

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P27: Procyanidin C1 from *Cynomorium songaricum* Targets SERCA2b to Alleviate Endoplasmic Reticulum Stress in T2DM

Zhihao Liu[1,2], Jihang Chen[1,2]*
[1]Shenzhen Key Laboratory of Steroid Drug Discovery and Development, Department of Pharmaceutical Science, Division of Biomedical Health Sciences, School of Medicine, The Chinese University of Hong Kong, Shenzhen, Guangdong, PR China
[2]The Chinese University of Hong Kong, Shenzhen Futian Biomedical Innovation R&D Center, Shenzhen, Guangdong, PR China

Cynomorium songaricum Rupr., a traditional edible and medicinal plant in China, exhibits hypoglycemic potential, yet its active constituents, direct targets, and mechanisms in endoplasmic reticulum (ER) stress-associated type 2 diabetes remain unclear. This study investigated the pharmacological basis of a polyphenol-enriched fraction from Cynomorii Herba (CSF) and its major bioactive constituents. UPLC/ESI-LTQ-Orbitrap-MS profiling, network pharmacology, and functional screening in high-insulin/high-glucose and palmitic acid/oleic acid-induced HepG2 cell models identified ER stress attenuation as a principal mechanism of CSF action. This effect was further supported in a 5-month high-fat diet-induced diabetic mouse model by integrated transcriptomic and lipidomic analyses, which showed that CSF improved insulin sensitivity while reducing ER stress, oxidative injury, and lipogenesis. Activity-guided screening subsequently identified procyanidin C1 (PCC1) as a potential active constituent. Integration of transcriptomic and Connectivity Map analyses prioritized SERCA2b as a central molecular target. Restoration of SERCA2b-dependent ER Ca^{2+} homeostasis was associated with suppression of the IRE1α-JNK-IRS1 and PERK-eIF2α-ATF4 pathways, thereby improving insulin signaling and redox homeostasis. Molecular docking, molecular dynamics simulations, surface plasmon resonance (SPR), cellular thermal shift assays (CETSA), pharmacological SERCA2b inhibition with thapsigargin, and SERCA2b knockdown in vitro and in vivo collectively supported a direct interaction between PCC1 and SERCA2b and demonstrated the SERCA2b dependence of its metabolic effects. These findings reveal that PCC1 might target SERCA2b to restore ER Ca^{2+} homeostasis, providing a mechanistic basis for developing innovative small-molecule lead compounds against ER stress-associated metabolic disorders.

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P28: *Dendrobium officinale*-Derived Exosome-like Nanovesicles Alleviate DSS-induced Colitis in Mice by Suppressing Inflammatory Response and Restoring Intestinal Mucus Barrier

Ziying Wang, Xiaodan Zhang, Zongsuo Liang*
Key Laboratory of Plant Secondary Metabolism and Regulation of Zhejiang Province, College of Life Sciences and Medicine, Zhejiang Sci-Tech University, Hangzhou-310018, China

Inflammatory bowel disease (IBD) is a relapsing inflammatory disorder of the gastrointestinal tract, characterized by symptoms including abdominal pain, weight loss, and diarrhea. The global prevalence of IBD has risen steadily over recent decades. Despite the availability of multiple pharmacological interventions, IBD continues to pose significant clinical challenges due to its heterogeneous pathogenesis and variable treatment response. Current evidence implicates dysregulated mucosal immunity and intestinal barrier dysfunction as central pathophysiological mechanisms. While existing therapies predominantly target immune suppression, their capacity to promote epithelial restitution and barrier restoration remains suboptimal. Extracellular vesicles (EVs), naturally secreted nano-sized particles enveloped by a lipid bilayer, mediate intercellular communication, cargo transport, and signal transduction. Owing to their low immunogenicity, intrinsic biocompatibility, structural stability, and ability to encapsulate diverse bioactive molecules, EVs have emerged as promising candidates for targeted drug delivery and regenerative therapeutics. *Dendrobium officinale*, as a traditional medicinal and edible Chinese medicinal herb, has been reported to release extracellular vesicles (TPEVs). However, their biological activity in colitis pathogenesis remains poorly characterized. In this study, we evaluated the therapeutic potential of TPEVs in a dextran sulfate sodium (DSS)-induced murine colitis model. The experimental results demonstrated that treatment with TPEVs significantly ameliorated clinical manifestations in mice with dextran sulfate sodium (DSS)-induced acute colitis, attenuated body weight loss, and suppressed the progression of disease activity index (DAI) scores. DSS administration induced pronounced oxidative stress and a robust pro-inflammatory response in colonic tissue, characterized by elevated levels of TNF-α and IL-1β. TPEV intervention markedly downregulated these pro-inflammatory cytokines and restored endogenous antioxidant capacity, as evidenced by modulation of superoxide dismutase (SOD) activity. Furthermore, TPEV treatment promoted goblet cell regeneration and significantly enhanced MUC2 expression, thereby facilitating structural and functional restoration of the intestinal mucosal barrier. Collectively, these findings these findings reveal the great potential of TPEVs as a novel nano-capsule carrier of medicinal and edible substances in IBD management.

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P29: A Comprehensive PK-PD and Metabolomic Approach to Evaluate the Therapeutic Effects of *Schisandra chinensis* Lignans in Diabetic Rats

Liqiang Shi[1], Shuang Cao[1], Guangxin Yuan[1]*
[1]College of Pharmacy, Beihua University, Jilin, Jilin 132013, P. R. China

Diabetes mellitus represents a significant global public health concern, with projections from the International Diabetes Federation indicating that the worldwide diabetic population will surpass 780 million by 2045[1]. Although conventional oral anti-diabetic medications are effective in lowering blood glucose levels, their clinical application is frequently constrained by adverse effects such as hypoglycemia and gastrointestinal disturbances, which can result in suboptimal patient adherence[2]. As a result, there is a growing interest in the exploration of active compounds derived from traditional Chinese medicine (TCM) as viable alternatives[3]. *Schisandra chinensis* (SC) is commonly employed in TCM for the management of diabetes, and various formulations containing SC have demonstrated notable clinical efficacy. The primary active components of SC, lignans, possess significant anti-inflammatory, antioxidant, and insulin-sensitizing properties, in addition to their capacity to inhibit vascular lesions [4]. Nonetheless, the precise hypoglycemic mechanisms and pharmacokinetic (PK) profiles of these lignans remain inadequately elucidated. This study explores the material basis and mechanisms underlying the anti-diabetic effects of SC lignans through an integrated approach that combines pharmacokinetics (PK), pharmacodynamics (PD), PK-PD modeling, and metabolomics. In diabetic rat models, SC administration significantly reduced serum levels of total cholesterol (TC), triglycerides (TG), and low-density lipoprotein cholesterol (LDL-C), while effectively mitigating hepatic inflammation induced by a high-fat diet. Metabolomic profiling of urine and fecal samples identified 21 and 24 potential biomarkers, respectively, primarily linked to the metabolic pathways of phenylalanine, tryptophan, the tricarboxylic acid (TCA) cycle, and bile acids. Additionally, a UPLC-TQ-MS/MS method was developed to simultaneously quantify PK and PD markers. Subsequent PK-PD association analysis revealed a complex, non-linear relationship characterized by a delayed PD response. These findings suggest that the pharmacological efficacy of SC is attributable to the synergistic interactions of multiple components rather than the action of a single active compound. Ultimately, this study elucidates the pharmacodynamic basis and therapeutic mechanisms of SC in the management of diabetes, thereby providing a crucial foundation for its further clinical development.

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P30: From Folk Medicine to Pharmacological Evidence: A Review of the Chemical Constituents and Bioactivities of Balanophora Harlandii Hook.f.

Yu Qing[1,2,3], Kefan Zhao[1,2,3], Guilin Chen[1,2,3,4], Minxia Fan[1,3,4]*, Guangwan Hu[1,2,3,4]*
[1]State Key Laboratory of Plant Diversity and Specialty Crops, Wuhan Botanical Garden, Chinese Academy of Sciences, Wuhan 430074, China
[2]University of Chinese Academy of Sciences, Beijing 100049, China
[3]Sino-Africa Joint Research Center, Chinese Academy of Sciences, Wuhan 430074, China
[4]Hubei Jiangxia Laboratory, Wuhan 430200, China

Balanophora harlandii Hook.f. (Balanophoraceae) is a perennial holoparasitic flowering plant with a long history of use in folk medicine. This review comprehensively examines the scholarly progress in its herbal textual research, chemical composition (including compounds from endophytic fungi), pharmacological properties, and the correlation between its holoparasitic nature and its bioactive constituents. Historical textual records reveal that this plant has been consistently documented in several Chinese materia medica works as "Ge Xun", with its traditional uses aligning with modern pharmacological findings, such as its efficacy in cooling blood, stopping bleeding, and detoxifying. Phytochemical analysis has identified diverse classes of compounds in *B. harlandii*, including polysaccharides, phenolic acids, flavonoids, triterpenoids, phenylpropanoids, and steroids, with phenylpropanoids and triterpenoids as the predominant components[错误!未找到引用源。,错误!未找到引用源。]. Pharmacological studies have demonstrated that plant extracts from *B. harlandii* exhibit diverse bioactivities, encompassing anti-inflammatory[错误!未找到引用源。], antioxidant, hepatoprotective (particularly against alcohol-induced damage), antitumor, and immunomodulatory effects[错误!未找到引用源。,错误!未找到引用源。]. Additionally, this review consolidates the findings of metabolomic investigations on plant host–parasite interactions, with the aim of guiding the sustainable utilization and conservation of this botanical resource. By synthesizing the existing literature, this paper not only provides a comprehensive overview but also outlines future research directions concerning sustainable resource management, identification of bioactive constituents, and elucidation of the underlying mechanisms.

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P31: Carbon-Efficient Upcycling of Agrifood Waste into Fatty Acid Ester by Engineered *Clostridium tyrobutyricum*

Zhenlei Liu[1], Ling Jiang[2]*
[1]College of Biotechnology and Pharmaceutical Engineering, Nanjing Tech University, Nanjing, China
[2]College of Food Science and Light Industry, Nanjing Tech University, Nanjing, China

Microbial conversion of renewable feedstocks into biofuels is gaining interest due to its sustainability. In this research article, we develop a carbon-and cost-efficient fermentation route in *Clostridium tyrobutyricum* to produce the biofuel butyl butyrate (BB) from abundant, low-cost agrifood waste. Using iterative, multimodule strain engineering—promoter engineering, multienzyme colocalization, nonoxidative glycolysis-driven carbon conservation, and cofac-tor engineering—we achieved high-selectivity BB production from rice straw hydrolysate and shrimp shell waste. The best strain delivered a 49.5-fold improvement, reaching 31.16 g/l BB with 98.4% selectivity and a productivity of 0.325 g/l/h in5-l batch fermentations. Techno-economic and carbon-footprint analyses indicate that, compared with conventional sugar biorefineries, agrifood-waste biorefineries cut feedstock costs by 53.6% and life-cycle carbon emissions by 63.4% perton of BB produced. These results show that engineered *C. tyrobutyricum* enables carbon-efficient upcycling of agrifood waste into high-yield BB and provides a blueprint for the biosynthesis of other biofuels.

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P32: Anti-Constipation Effects of *Prunus domestica* L.-Derived Vesicles

Lili Zhang[1,2], Mingqing Kuang[1,2], Zhangfeng Zhong[1,2]*
[1]Macao Centre for Research and Development in Chinese Medicine, State Key Laboratory of Quality Research in Chinese Medicine, Institute of Chinese Medical Sciences, University of Macau, Macao SAR 999078, China
[2]Zhuhai UM Science and Technology Research Institute, Zhuhai 519031, China

Constipation is a common functional gastrointestinal disorder, and current therapeutic options are limited by safety concerns, suboptimal efficacy, and long-term dependence. *Prunus domestica L. exhibits* notable laxative effects; however, its key bioactive carriers remain unclear, and its innovative form needs to be developed. Growing evidence indicates that plant-derived vesicles possess favorable biocompatibility and intestinal regulatory functions, yet studies on *Prunus domestica* L.-derived vesicles (PDVs) are completely lacking. This study aims to isolate and characterize PDVs, evaluate their anti-constipation effects, and explore the preliminary mechanisms. PDVs were isolated and purified with typical vesicular structures, stable particle size, and were enriched in miRNAs, lipids, and proteins. Cellular uptake assays demonstrated efficient internalization by intestinal epithelial cells, and in vivo distribution revealed targeted accumulation in the colon. Biosafety evaluation showed no significant hemolysis, organ toxicity, or abnormal serum biochemical indices. In the constipation model, PDVs significantly shortened total gastrointestinal transit and promoted defecation. Mechanistic studies revealed that PDVs modulated gut microbiota composition, altered metabolite profiles, and regulated intestinal protein expression. PDVs possess good biosafety and intestinal targeting, as well as effectively alleviate constipation in mice through multidimensional regulation of gut microbiota, metabolites, and protein expression, representing a promising natural nanoscale intervention strategy against constipation.

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P33: Improving Soluble Expression of Sweet Protein Thaumatin II Through Directed Evolution in *Escherichia coli*

Lefei Wang[1], Ling Jiang[2]*
[1]College of Biotechnology and Pharmaceutical Engineering, Nanjing Tech University, Nanjing, China
[2]College of Food Science and Light Industry, Nanjing Tech University, Nanjing, China

Thaumatin is a natural sweet protein valued for its intense sweetness, long-lasting effect, low-calorie content, and safety[1]. However, limited solubility and low yields hinder microbial fermentation[2]. To overcome these challenges, we engineered *Escherichia coli* to express thaumatin II and implemented three strategies to improve its solubility, then co-expression with molecular chaperones has proved to be the most effective in significantly enhancing the soluble expression of thaumatin II. Furthermore, we applied directed evolution to further refine thaumatin II, resulting in the M-882 mutant, which achieved a thaumatin titer of 42 mg/L, representing a 45% increase compared to the original protein yield. Structural analysis revealed that disruption of two adjacent disulfide bonds in the M-882 mutant minimized mispairing during peptide folding, thereby improving protein solubility. Additionally, molecular dynamics simulations showed that the M-882 variant enhanced solvent accessibility and structural flexibility, both of which contributed to improved solubility. The interaction between thaumatin II and sweet taste receptors, as well as the analysis of surface positive charges, indicates that the M-882 variant is capable of binding to the receptors, thereby retaining its sweetness[3]. Overall, this study not only offers valuable insights into optimizing thaumatin expression but establishes a foundation for engineering other sweet proteins with broad industrial applications.

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P34: Flavonoids From Ougan (*Citrus suavissima*) Peel: Extraction, Characterization and Hypouricemic Activity Evaluation

Chenhao Yu[1], Hailong Yang[1], Hang Qu[1]*
[1]College of Life & Environmental Science, Wenzhou University, Wenzhou, China

Hyperuricemia is a chronic metabolic disorder characterized by elevated serum uric acid (UA) levels and is closely associated with the progression of multiple pathological conditions[1]. Accumulating evidence in recent years has demonstrated that hyperuricemia serves as an independent risk factor for a variety of common chronic diseases, including hypertension, chronic kidney disease, and type 2 diabetes[2]. Accordingly, the prevention and management of hyperuricemia have emerged as prominent areas of current research. Natural bioactive compounds with therapeutic potential against hyperuricemia have attracted growing scientific interest[3]. Flavonoids are known to selectively inhibit xanthine oxidase and modulate renal tubular urate transporters[4]. Ougan (*Citrus suavissima*) peel is abundant in flavonoids[5], yet relevant studies remains scarce, and its resource utilization remains inadequate, resulting in considerable waste. In the present study, deep eutectic solvents (DES) were employed for the efficient extraction of flavonoids from Ougan peel. The primary chemical constituents were characterized by LC-MS, and the major flavonoids, including neohesperidin, hesperetin, tangeretin, nobiletin, naringenin, naringin, isosakuranetin, casticin, orientin, and methyl deoxycholate were further quantified using HPLC[6]. Core targets against hyperuricemia were predicted via network pharmacology, and xanthine oxidase inhibition assays were performed to evaluate the inhibitory effect. Finally, a cellular hyperuricemia model was established using HK-2 cells for functional validation of the flavonoids. The results showed that flavonoids from Ougan peel exhibited significant xanthine oxidase inhibitory activity, enhanced the transcription and expression of urate transporters in HK-2 cells, and alleviated hyperuricemia primarily through the PI3K/AKT signaling pathway. These findings suggest that flavonoids from Ougan peel possess promising potential for the prevention and treatment of hyperuricemia.

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P35: Research Progress on Chemical Constituents and Pharmacological Activities of Neopicrorhiza Plants

Kefan Zhao[1,2,3], Yu Qing[1,2,3], Guilin Chen[1,2,3,4], Minxia Fan[1,3]*, Guangwan Hu[1,2,3,4]*
[1]State Key Laboratory of Plant Diversity and Specialty Crops, Wuhan Botanical Garden, Chinese Academy of Sciences, Wuhan, 430074, China
[2]University of Chinese Academy of Sciences, Beijing, 100049, China
[3]Sino-Africa Joint Research Center, Chinese Academy of Sciences, Wuhan, 430074, China
[4]Hubei Jiangxia Laboratory, Wuhan, 430200, China

Neopicrorhiza is an important medicinal genus used in traditional Chinese medicine for clearing deficiency heat, and its representative species *N. scrophulariiflora* is widely utilized in Tibetan and Ayurvedic medicine for treating hepatobiliary diseases[1,2]. This paper systematically reviews the research progress on the ethnobotany, phytochemistry, pharmacological activities, and toxicology of plants in the genus *Neopicrorhiza*. To date, researchers have isolated and identified various types of secondary metabolites from Neopicrorhiza species[1]. The main structural types are iridoid glycosides, cucurbitane-type tetracyclic triterpenoids, phenylpropanoids, and phenylethanoid glycosides; among these, iridoid glycosides (exemplified by picroside I and II) are the characteristic active constituents. Pharmacological studies have shown that extracts and monomeric compounds from *Neopicrorhiza* exert extensive pharmacological effects, including hepatoprotective, anti-inflammatory, antioxidant, neuroprotective, antitumor, and immunomodulatory activities[3,4]. These effects are mediated through the activation of the Keap1/Nrf2/ARE antioxidant pathway, inhibition of the NF-κB and NLRP3 inflammasome pathways, and regulation of the JAK2/STAT3 and MEK/ERK signaling pathways. Toxicological studies indicate that the total glycosides of *Neopicrorhiza* have a good safety profile at conventional doses[4]. Currently, *N. scrophulariiflora* has been listed as a second-class national protected plant in China, and its wild populations are endangered, necessitating urgent research on artificial cultivation and sustainable utilization[5]. In the future, it will be essential to integrate ethnobotany, natural product chemistry, systems pharmacology, and omics technologies to establish a full-chain research paradigm encompassing "resources-constituents-targets-therapeutic effects" for *Neopicrorhiza*, thereby providing scientific support for the sustainable utilization and modern development of this rare and endangered medicinal resource.

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P36: Morroniside Ameliorates Diabetic Kidney Disease Proteinuria by Targeting Drp1 and Preserving Glomerular Filtration Barrier Integrity via Inhibition of Its Ubiquitin-Proteasome Degradation

Jiaxiang Yu[1], Yi Wu[2], Yan Shi[3], Wenshun Zhang[2]*, Hanwen Zhang[3]*
[1]College of Health Preservation and Rehabilitation, Liaoning University of Traditional Chinese Medicine, Shenyang,110847, China
[2]Liaoning Province Traditional Chinese Medicine Research Institute, Shenyang,110034, China
[3] College of Basic Medical Sciences, Liaoning University of Traditional Chinese Medicine, Shenyang,110847, China

Aim of the study: This study aimed to investigate whether morroniside, an active compound derived from *Cornus officinalis*, protects against proteinuria in diabetic kidney disease (DKD) and to elucidate the underlying mechanism, focusing on its direct target protein, Drp1, and the regulation of Drp1 ubiquitination and proteasomal degradation. Material and methods: Sixteen-week-old db/db mice were treated with morroniside by gavage for 8 weeks. General metabolic parameters, renal function, including SCr, BUN, and cystatin C, as well as 24-h urine protein and urinary albumin-to-creatinine ratio (UACR), were assessed. Renal histopathology and fibrosis were evaluated by PAS and Sirius red staining, and glomerular ultrastructure by transmission electron microscopy. Expression of slit diaphragm proteins, including nephrin, podocin, and CD2AP, and endothelial junction proteins, including VE-cadherin and ZO-1, was measured by Western blot and immunofluorescence. To identify the direct target of morroniside, we used affinity-based chemical probes and binding assays. The direct interaction was validated by molecular docking, surface plasmon resonance, pull-down, and cellular thermal shift assays. Ubiquitination and proteasomal degradation of Drp1 were examined by cycloheximide chase, MG132 inhibition, and immunoprecipitation-ubiquitin blotting. CRISPR/Cas9-mediated knockout and overexpression of Drp1 in podocytes and glomerular endothelial cells in vitro, as well as podocyte-specific AAV-mediated Drp1 knockout in vivo, were performed to determine the dependency of morroniside's effects on Drp1. Results: Morroniside treatment significantly lowered random blood glucose and HbA1c, reduced 24-h urine protein and UACR, improved renal function, and attenuated glomerular mesangial expansion and collagen deposition. Ultrastructural analysis showed that Morroniside alleviated foot process effacement and glomerular basement membrane thickening. Molecularly, morroniside restored the expression of nephrin, podocin, CD2AP, VE-cadherin, and ZO-1, preserving the filtration barrier integrity. We identified Drp1 as the direct binding target of morroniside, with high affinity. Morroniside inhibited the ubiquitination of Drp1, prolonged its half-life, and prevented its proteasomal degradation. Knockout of Drp1 in cultured podocytes and endothelial cells completely abolished the protective effects of morroniside on cell integrity and barrier function, while Drp1 overexpression mimicked its protection. In vivo, podocyte-specific Drp1 knockout fully blocked the renoprotective actions of morroniside, including the reduction of proteinuria and the preservation of the glomerular filtration barrier. Conclusion: Morroniside ameliorates DKD proteinuria by directly targeting Drp1, inhibiting its ubiquitin-proteasome degradation, and thereby maintaining glomerular filtration barrier integrity. This work identifies a novel target and mechanistic pathway for morroniside in the treatment of DKD.

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P37: From Peel Waste to Functional Ingredient: Green pH-Driven Self-Assembly of Tilapia Protein-Chondroitin Sulfate Nanoparticles for Enhancing the Stability and Bioavailability of Betanin

An Luo[1], Qiaoli Zhao[1]*, Xuan Zhang[1], Zhuo Wang[1], Rui Li[1], Saiyi Zhong[1,2]*
[1]College of Food Science and Technology, Guangdong Ocean University, Guangdong Provincial Key Laboratory of Aquatic Product Processing and Safety, Guangdong Province Engineering Laboratory for Marine Biological Products, Guangdong Provincial Engineering Technology Research Center of Seafood, Guangdong Provincial Science and Technology Innovation Center for Subtropical Fruit and Vegetable Processing, Zhanjiang 524088, China
[2]Shenzhen Research Institute, Guangdong Ocean University, Shenzhen 518108, China

Red-fleshed dragon fruit is a characteristic tropical fruit, but its peel, which accounts for 20-30% of the fruit mass, is commonly discarded by landfilling or incineration, causing resource loss, environmental pressure and disposal costs. The dragon fruit peel is rich in betanin, a water-soluble natural pigment with antioxidant and anti-inflammatory, and can function as both a colorant and a nutritional fortifier. However, betanin is readily degraded by heat, pH, oxygen and light, resulting in poor stability and low bioaccessibility. To overcome this limitation, we developed betanin-loaded tilapia protein isolate-chondroitin sulfate nanoparticles (TPI-CS/Bt) using a green pH-driven self-assembly strategy. Results indicate that at an optimal CS concentration of 2 mg/mL, the nanoparticles showed a particle size of 567.26 nm, a zeta potential of -35.93 mV, an encapsulation efficiency of 81.43% and a loading capacity of 11.63 μg/mg. Spectroscopic analyses (UV–vis, fluorescence, circular dichroism and FT-IR) revealed that betanin was incorporated primarily through hydrogen bonding and hydrophobic interactions. Compared with free betanin, TPI-CS/Bt improved thermal and ultraviolet stability and increased bioaccessibility by 2.44-fold, from 18.31% to 44.66%. In vitro gastrointestinal digestion experiments demonstrated that the release profiles of betanin showed reduced premature gastric release and fitted the Logistic model, while Ritger–Peppas kinetics indicated Fickian diffusion as the dominant release mechanism. This work offers a sustainable and efficient delivery platform that simultaneously valorizes dragon fruit peel waste and boosts betanin stability and bioavailability, opening a new avenue for the high-value utilization of fruit processing by-products in functional food applications.

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P38: Deep Learning in Food Science: Innovative Approaches for Predicting and Simulating Food-Derived Protein-Peptides

Shilong Cheng[1], Yao Chen[2], Yi Cao[1], Xuyao Huang[3], Bin Liu[4], Minghui Liu[5], Shuai Jiang[1]*, Ling Jiang[1,6]*
[1]College of Food Science and Light Industry, Nanjing Tech University, Nanjing 211816, China
[2]Taizhou Key Laboratory of Biomass Functional Materials Development and Application, School of Life Science, Taizhou University, Taizhou 318000, China
[3]School of Electronic Information and Electrical Engineering, Shanghai Jiao Tong University, Shanghai 200240, China
[4]School of Life Sciences, Nankai University, Tianjin 300071, China
[5]School of Pharmaceutical Sciences, Nanjing Tech University, Nanjing 211816, China
[6]State Key Laboratory of Materials-Oriented Chemical Engineering, Nanjing Tech University, Nanjing 211816, China

Background: Food-derived peptides possess diverse bioactivities, and the prediction and simulation of protein–peptide interactions are instrumental in identifying functional peptides in foods. However, traditional methods for predicting and simulating protein–peptide interactions are often inefficient and costly, making them inadequate for the demands of modern high-throughput screening and rational design. Deep learning techniques can learn complex interaction patterns from large-scale sequence and structural data, thereby facilitating the discovery and application of functional peptides in the food sector.

Scope and approach: This review systematically summarizes recent advances in the application of deep learning for the prediction and simulation of food-derived protein–peptide interactions. It focuses on the biological functions of food-derived peptides, the development and utilization of protein and peptide databases, as well as the application of deep learning algorithms in the prediction of protein–peptide structure and function, molecular docking, and molecular dynamics simulation. Furthermore, current challenges and future perspectives in this field are discussed.

Key findings and conclusions: Deep learning techniques have significantly improved the efficiency and accuracy of predicting and simulating food-derived protein–peptide interactions, facilitating the precise identification of active sites and structure-activity relationships. By integrating advanced algorithms with comprehensive databases, researchers can efficiently screen and design functional peptides, thereby accelerating the innovation and development of functional foods. This review provides valuable insights for a deeper understanding of protein–peptide interaction mechanisms and offers important reference for advancing the functional research and application development of food-derived proteins and peptides.

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P39: Regulatory Effects of Ethanol Extract from Helianthus Tuberosus L. on Glucose Metabolism and Gut Microbiota Homeostasis in Type 2 Diabetic Mice

Wang Miaohui[1], Yin Xuemei[1], Xu Wei[1], Shao Rong[1]*
[1]College of Marine and Bioengineering, Yancheng Institute of Technology, Yancheng, 224051, China

Type 2 diabetes mellitus (T2DM) has become a global metabolic epidemic, characterized by intricate interactions among insulin resistance, dyslipidemia, and gut microbiota dysbiosis[1,2]. Plant-derived natural products, with their multi-target characteristics and favorable safety profiles, offer promising alternatives for T2DM management[3,4]. *Helianthus tuberosus* L. (*H. tuberosus*) is rich in inulin, polyphenols and flavonoids, yet the comprehensive effects of its non-polysaccharide lipophilic components on T2DM remain underexplored. In this study, we prepared the 70% ethanol extract of *H. tuberosus* (HTE) and characterized 1735 compounds via UPLC-Q-TOF-MS, predominantly flavonoids and carboxylic acids. Using a high-fat/high-sugar diet combined with streptozotocin-induced T2DM mouse model, we evaluated the metabolic benefits of HTE at different dosages over a 4-week intervention. Our results demonstrated that HTE significantly reduced fasting blood glucose, improved oral glucose tolerance and insulin sensitivity (HOMA-IS), enhanced β-cell function (HOMA-β), and ameliorated dyslipidemia in both serum and liver. Mechanistically, HTE up-regulated hepatic AKT-1 and GLUT-2 mRNA expression, indicating improved insulin signaling and glucose utilization. Furthermore, 16S rRNA sequencing and gas chromatography revealed that HTE reshaped the gut microbial community by lowering the Bacillota/Bacteroidota ratio and increasing short-chain fatty acids (especially butyrate) in cecal contents. Notably, the genera Turicibacter and Ligilactobacillus showed strong negative correlations with key glycemic and lipid parameters, suggesting their potential roles as microbial targets. Collectively, HTE exerts its anti-diabetic effects through a synergistic axis involving gut microbiota remodeling, SCFA elevation, and activation of hepatic AKT-1/GLUT-2 signaling, highlighting its potential as a functional food ingredient for T2DM intervention.

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P40: Ancestral Sequence Reconstruction and Machine Learning Driven Redesign of Superoxide Dismutase for Enhanced Performance

Ruitong Ding[1], Lin Li[1], Zhengming Zhu[2]*, Ling Jiang[2]*
[1]College of Biotechnology and Pharmaceutical Engineering, Nanjing Tech University, Nanjing 211816, China
[2]College of Food Science and Light Industry, Nanjing Tech University, Nanjing 211816, China

Superoxide dismutase (SOD) is a redox metalloenzyme that scavenges superoxide anion radicals, with extensive applications in food and cosmetics. However, its industrial production is hindered by limited catalytic activity and thermal stability. In this study, we targeted SOD from *Deinococcus wulumuqiensis* R12 and employed a strategy combining multiplexed ancestral sequence reconstruction (mASR), directed evolution, and machine learning to enhance its performance. Through mASR, we resurrected 13 ancestral enzymes, with Ancestral_117 exhibiting a specific activity of 1592.46 U/mg and Ancestral_148 retaining 93% activity at 80°C. Utilizing ambiguous sites identified during ASR, we constructed a Combinatorial Libraries of Ancestors for Directed Evolution (CLADE) library. Screening of 57 single-point mutants yielded variants with significantly improved properties, including mutant 164_V36I with a specific activity of 3231.35 U/mg and mutant 152_G69T showing no activity loss at 80°C. To explore synergistic multi-site mutations, we developed a machine learning model trained on the CLADE dataset. Virtual screening and experimental validation identified a five-point mutant (Ancestral_164_D37N_N69G_V70A_V87I_N104D) with a balanced phenotype: a specific activity of 2368.08 U/mg and 65% residual activity at 80°C. Molecular dynamics simulations revealed that improved performance stems from a dynamic balance between structural rigidity and active-site flexibility, as well as enhanced intersubunit interactions. This study demonstrates that evolution-driven ASR, combined with machine learning-guided engineering, is a powerful strategy for simultaneous improvement of enzyme activity and stability, providing a valuable reference for SOD optimization and future enzyme engineering.

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P41: Functional Water Kefir Beverage Formulated with Lilac (*Syringa vulgaris* L.) Flower Syrup

Nenad Mićanović[1]*, Gordana Zdunić[2], Đorđe Boškov[1], Nemanja Krgović[2], Jelena Popović-Đorđević[1]*
[1]University of Belgrade, Faculty of Agriculture, Belgrade, Serbia
[2]Institute for Medicinal Plants Research "Dr Josif Pančić", Belgrade, Serbia

Functional foods have gained increasing attention due to the growing awareness of the relationship between diet and health. Among them, fermented beverages are recognized as a valuable source of beneficial microorganisms and bioactive compounds that may promote overall health[1]. Water kefir is a traditional fermented beverage produced by fermenting a sugar solution with water kefir grains, a symbiotic consortium of lactic acid bacteria, acetic acid bacteria, and yeasts. During fermentation, these microorganisms produce organic acids, vitamins, enzymes, exopolysaccharides, and other bioactive metabolites that contribute to the beverage's nutritional, sensory, and functional properties [1]. Lilac (*Syringa vulgaris* L.) is an ornamental plant native to the Balkan Peninsula, whose edible flowers are rich in phenolic compounds. Due to their pleasant aroma and distinctive flavor, lilac flowers are traditionally used in the production of syrups, beverages, and other food products[2].

Water kefir based on lilac (*S. vulgaris* L.) flower syrup is fermented beverage produced by using lilac flower syrup as the fermentation substrate. This study investigated the effect of lilac flower syrup on the technological properties of water kefir. Following parameters were examined: total soluble solids (TSS), pH, titratable acidity (TA) and soluble solids/titratable acidity ratio TSS/TA, and bioactive compounds including total phenolic content (TPC), total flavonoid content (TFC), and total hydroxycinnamic acid derivatives (THCA). The obtained water kefir formulation with lilac flower syrup (WKLF) was compared with a conventional water kefir (CWK). Lilac flower syrup was prepared using the hot maceration process that resulted in TPC - 94.42±1.36 mg GAE/100 g, TFC - 59.81±1.27 mg CE/100 g, and THCA - 88.47±1.01 mg ChAE/ 100 g.

The comparison between conventional water kefir and lilac flower syrup-based water kefir revealed differences in total TSS (CWK: 3.35±0.07% / WKLF: 2.60±0.00%), pH (CWK: 4.80±0.00 / WKLF: 3.82±0.00), TA (CWK: 0.048±0.00% / WKLF: 0.074±0.00%), and TSS/TA ratio (CWK: 69.80±0.58 / WKLF: 35.38±0.34). Furthermore, lilac syrup-based water kefir exhibited higher levels of bioactive compounds, including TPC (10.82±0.34 vs. 1.33±0.05 mg GAE/100 g), TFC (5.11±0.04 vs. 0.08±0.03 mg CE/100 g), and THCA (7.77±0.13 vs. 1.59±0.12 mg ChAE/100), compared with conventional water kefir. The results demonstrated that lilac (*S. vulgaris* L.) flower syrup can be successfully used for water kefir production, enhancing its technological properties and bioactive compounds content. In respect of obtained results, water kefir formulation with lilac flower syrup is a promising formulation for the development of a novel functional fermented beverage.

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P42: Mechanistic Study on the Anti-hyperuricemic Effect of *Polygonatum hunanense* Based on Multi-Target Regulation of Urate Transport and the Inflammatory-Oxidative Stress Network

Yu Qing[1,2,3], Kefan Zhao[1,2,3], Guilin Chen[1,2,3,4], Minxia Fan[1,3,4]*, Guangwan Hu[1,2,3,4]*
[1]State Key Laboratory of Plant Diversity and Specialty Crops, Wuhan Botanical Garden, Chinese Academy of Sciences, Wuhan 430074, China
[2]University of Chinese Academy of Sciences, Beijing 100049, China
[3]Sino-Africa Joint Research Center, Chinese Academy of Sciences, Wuhan 430074, China
[4]Hubei Jiangxia Laboratory, Wuhan 430200, China

Polygonatum hunanense, a traditional medicinal plant, exhibits various pharmacological activities, but its anti-hyperuricemic effects and mechanisms remain unclear[1]. In this study, systematic solvent extraction yielded four polarity fractions: n-hexane, ethyl acetate (EA), n-butanol, and water. Through comprehensive chemical profiling and bioactivity-guided screening in cellular and animal models, the EA fraction was identified as the most active, containing the highest levels of total flavonoids, polyphenols, and saponins, and showing superior antioxidant, xanthine oxidase (XOD), and cyclooxygenase-2 (COX-2) inhibitory activities[2]. UPLC-Q-TOF-MS/MS analysis tentatively identified 12 compounds from the EA fraction, including phenolic acids, phenolic amides, homoisoflavonoids, and organic acids. In HK-2 cells, the EA fraction (0.3125-1.25 μg/mL) concentration-dependently attenuated adenosine-induced oxidative injury, inflammatory cytokine release, and uric acid production, associated with downregulation of URAT1 and NLRP3 and upregulation of HO-1. In hyperuricemic mice induced by potassium oxonate, the EA fraction not only lowered serum uric acid, creatinine, and blood urea nitrogen levels but also ameliorated renal histopathology. Mechanistically, these effects were attributed to coordinated regulation of urate transporters (downregulation of URAT1/GLUT9 and upregulation of OAT1/ABCG2), suppression of the TLR4/NF-κB/NLRP3 inflammatory cascade, and activation of the Keap1/Nrf2/HO-1 antioxidative pathway[3-5]. Collectively, this study provides the first systematic evidence that the EA fraction of *P. hunanense* exerts urate-lowering and renoprotective effects through multi-target regulation of urate transport and the inflammatory-oxidative stress network, offering a promising candidate for treating hyperuricemia-associated renal injury.

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P43: Ultrasound-Assisted Glycation with Xylose and Sodium Alginate for Modulating Pickering Emulsion and Hydrogel Properties of Silkworm Pupa Protein

Xinyang Wang[1], Haining Xu[1]*, Yingchun Ma[1], Yan Ye[1], Xueyue Huang[2], Ronghai He[3], Jun Tian[1]*
[1]School of Life Sciences, Jiangsu Normal University, 221116 Xuzhou, China
[2]WuXi AppTec (Suzhou) Co., Ltd., 215104 Suzhou, China
[3]School of Food and Biological Engineering, Jiangsu University, 212013 Zhenjiang, China

Silkworm pupa protein isolate (SPPI) exhibits poor emulsifying and gelling properties, which restricts its application in food products[1,2,3]. In this study, synergistic modification via the Maillard reaction was performed by combining dual-frequency ultrasonication with either low-molecular-weight xylose or high-molecular-weight sodium alginate. The effects of these two modification systems on the interfacial characteristics of SPPI, as well as the properties of the resulting Pickering emulsions and emulsion-filled hydrogels, were systematically compared. Results demonstrated that ultrasonication-assisted xylose modification significantly improved the amphiphilic balance of SPPI, reduced droplet size, and enhanced interfacial adsorption, resulting in emulsions with greatly improved freeze-thaw stability; the corresponding hydrogels displayed a soft texture and excellent water-holding capacity, making them suitable for dysphagic populations[4]. In contrast, ultrasound-assisted sodium alginate modification further improved protein hydrophilicity and refrigeration stability, while enhancing disulfide crosslinking to increase gel hardness, catering to consumers preferring chewy and firm textures[5]. Ultrasonication disrupted hydrophobic protein aggregates and promoted the exposure of hydrophilic residues, thereby improving glycation efficiency and enabling the formation of stable elastic interfacial films that enhanced the environmental tolerance of the emulsions[4,5,6]. This dual modification strategy enables targeted modulation of silkworm pupa protein functionality and offers a green technological approach for the development of insect protein-based composite foods.

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P44: Study on the Mechanism of *Salvia miltiorrhiza* Bge. Extract in Improving Gastric Precancerous Lesions via the HSP90/NOD-like Signaling Pathway

Xinyue Huang[1], Guoyin Kai[1]
[1]Zhejiang Provincial International S&T Cooperation Base for Active Ingredients of Medicinal and Edible Plants and Health, Zhejiang Provincial Key TCM Laboratory for Chinese Resource Innovation and Transformation, School of Pharmaceutical Sciences, Jinhua Academy, Zhejiang Chinese Medical University, Hangzhou, Zhejiang, 310053, China

Gastric precancerous lesions (GPLs) represent a critical pathological stage in the progression of chronically injured gastric mucosa toward gastric cancer. Extracts of *Salvia miltiorrhiza*[1] possess anti-inflammatory and tissue-protective effects; however, their efficacy against GPLs and the underlying molecular mechanisms have not been systematically investigated. In this study, the pharmacological effects of *S. miltiorrhiza* extracts were evaluated through animal and cell experiments, and their potential mechanisms were analyzed using transcriptomics, network pharmacology, quantitative polymerase chain reaction (qPCR), and Western blotting. Animal experiments showed that both aqueous and ethanolic extracts of *S. miltiorrhiza* improved gastric mucosal morphology in GPL model animals and alleviated histopathological damage to some extent. Transcriptomic and network pharmacological analyses suggested that protein processing, inflammatory responses, and NOD-like receptor-related signaling pathways may be involved in the effects of *S. miltiorrhiza* extracts, with HSP90-related molecules[2] potentially playing an important regulatory role. Cell experiments further demonstrated that S. miltiorrhiza extracts inhibited the migration and invasion of model cells, partially reversed epithelial-mesenchymal transition-related phenotypes[3], and modulated the expression of inflammation-related molecules, including HSP90, NLRP3, N-GSDMD, and interleukin-18. These findings suggest that S. miltiorrhiza extracts ameliorate gastric precancerous lesions by regulating the HSP90-NOD/inflammasome signaling pathway, providing an experimental basis for the application of *S. miltiorrhiza* in the prevention and treatment of GPLs.

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P45: Identification and Functional Analysis of the WRI1 (WRINKLED1) Transcription Factor Family Involved in Oil Biosynthesis in *Coix* (*Coix lacryma-jobi L.*)

Lijun Yang[1], Tinghui Feng[1], Lingxia Peng[1], Zhiwei Wang[1], Lietao Cai[3], Chaojun Zhang[3], Yuyang Zhao[4], Yan Jin[4], Dongfeng Yang[1], Zongsuo Liang[1,2], Xiaodan Zhang[1,2]*
1. Key Laboratory of Plant Secondary Metabolism and Regulation of Zhejiang Province, College of Life Sciences and Medicine, Zhejiang Sci-Tech University, Hangzhou 310018, China
2. Zhejiang Sci-Tech University Shaoxing Academy of Biomedicine Co., Ltd, Shaoxing, China
3. R&D Center of Kanglaite, Hangzhou, 310018, China
4. State Key Lab Breeding Base Dao-Di Herbs, National Resource Center Chinese Materia Medica, Beijing, China Academy of Chinese Medical Sciences, Beijing, 100700, China

Coix (*Coix lacryma-jobi L.*), known as a medicinal and edible plant, yields seed kernels with an average oil content ranging from 5% to 10%. *Coix* oil is noted for its ability to hinder the proliferation of cancerous tissues and its overall health benefits which bolster human resistance. This study aimed to elucidate the molecular mechanisms of oil biosynthesis in *Coix*, focusing on the WRI1 (WRINKLED1) transcription factor family. Through transcriptomics, lipidomics, and functional validation in yeast and Arabidopsis, the regulatory role of the *Coix* WRI1 family was revealed.Oil biosynthesis in *Coix* is primarily concentrated in the embryo, with key lipid metabolites significantly enriched. WGCNA identified a lipid-associated module (blue module) with ClWRI1-02 as a hub gene, highly expressed in the embryo and driving lipid accumulation by regulating glycolysis and fatty acid elongation pathways. A total of 20 WRI1 homologs were identified and categorized into three phylogenetic clades. Promoter analysis revealed that all members contained jasmonic acid-responsive elements (CGTCA-motif), indicating potential roles in integrating developmental and environmental signals.Tissue-specific expression profiling showed that ClWRI1-02 and ClWRI1-03 were predominantly expressed in seeds, while ClWRI1-18 and ClWRI1-20 were stem-enriched and significantly upregulated under stress. Subcellular localization confirmed that ClWRI1 proteins reside in the nucleus. Yeast two-hybrid assays demonstrated extensive protein-protein interactions, including between ClWRI1-02 and ClWRI1-20. Overexpression of ClWRI1-02 in yeast and Arabidopsis significantly increased lipid, upregulating key genes involved in glycolysis, fatty acid biosynthesis, and oil body assembly. ClWRI1 was identified as a key regulator of oil biosynthesis in *Coix*, providing valuable genetic resources for breeding high-oil varieties.

P46: Study of Dihydrotanshinone I Inhibiting Colorectal Cancer Growth by Regulating the LAMA5/ITGB8-Mediated Hippo Pathway

Shengqian Deng[1], Chengtao Sun[1], Guoyin Kai[1]
[1]Zhejiang Provincial International S&T Cooperation Base for Active Ingredients of Medicinal and Edible Plants and Health, School of Pharmaceutical Science, The First Affiliated Hospital, Zhejiang Chinese Medical University, Hangzhou 310053, China

Colorectal cancer (CRC) is a highly prevalent malignant tumor of the digestive tract, and its incidence rate and mortality continue to rise worldwide. The limited efficacy of current clinical protocols, severe toxic side effects, and frequent drug resistance remain major treatment challenges, highlighting the urgent need for novel, effective, and low toxicity anti CRC drugs. In this study, we systematically investigated the anti-tumor activity of dihydrotanshinone I (DHT) on CRC and elucidated its potential molecular mechanism targeting the LAMA5/ITGB8 integrin Hippo signaling axis. In vitro functional experiments have shown that DHT dose dependently inhibits the proliferation, colony formation, migration, and invasion of CRC cells. In vivo studies using subcutaneous transplant tumor models have confirmed that DHT significantly inhibits tumor growth and has good biocompatibility. Comprehensive transcriptomics and untargeted metabolomics analysis showed that DHT intervention mainly disrupted the extracellular matrix (ECM) receptor interaction pathway and lipid metabolism pathway in CRC cells, and significantly downregulated the expression of core ECM components LAMA5 and ITGB8. Mechanistically, DHT inhibits the phosphorylation of focal adhesion kinase (FAK) downstream of ITGB8, thereby promoting YAP phosphorylation and isolating YAP in the cytoplasm, independent of the typical MST1/2-LATS1/2 kinase cascade. In vivo experiments have shown that overexpression of ITGB8 significantly accelerates the growth of xenografts and partially antagonizes the anti-tumor effect of DHT, while knockout of ITGB8 replicates the inhibitory effect of DHT on tumors and eliminates its further inhibitory activity. In addition, the MST1/2 kinase inhibitor XMU-MP-1 partially reversed tumor growth inhibition induced by DHT therapy or ITGB8 silencing. Overall, our research findings indicate that DHT exerts anti CRC effects by downregulating LAMA5/ITGB8 expression and inactivating YAP through the integrin Hippo signaling axis. This study not only elucidates the molecular mechanism of DHT anticancer therapy, but also provides promising therapeutic targets and scientific basis for the clinical translation of DHT in the treatment of colorectal cancer.

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P47: Targeting the Hepatic Saa Inflammatory Network: Gegen Qinlian Decoction Polysaccharide Remodels the Gut-Liver Axis to Improve Insulin Resistance

Dongwei Wang[1], Jun Yi[1], Yong Zhu[1], Yishan Tong[1], Xuwei Liu[3], Judyta Cielecka-Piontek[2], Jihang Chen[1]*
[1]School of Medicine, The Chinese University of Hong Kong, Shenzhen, Guangdong 518172, China
[2]Department of Pharmacognosy and Biomaterials, Poznan University of Medical Sciences, Rokietnicka 3 Str., 60-806 Poznan, Poland
[3]Guangdong Provincial Key Laboratory of Food Quality and Safety, College of Food Science, South China Agricultural University, Guangzhou 510642, China

Insulin resistance is a central pathological feature of metabolic diseases and is closely associated with gut microbiota dysbiosis and chronic inflammation[1]. This study investigated the beneficial effects and mechanisms of Gegen Qinlian Decoction polysaccharide (GQDP), an α-(1→4)-linked glucan isolated from the traditional Chinese formula Gegen Qinlian Decoction, on high-fat diet-induced insulin resistance[2]. Using a C57BL/6J mouse model, GQDP administration significantly improved glucose tolerance, enhanced insulin sensitivity, and reduced hepatic lipid accumulation. Integrated multi-omics analyses, including gut microbiome, intestinal metabolome, serum metabolome, and hepatic transcriptome profiling, revealed that GQDP reshaped the gut microbial community, particularly enriching beneficial bacteria such as *Lactobacillus johnsonii*. GQDP also regulated microbial and host metabolic profiles, especially pathways related to amino acid and lipid metabolism. Mechanistically, GQDP acted through the gut-liver axis to suppress hepatic inflammation by reducing the activation of the IL-6/JAK/STAT3 and NF-κB/IL-17 signaling pathways, thereby decreasing the hepatic Saa-centered acute-phase inflammatory network. These findings demonstrate that GQDP alleviates high-fat diet-induced insulin resistance through microbiota-driven metabolic and inflammatory reprogramming. This work provides new evidence supporting polysaccharides from traditional Chinese medicine as potential therapeutic agents for metabolic disorders.

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P48: Biosynthesis and Nutritional Mechanisms of Fucosylated Oligosaccharides

Chao Zhao*
College of Marine Sciences, Fujian Agricultural and Forestry University, Fuzhou 350002, China

Fucosylated oligosaccharides are a class of sugar chains formed by the attachment of fucose to oligosaccharide molecules catalysed by fucosyltransferases. These oligosaccharides have a wide range of bioactivities and important physiological functions with benefits for human health, including the promotion of neurodevelopment, the establishment of intestinal barriers, and the maturation of the immune system[1]. Previous studies have shown that lactoyl-N-fucoidan I (LNFPI) has a significant antiviral effect on hand-foot-mouth disease caused by enterovirus 71 (EV71)[2]. It not only attenuated the host inflammatory storm triggered by EV71 infection, but also significantly inhibited the proliferation of EV71 in a dose-dependent manner. In addition, EV71 infection leads to abnormal energy metabolism in host cells, which creates a favourable environment for viral replication, and LNFPI treatment was able to effectively reverse EV71-induced aberrant glycolysis in the host and reduce the number of cytopathic lesions. In in vitro cellular experiments, when LNFPI reaches a certain concentration, it can significantly inhibit the replication of EV71 capsid protein VP1 and reduce the damage of the virus to cells. LNFPI can be obtained by four ways: biological extraction, enzymatic synthesis, chemical synthesis and biosynthesis.In the previous study, the group isolated an efficient and stable α-1,2-fucosyltransferase (Te2FT) from thermophilic cyanobacteria, and successfully synthesised LNFPI using a highly efficient one-pot multi-enzymatic fucosylation system with lactose-N-tetrasaccharide (LNT) and GDP-fucose (GDP-L-Fucose) as the substrates with the yield as high as 94%. In recent years, the group further used *Escherichia coli* as a biosynthetic chassis, and systematically designed and modified the sugar metabolic pathway of the chassis strain using CRISPR-Cpf1 as a gene editing tool to achieve the biosynthesis of the LNFPI precursors LNT and LNTII. At present, the group has successfully constructed the first strain without plasmid to synthesise LNFPI from scratch, which provides a broad prospect for the stable and efficient production of LNFPI.

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P49: Analysis of Composition and Study on Antioxidant Activity Mechanism of *Rubus chingii* Fruit Juice

Hongju Li[1], Zheng Xiang[2], Xiaodan Zhang[1]*
[1]College of Life Sciences and Medicine, Zhejiang Sci-Tech University, Hangzhou 310018, China
[2]Medical School, Hangzhou City University, Hangzhou 310015, China

This study explored the medicinal properties of *Rubus chingii* fruit juice. The total flavonoid and phenolic content of the fruit juice was determined by sodium nitroprusside-aluminum nitrate colorimetry and the Folin-Ciocalteu method, and the results showed that the fruit juice had high levels of these compounds. The DPPH, ABTS and FRAP tests revealed that it had significant in vitro antioxidant activity. A total of 198 compounds in the fruit juice were identified by ultrahigh-performance liquid chromatography coupled with quadrupole-orbitrap mass spectrometry (UPLC-Q-Orbitrap-MS). Non-targeted metabolomics showed that the fruit juice could reverse 31 metabolites in mice with ethanol-induced liver injury. Metagenomic sequencing indicated that the fruit juice could regulate gut microbiota. Molecular docking and Western blot assays demonstrated that it worked by modulating CDK1 and COX2. Overall, the study provided a theoretical basis for the antioxidant and liver-protective effects of *Rubus chingii* Hu fruit juice, confirmed its protective effect against ethanol-induced oxidative liver injury in mice, and supported the development of *Rubus chingii* Hu-related health products.

P50: Medicine-Food Homologous Citrus Alleviated High-fat Diet-induced Obesity via Modulation of the Gut Microbiota

Yixin Hu[1], Jiebiao Chen[1,2], Jiaojiao Liang[1], Yunyi Chen[1], Hui Xu[1], Yue Wang[1], Jinping Cao[1], Haizhen Zhang[2], Chongde Sun[1]*
[1]Fruit Science Institute, College of Agriculture and Biotechnology, Zhejiang University, Hangzhou, People's Republic of China
[2]Hangzhou Botanical Garden, Hangzhou West Lake Academy of Landscape Science, Hangzhou, People's Republic of China

The rising prevalence of obesity underscores the need for safe, sustainable dietary interventions. Medicine-food homologous (MFH) citrus species possess nutritional and pharmacological potential, yet their functional diversity remains unclear. This study characterized the phytochemical profiles of five MFH citrus species (Daidaihua, Foshou, Huajuhong, Xinhui Chenpi, and Xiangyuan) and evaluated their comparative effects on gut microbiota and obesity in healthy and high-fat diet (HFD)-induced obese mice. High- performance liquid chromatography (HPLC) analysis revealed eight characteristic compounds, including three flavanone-O-glycosides (naringin, hesperidin, neohesperidin), three polymethoxyflavones (PMFs, nobiletin, tangeretin, 5-demethylnobiletin), one flavanone aglycone (naringenin), and one coumarin (5,7-dimethoxycoumarin), with each species exhibiting distinct profiles. All MFH citrus extracts were found to modulate the gut microbiota by increasing diversity, enriching beneficial genera (e.g., Akkermansia), and suppressing the opportunistic pathogen *Staphylococcus*. Metabolically, all MFH citrus significantly lowered fasting or random glucose, although dynamic glucose tolerance was not significantly improved; Daidaihua, Huajuhong, and Xiangyuan reduced serum triglyceride levels, while Foshou increased serum HDL-C level, inhibited weight gain and white adipose tissue accumulation. The identified characteristic compounds are likely responsible for the observed bioactivities. These findings suggest species-specific metabolic benefits potentially linked to gut microbiota modulation of MFH citrus, providing a preliminary basis for targeted development of citrus- derived functional foods for personalized nutrition.

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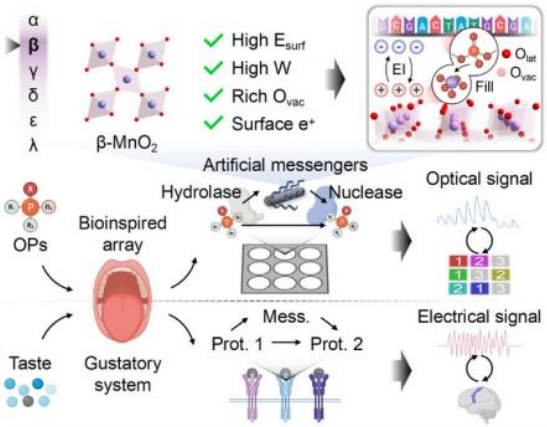
P51: Crystal Phase-Driven MnO_2-DNA as Editable Artificial Messengers Enabling a Bioinspired Array for High-Resolution Biosensing

Yi Liu, Jingyu Feng, Shuo Wang*, Haiyan Fu*
The Modernization Engineering Technology Research Center of Ethnic Minority Medicine of Hubei Province, School of Pharmaceutical Sciences, South-Central Minzu University, Wuhan 430074, China

High-precision identification of structurally similar compounds serves as a core technological foundation in research fields such as chemistry, biology, and medicine[1]. However, the current recognition mechanisms for structurally similar compounds using multi-channel array sensors exhibit homogenization and low sensitivity, making it difficult to achieve integrated qualitative-quantitative high-resolution biosensing[2]. This study proposes a high-resolution biosensor array constructed from a complex of β-phase MnO_2 nanomaterials and single-stranded DNA (ssDNA) for detecting structurally similar organophosphorus compounds[3]. By leveraging the adsorption and desorption properties of MnO_2 in different crystalline phases toward ssDNA, combined with a nuclease cascade reaction, a multi-channel sensor array was successfully developed. This array enables high-resolution detection of 19 organophosphorus compounds through digital encoding and machine learning algorithms. Experimental results demonstrated that the target compounds (e.g., chlorpyrifos) significantly enhance fluorescence signal output in the cascade reaction through interaction with the enzyme system, and the array exhibits strong selectivity and interference resistance. Studies demonstrate that this MnO_2-based multi-enzyme array provides a novel application paradigm for high-resolution biosensing, with significant potential in environmental monitoring and food safety detection.



Acknowledgments
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P52: Effects of Different Edible Mushroom Stipes as Partial Animal Fat Replacers on Gel Properties and Digestion Behavior of Pork Gels

Huizhi Chen[1], Xieyu Wang[1], Wei Xia[2], Hangjun Chen[1], Maratab Ali[1], Yangchao Yu[4], Weijie Wu[5], Yan Xu[3]*, Weijie Wu[1]*, Haiyan Gao[1]*
[1]Zhejiang Key Laboratory of Intelligent Food Logistic and Processing, Key laboratory of post-harvest handling of fruits, Ministry of Agriculture and Rural Affairs, Key Laboratory of Postharvest Preservation and Processing of Vegetables (Co-construction by Ministry and Province), Key laboratory of postharvest preservation and processing of fruits and vegetables, China National Light Industry, Food Science Institute, Zhejiang Academy of Agricultural Sciences, Hangzhou 310021, P. R. China
[2]Zhejiang International Joint Laboratory on Low-Carbon Pollution Control and Resource Utilization, College of Biological and Environmental Engineering, Zhejiang Shuren University, Hangzhou, 310015, P. R. China
[3]School of Food and Pharmacy, Zhejiang Ocean University, Zhoushan, 316022, P. R. China
[4]Jiangsu Chinagreen Biological Technology Group Co., Ltd., Siyang, 223700, P. R. China
[5]Jiangsu Alphay Bio-technology Co., Ltd., Nantong, 226009, P. R. China

This study investigated the effects of five edible mushroom stipes as partial fat replacers on the gel properties and digestion behavior of minced pork gels. Incorporation of mushroom stipes significantly improved gel hardness, reduced cooking loss, improved water-holding capacity, and flavor characteristics, with *Lentinula edodes* stipes showing the most pronounced effects. Compared with the control, gels containing *Lentinula edodes* stipes exhibited a 1.1-fold increase in hardness ($P < 0.05$), cooking loss below 8%, and an increase in water-holding capacity from 79% to 85%. Low-field nuclear magnetic resonance and dynamic rheological analyses showed a shift in water distribution toward a semi-bound state with peak area ratio exceeding 90%, while elastic-dominant behavior ($G' > G''$) was maintained during heating. Microstructural and molecular interaction analyses indicated hydrogen-bond-dominated noncovalent interactions, resulting to a denser and more uniform gel network. Digestion studies demonstrated that *Lentinula edodes* stipes maintained normal gastric protein hydrolysis while modulating intestinal digestion and promoting beneficial short-chain fatty acid production during fermentation. These findings suggest the *Lentinula edodes* stipes are promising natural fat replacers for improving the structural and digestion-related functionality of low-fat minced pork gels.

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P53: Anti-Psoriasis Effects of *Salvia officinalis*-Derived Vesicles

Jingbin Zheng[1,2], Zhangfeng Zhong[1,2]*
[1]Macao Centre for Research and Development in Chinese Medicine, Institute of Chinese Medical Sciences, University of Macau, Macao SAR 999078, China
[2]Zhuhai UM Science and Technology Research Institute, Zhuhai 519031, China

Psoriasis is an intractable chronic inflammatory skin disorder lacking safe long-term therapeutic regimens[1]. Plant-derived vesicles (PDVs) display remarkable anti-inflammatory properties accompanied by low cytotoxicity[2]. *Salvia officinalis*-derived vesicles (SODVs), loaded with abundant microRNAs, lipids, proteins, and metabolites, possess favorable nanovesicle physicochemical features and transdermal delivery effects. Nevertheless, the potential therapeutic efficacy of PDVs against psoriasis has not been comprehensively verified. In the present study, we were aiming to explore the potential PDVs against psoriasis. We firstly characterized the morphological structure, particle size distribution and microRNA expression profiles of SODVs. Cellular uptake experiments confirmed that human keratinocytes could efficiently internalize SODVs. Furthermore, an imiquimod (IMQ)-triggered murine psoriasis-like dermatitis model was established to assess the alleviative effects of SODVs on inflammatory skin lesions. Collectively, our findings validate the anti-psoriatic potential of SODVs, which provides a novel and natural biomaterial candidate for the intervention of psoriasis and related inflammatory skin diseases.

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P54: A Hierarchical Design of Zein-Pectin Stabilized Double Emulsion Gel for Enhanced Anthocyanins Delivery: Interfacial and Gel-Network Synergy

Ming Yin[1], Haopeng Zhang[1], Ruiling Liu[1], Xiangjun Fang[1], Weijie Wu[1], Huizhi Chen[1]*, Haiyan Gao[1]*
[1]Zhejiang Key Laboratory of Intelligent Food Logistic and Processing, Key laboratory of post-harvest handling of fruits, Ministry of Agriculture and Rural Affairs, Key Laboratory of Postharvest Preservation and Processing of Vegetables (Co-construction by Ministry and Province), Key laboratory of postharvest preservation and processing of fruits and vegetables, China National Light Industry, Food Science Institute, Zhejiang Academy of Agricultural Sciences, Hangzhou 310021, P. R. China

A hierarchical double-emulsion gel based on zein-pectin composites was fabricated to protect anthocyanins (ACNs) and modulate their gastrointestinal release. Zein-high methoxyl pectin (HMP) particles at a 1:2 ratio afforded optimal interfacial properties and an encapsulation efficiency of 93.4%. Subsequent Ca^{2+}-induced cross-linking of low-methoxyl pectin, optimized at 3% $CaCl_2$, generated a dense gel network, as evidenced by rheological, textural, and water-distribution analyses. This dual architecture conferred marked resistance to light and heat induced degradation, delayed gastric efflux, and sustained intestinal release, with Ritger–Peppas kinetics indicating anomalous diffusion coupled with matrix swelling and erosion. In alcohol-challenged mice, gel-loaded ACNs significantly attenuated hepatic steatosis, transaminase elevation, oxidative stress (GSH, SOD, CAT), and pro-inflammatory cytokines (TNF-α, IL-1β, IL-6), while restoring IL-10. The combined interfacial shielding and gel-network confinement thus offer a mechanistic rationale for enhancing both the physicochemical stability and in vivo hepatoprotective efficacy of labile polyphenols.

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P55: *Cynomorium songaricum* Flavonoid-Enriched Fraction and Procyanidin C1 Protect Skeletal Muscle in Type 2 Diabetes-Associated Sarcopenia

Yi Shan Tong[1]*, Ji Hang Chen[1]
[1]Shenzhen Key Laboratory of Steroid Drug Discovery and Development, School of Medicine, The Chinese University of Hong Kong, Shenzhen, Guangdong, 518172, China

Diabetic sarcopenia is characterized by metabolic dysfunction accompanied by progressive loss of skeletal muscle mass and function [1]. *Cynomorium songaricum* is an edible medicinal plant rich in flavonoids and polyphenols with potential metabolic and myoprotective activities. In our previous study, *Cynomorium songaricum* Flavonoid-Enriched Fraction (CSF) was prepared from *Cynomorium songaricum* by 70% ethanol reflux extraction followed by AB-8 macroporous resin enrichment, and 36 flavonoid compounds were identified by UHPLC-Q-Exactive Orbitrap MS/MS, with catechin, epicatechin gallate, procyanidin C1 (PC1), and ellagic acid as relatively abundant constituents [2]. The present study further investigated the myoprotective effects of CSF and its representative active compound PC1. A stable lipotoxic muscle atrophy model was established by exposing differentiated C2C12 myotubes to palmitic acid. CSF and PC1 reduced intracellular lipid accumulation, attenuated myotube atrophy, preserved myosin heavy chain expression, and increased the expression of the myogenic differentiation marker myogenin, suggesting that PC1 may be an important myoprotective constituent of CSF. A high-fat diet-induced mouse model of diabetic sarcopenia was subsequently established. Treatments with CSF and PC1 alleviated skeletal muscle fiber disorganization, collagen deposition, mitochondrial ultrastructural damage, and metabolic abnormalities. Skeletal muscle transcriptomic analysis showed that both interventions regulated biological processes related to lipid metabolism, muscle structural development, and cytoskeletal remodeling. Notably, the Apelin signaling pathway was commonly enriched following CSF and PC1 treatment. Molecular validation further demonstrated partial restoration of Apln and Aplnr expression and increased MyoG protein levels in skeletal muscle. These findings indicate that CSF and PC1 exert coordinated metabolic and myogenic protective effects against diabetic sarcopenia, potentially associated with the regulation of the Apelin/APJ signaling axis. PC1 may therefore represent an important functional constituent of CSF for developing nutritional interventions targeting diabetes-associated skeletal muscle dysfunction.

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P56: A Prebiotic α-Glucan from *Pseudostellaria heterophylla* Targets the Microbiota-OEA-Brain Axis to Alleviate Alzheimer's Pathology

Xiaobo Kang[1], Longjian Zhou[1], Yi Zhang[1], Yuewei Ge[2], Yuntao Zhao[1], Zhiyou Yang[1]*
[1]College of Food Science and Technology, Shenzhen Institute of Guangdong Ocean University, Guangdong Provincial Key Laboratory of Aquatic Product Processing and Safety, Guangdong Province Engineering Laboratory for Marine Biological Products, Zhanjiang Municipal Key Laboratory of Marine Drugs and Nutrition for Brain Health, Guangdong Ocean University, Zhanjiang 524088, China
[2]Key Laboratory of Digital Quality Evaluation of Chinese Materia Medica of State Administration of TCM, Guangdong Pharmaceutical University, Guangzhou 510006, China

Alzheimer's disease (AD) is a progressive neurodegenerative disorder characterized by amyloid-beta (Aβ) plaque accumulation, chronic neuroinflammation, and cognitive decline, for which effective multi-targeted therapeutic strategies remain urgently needed. Natural bioactive polysaccharides have emerged as promising candidates due to their pleiotropic pharmacological properties and favorable safety profiles. This study aimed to purify and structurally define the neuroprotective polysaccharide from *Pseudostellaria heterophylla* and elucidate its microbiota-dependent mechanisms against AD-like pathology. Using bioactivity-guided fractionation coupled with an $A\beta_{1-42}$-induced zebrafish model, we isolated the active polysaccharide PF30-1, characterized as a branched α-D-glucan (17.18 kDa) with a →4)-Glcp-(1→ linked backbone and Glcp-(1→6)-branched residues. Oral administration of PF30-1 to APP/PS1 mice attenuated cognitive impairments, reduced Aβ plaque burden, preserved synaptic integrity, suppressed neuroinflammation, and restored intestinal barrier function. Antibiotic-induced microbiota depletion abolished these effects, demonstrating the essential role of gut microbes in mediating PF30-1's neuroprotection. Mechanistically, PF30-1 enriched *Lactobacillus*-related taxa and elevated serum levels of 9-Octadecenamide (OEA) and glycerophospholipid metabolites. Exogenous OEA recapitulated PF30-1's neuroprotective effects in 5×FAD mice. Transcriptomic and immunoblotting analyses revealed that both PF30-1 and OEA convergently upregulated PLA2G4E and activated the PPARα/AMPK–TFEB–LAMP2 lysosomal clearance pathway. These findings establish PF30-1 as a structurally defined prebiotic α-glucan that targets the microbiota-OEA-brain axis to alleviate AD pathology via PLA2G4E–PPARα/AMPK–TFEB–LAMP2 signaling, providing a mechanistic framework for *P. heterophylla-derived* polysaccharides as phytomedicine candidates against AD.

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P57: Yitangkang Decoction Ameliorates Renal Fibrosis in Diabetic Kidney Disease via Suppressing Ferroptosis through the STAT3-PECR Transcriptional Axis

Jiaxiang Yu[1], Hanwen Zhang[2], Yi Wu[3], Yan Shi[2], Wenshun Zhang[3]*
[1]College of Health Preservation and Rehabilitation, Liaoning University of Traditional Chinese Medicine, Shenyang,110847, China
[2]College of Basic Medical Sciences, Liaoning University of Traditional Chinese Medicine, Shenyang,110847, China
[3]Liaoning Province Traditional Chinese Medicine Research Institute, Shenyang,110034, China

Aim of the study: This study aimed to elucidate the mechanism by which Yitangkang decoction (YTK) ameliorates renal fibrosis in diabetic kidney disease (DKD), with a focus on ferroptosis and the STAT3-PECR transcriptional axis. Material and methods: Sixteen-week-old db/db mice (DKD model) were treated with YTK water extract or a positive control (finerenone) by gavage for 12 weeks, with db/m mice as the normal control. General conditions, renal function, including FBG, Scr, BUN, UACR, NAG, and β2-MG, and systemic inflammatory cytokines, including TNF-α, IL-1β, IL-6, and CCL2, were evaluated. Renal pathological injury and fibrosis were assessed by HE, Masson, and PAS staining, and tubular integrity was assessed by immunohistochemistry for AQP1, ZO-1, and E-cadherin. Ferroptosis markers, including MDA, GSH, Fe^{2+}, SOD, CAT, GSH-Px, 4-HNE, 8-OHdG, GPX4, SLC7A11, and FTH1, and key proteins of the STAT3-PECR and Nrf2/HO-1 pathways were measured. Single-cell RNA sequencing was performed to profile renal cell subpopulations and ferroptosis-related gene signatures. In vitro, HK-2 cells cultured under high glucose were treated with Corydalmine (the active monomer of YTK); cell viability, injury, ATP, mitochondrial membrane potential, Lipid-ROS, and ferroptosis-related proteins were examined. Molecular docking, surface plasmon resonance (SPR), cellular thermal shift assay (CETSA), dual-luciferase reporter assays, and ChIP-qPCR were used to validate the direct binding of Corydalmine to STAT3 and its regulation of the PECR promoter activity. Results: YTK treatment significantly improved general status and renal function, reduced systemic inflammation, attenuated renal tubular injury and fibrosis, and suppressed ferroptosis in DKD mice. Single-cell sequencing revealed that YTK reshaped the renal cell landscape, particularly reducing ferroptosis signatures in proximal tubular subpopulations. Corydalmine protected HK-2 cells against high-glucose-induced injury and ferroptosis, as evidenced by increased viability, ATP, and mitochondrial function, and decreased LDH, MDA, and Lipid-ROS. Mechanistically, corydalmine directly bound to STAT3, inhibited its phosphorylation, and downregulated PECR expression. Overexpression of STAT3 enhanced the PECR promoter activity, and ChIP-qPCR confirmed that STAT3 directly binds to the PECR promoter. Moreover, PECR overexpression reversed the protective effects of corydalmine. Conclusion: YTK ameliorates DKD renal fibrosis by suppressing ferroptosis via its active monomer, corydalmine, which directly targets STAT3 and inhibits PECR transcription. These findings provide a novel mechanistic basis for YTK as a therapeutic agent against DKD.

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P58: The Conversion of Black Chokeberry Condensed Tannins into Anthocyanins Have a Better Repair Effect on Imbalance of Gut Microbiota Caused by High-Salt Diet

Ningxuan Gao[1], Bin Li[1]*
[1]Shenyang Agricultural University, College of Food Science, Shenyang, China

Black chokeberry is rich in polyphenols such as cyanidins, which makes it have a good effect on regulating intestinal flora[1,2]. However, in these polyphenols, different polyphenols show completely different activities due to the difference in their molecular structure. Especially the proanthocyanidins which account for the largest proportion, because of the high polymerization of proanthocyanidins in black chokeberry, it has the characteristics of low activity and can not be absorbed by the human body[3]. If these polymeric proanthocyanidins can be converted into cyanidins with high activity by means of processing, it can greatly improve the regulation of intestinal flora of black chokeberry[4,5]. Especially the destruction of specific intestinal flora caused by high-salt diet. In this study, black chokeberry was used as the material, on the basis of not reducing its antioxidant activity, by means of converting the black chokeberry components which had low contribution to the regulation of intestinal flora into substances with high contribution to intestinal flora, through the effective regulation of intestinal flora, and then inhibit the imbalance of intestinal flora caused by high-salt diet. Through the analysis of total antioxidant activity and cellular antioxidant activity, it can be proved that the conversion treatment black chokeberry extract was not at the expense of high antioxidant activity to obtain better regulation of intestinal flora. On the contrary, its antioxidant activity has been further improved. Through the analysis, we found that the high-salt diet can destroy the structure of the intestinal flora, especially the inhibition of *Lactobacillus*. Intervention with conversion treatment black chokeberry extract significantly improved the relative abundance of *Lactobacillus* and Bifidobacterium in the intestinal flora of rats fed a high-salt diet.

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P59: Supramolecular Self-Assembled *Polygonatum* Sibiricum Polysaccharides-Based Hydrogel for Suspension 3D Printed Diabetic Wound Dressing

Yong Zhu[1]*, Jihang Chen[1]*
[1]Shenzhen Key Laboratory of Steroid Drug Discovery and Development, School of Medicine, The Chinese University of Hong Kong, Shenzhen, Guangdong, 518172, China

Diabetic wounds (DW) are affected by factors such as chronic inflammation, oxidative stress, and infection risks [1], and are serious chronic complications of diabetes that pose a significant threat to public health. Developing personalized dressings that are compatible with wound morphology, manage exudates, and have multiple biological activities is an important strategy for achieving precise DW repair [2,3]. This study constructs a PSP/CS hydrogel wound dressing based on the supramolecular self-assembly effect between *Polygonatum* Sibiricum polysaccharides (PSP) and chitosan (CS) and combined with suspension 3D printing technology [4]. The resulting hydrogel has a continuous three-dimensional porous network and adjustable pore size (0.67–13.67 μm), and exhibits good structural stability ($G' \gg G''$, $\tan\delta<1$), mechanical properties (compression modulus 0.76 kPa), swelling ability (2673±65%), and water retention properties (78.26±1.58%). Molecular dynamics simulation and experimental verification indicate that hydrogen bonds are the main driving force for the formation of the PSP/CS hydrogel network. In vitro experiments show that the PSP/CS hydrogel has better hemostasis, coagulation promotion, cell migration promotion, antioxidant, and antibacterial capabilities compared to pure CS hydrogel. In the diabetic wound model in vivo, the wound closure rate of the hydrogel treatment group reached 85.83% on the 3rd day and 98.67% on the 14th day; histological results show that it can promote collagen deposition, granulation tissue formation, and skin appendage regeneration. In summary, the PSP/CS supramolecular self-assembled hydrogel has printing formability, moist wound healing regulation, and multi-dimensional promoting repair activity, and has good application potential in personalized wound repair of diabetes and provides a new idea for the design of drug-active polysaccharide-based hydrogel dressings.

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P60: Green Modification Strategy for Legume Proteins: Pulsed Electric Field-Mediated Unfolding and Refolding of Globulin

Yongxin Teng[1]
[1]College of Biological Science and Engineering, Fuzhou University, Fuzhou 350108, Fujian, China

Driven by health and sustainability demands, plant proteins are emerging as mainstream food proteins; however, their dense native structures and poor processing properties severely limit industrial applications [1]. Conventional pH-shifting utilizes electrostatic repulsion in extreme environments to induce unfolding, followed by refolding during neutralization into a "molten globule" state[2]. Although this intermediate retains secondary structures and exposes hydrophobic groups to improve physicochemical properties, it consumes excessive strong acids/bases, causing inevitable high salt residues. To address this, we propose Pulsed Electric Field (PEF) as a green, additive-free physical alternative. PEF polarization forces the directional alignment of charged amino acid residues, disrupting non-covalent interactions (e.g., hydrogen bonds) to trigger structural unfolding and hydrophobic core exposure. During pulse intervals, proteins spontaneously refold. This physical "unfolding-refolding" achieves green modification comparable to pH-shifting[3,4]. Furthermore, to overcome PEF's reliance on extreme electric field intensities for modifying rigid structural proteins, we innovatively introduced a heterologous protein co-folding strategy[5]. By coupling PEF with this technique, a chickpea protein isolate-bovine serum albumin (CPI-BSA) binary composite was constructed. This synergistic approach compensates for single-field limitations, significantly enhancing the functional properties and nutritional value of plant proteins. Ultimately, this research provides a novel theoretical and technical pathway for the green, high-performance processing of plant-based proteins.

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P61: Plant-Derived Exosome-like Nanovesicles as New Functional Ingredients and Their Applications

Zhenzhu Zhu
College of Food Science and Engineering, Nanjing University of Finance and Economics, Nanjing, 210023, China

Plant-derived exosome-like nanovesicles (PELNs) play an important role in transferring their biological cargos to recipient cells. PELNs are highly biocompatible, biodegradable, and stable, exhibit low immunogenicity. PELNs have emerged as a type of bioactive component discovered in foods and exhibit excellent functions. The extraction of exosome-like vesicles from edible plants, fungi and bacteria are used several traditional methods[1]. Garlic-derived exosome-like nanovesicles (GELNs) and soybean-derived exosome-like nanovesicles (SELNs) were isolated and purified by ultracentrifugation and sucrose density gradient centrifugation methods. The effect of GELNs against inflammatory bowel disease (IBD) was explored. Data showed that specific miRNAs carried by GELNs were predicted to target the inflammatory-related genes in the recipient cells. GELNs significantly up-regulated the expression of barrier-related proteins and inhibited the overproduction of pro-inflammatory cytokines in LPS-induced Caco-2 cells, which was closely related to toll-like receptor 4 (TLR4). As a result, pretreatment with GELNs at a moderate dosage (100 mg/kg) efficiently ameliorated inflammatory bowel behavior, intestinal histological pathological damage, and tight junction proteins dysfunction induced by dextran sulphate sodium (DSS) in the colon tissue. Intake of GELNs had a potential to protect colon against DSS-induced damage through inhibiting the TLR4/MyD88/NF-κB signaling pathway. This study identified the main components of GELNs and proved that GELNs had a potential application for IBD prevention[2]. The effect of SELNs on lipid metabolism was investigated. The stability of SELNs was evaluated by in vitro digestion simulation. Sodium palmitate (SP)-induce hyperlipidemic *C. elegans* model and the human adipocytes model were used. Results showed that SELNs was stable in the stomach acid environment and ruptures in intestinal fluid. Intake moderate of SELNs have potential to regulate the expression of key genes of lipid metabolism (fat-5, fat-6 and fat-7), inhibit lipid droplet generation, reduce lipid deposition. Therefore, SELNs exhibit the promising anti-adipogenic activity[3]. In addition, PELNs–based drug delivery system boosts phytochemicals' therapeutic effect for neurodegenerative diseases[4]. Herein, plant-derived exosome-like nanovesicles are promising functional ingredients and exhibit multiple applications in food and medicine industry.

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P62: Pulvis Fellis Suis Ameliorates Metabolic Dysfunction-associated Steatotic Liver Disease through the Synergistic Regulation of the Farnesoid X Receptor in Hepatic and Intestinal Tissues in Mice

Hui Li, Songsong Wang*
School of Pharmaceutical Sciences & Institute of Materia Medica, Shandong First Medical University & Shandong Academy of Medical Sciences, Jinan 250017, P.R. China

The pathogenesis of metabolic dysfunction-associated steatotic liver disease (MASLD) is intricate, necessitating the coordinated involvement of multiple organs for effective treatmen[1,2]. Pulvis Fellis Suis (PFS), a traditional Chinese medicinal substance derived from pig bile, may exert therapeutic effects on MASLD through its action on multiple organs[3]. However, the underlying molecular mechanisms of PFS in MASLD remain unclear. In this study, offline two-dimensional liquid chromatography-mass spectrometry (2D-LC-MS) was employed to characterize the chemical composition of PFS[4], and the therapeutic effects of PFS were evaluated using established cell, zebrafish, and mouse models of MASLD. Multi-omics analyses, including transcriptomics, proteomics, and metabolomics, combined with Western blotting (WB), reverse transcription quantitative polymerase chain reaction (RT-qPCR), and immunofluorescence, were employed to elucidate and verify the underlying molecular mechanisms. A total of 139 bile acids were identified in PFS, and administration of PFS significantly alleviated hepatic steatosis, inflammatory responses, and serum lipid metabolic disorders. In the liver, PFS activated hepatic farnesoid X receptor (FXR) signaling, thereby facilitating the synthesis and excretion of hepatic bile acids, regulating bile acid pool homeostasis, and regulating lipid metabolism[5]. Meanwhile, PFS enhanced intestinal FXR signaling, which suppressed intestinal fatty acid uptake and promoted cholesterol efflux, thus decreasing lipid influx to the liver and effectively mitigating hepatic lipid accumulation. PFS exerts protective effects by coordinating FXR signaling in both hepatic and intestinal tissues, significantly reducing lipid accumulation and alleviating MASLD[6].

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P63: Anti-Alzheimer Natural Products from Marine Fungi and Seaweeds

Yi Zhang[1,2*], Longjian Zhou[1,2], Zhiyou Yang[1,2], Yayue Liu[1,2], Yongping Zhang[1,2]
[1]College of Food Science and Technology, Guangdong Ocean University, Zhanjiang 524088, China
[2]Shenzhen Institute of Guangdong Ocean University, Shenzhen 518120, China

Alzheimer's disease (AD) has been severely threatening the global public health. The damage and loss of neurons in central nerve system and their dysfunction are the critical pathology. The previous studies indicated that oxidative stress and neuroinflammation play crucial and universe role in the occurrence and development of AD. Marine natural products (MNPs) are important source of new drug leading compounds. However, the anti-AD potential of MNPs is far from well investigated compared with their other usages.
In this lecture, we introduce our work on the anti-AD MNPs from marine fungi and seaweeds which possess the advantage of sustainable utilization. A compound butyrolactone I from a marine coral derived fungus *Aspergillus terreus* exhibited remarkable neuroprotective effects on amyloid peptide $A\beta_{25-35}$ induced neuronal injury in PC-12 cells and on 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine (MPTP) induced injury in SH-SY5Y cells. Besides, it also displayed anti-inflammatory activity on LPS induced BV-2 cells with NF-KB as possible key target. On $AlCl_3$ and LPS induced zebrafish memory deficient models and in Aβ induced AD mouse model, this compound also showed significant cognition improving effect and in vivo antioxidant, anti-neuroinflammatory, and cholinergy enhancing activities. In addition, a lipid subfraction HFFO extracted from an edible seaweed *Hizikia fusiforme* displayed acetylcholinesterase (AChE) inhibition, antioxidation, and anti-neuroinflammation activities. GC-MS analysis and bioactivity tracing indicated that arachidonic acid (ARA) and 11,14,17-eicosatrienoic acid (ETrA) are its main AChE inhibitory components. Furthermore, a microcapsule (HFFOM) was prepared by subcritical extraction and complex coacervation method, which exhibited acceptable stability and improves LPS induced zebrafish memory impairment and enhances normal rodents memory and cognition.
The above results showed good prospective of marine fungal and algal natural products in AD preventing or treatment.

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P64: Unveiling the Structure-Activity Relationships of Gonggan Mandarin Pectin: From Molecular Characterization to Processing Innovationand Juice Quality Enhancement

Zhang Shudie, Lui Huifan, Xie Xi, Liu Dongjie, Peng Jinming, Xiao Gengsheng, Wang Qin
[1]Key Laboratory of Green Processing and Intelligent Manufacturing of Lingnan Specialty Food of Ministry and Rural Affairs, College of Light Industry and Food, Zhongkai University of Agriculture and Engineering, Guangzhou, 510225, China
[2]Guangdong Provincial Key Laboratory of Lingnan Specialty Food Science and Technology, Zhongkai University of Agriculture and Engineering, Guangzhou, 510225, China
[3]Lingnan Special Food-Medicine Homology Diet Nutrition and Health Engineering Research Center, Guangzhou, 510225, China

Previous work on Lingnan pomelo fruitlets showed that mechanical injury disrupted cellular organization and activated flavonoid-associated antioxidant defenses, indicating that citrus tissues undergo coordinated structural and biochemical remodeling under external stress[错误!不能识别的开关参数。]. Against this background, Gonggan mandarin pectin was examined as a determinant of cloudy-juice stability, aroma retention, and biological activity. Molecular characterization revealed differences in backbone organization, branching, functional groups, and aggregation, providing a basis for interpreting processing-induced changes. High-pressure homogenization disrupted cell-wall structures and increased soluble pectin release by 94.26% at 400 bar. At this pressure, the volatile profile became terpene-dominant, whereas 600 bar promoted undesirable flavor formation[错误!不能识别的开关参数。]. Thermal sterilization induced pectin depolymerization, aggregation, and local structural rearrangement. Treatment at 80°C preserved turbidity and citrus–floral notes more effectively than treatment at 100 or 120°C[错误!不能识别的开关参数。]. Enzymatic hydrolysis cleaved pectin backbones, reduced molecular weight and methyl esterification, and converted compact aggregates into dispersed, porous structures. Increased structural flexibility was accompanied by stronger anti-inflammatory activity, including MAPK/ERK suppression and lower iNOS and COX-2 expression[错误!不能识别的开关参数。]. Beyond pectin modification, process-compatible α-L-rhamnosidase and cold-active protease-based systems were developed for citrus debittering and mild whole-fruit processing[错误!不能识别的开关参数。,错误!不能识别的开关参数。]. These findings link pectin architecture with processing response, juice quality, and functional performance, providing a practical basis for improving Gonggan cloudy-juice stability and aroma.

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P65: Development of a Scalable Vascularized Chip Platform Using Cell Line-derived Lung 3D Structures For Tumor Modeling and Drug Evaluation

Taeyeon Kwon[1], Bumjun Park[2], and Yun Suk Huh[1]*
[1]Department of Biological Sciences and Bioengineering, Inha University, Incheon, Republic of Korea
[2]Department of Bioengineering, University of Pennsylvania, Philadelphia, PA 19104, USA

Lung diseases and lung cancer are among the leading causes of mortality worldwide. However, conventional 2D cell culture and animal-based models do not adequately recapitulate the complex physiological and pathological microenvironment of human lung tissue. In particular, the development, metastasis, and drug responsiveness of lung cancer are strongly influenced not only by tumor cells but also by the tumor microenvironment, in which blood vessels, stromal cells, and the extracellular matrix interact in a highly coordinated manner. Therefore, there is a growing need for biomimetic platforms capable of reproducing these features with high precision. This study aims to establish a lung-on-a-chip platform that can simultaneously reflect lung-specific function and the tumor microenvironment by forming normal and cancerous lung 3D structures using a custom-designed U-shaped PDMS platform and inducing vascularization within a microfluidic chip. Normal and cancerous lung 3D structures were generated using HPAEpiC and A549 cells, respectively, and vascularization was induced in the chip by co-culturing HUVECs and NHLFs. Histological analysis showed that, compared with spheroid-like structures, organoid-like structures formed an internal lumen-like architecture. Fluorescence-based analysis of cisplatin treatment further demonstrated that the 3D structures exhibited greater drug resistance than 2D cultures, likely due to limited drug penetration caused by their dense outer layer. In addition, simulation of solution leakage according to micropillar spacing revealed that leakage into the side channel increased when the spacing exceeded 0.2 mm, and this finding was used to optimize the chip design for vascular formation. In future studies, the organoid-like structures and vascular chip will be integrated to quantitatively analyze vascular-mediated metastatic behavior and cellular responses following treatment with drug carriers, thereby validating the platform as a useful tool for modeling lung cancer metastasis and evaluating therapeutic responses.

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P66: Morroniside Ameliorates Diabetic Kidney Disease Proteinuria by Targeting Drp1 and Preserving Glomerular Filtration Barrier Integrity via Inhibition of Its Ubiquitin-Proteasome Degradation

Jiaxiang Yu[1], Yi Wu[2], Yan Shi[3], Wenshun Zhang[2]*, Hanwen Zhang[3]*
[1]College of Health Preservation and Rehabilitation, Liaoning University of Traditional Chinese Medicine, Shenyang,110847, China
[2]Liaoning Province Traditional Chinese Medicine Research Institute, Shenyang,110034, China
[3]College of Basic Medical Sciences, Liaoning University of Traditional Chinese Medicine, Shenyang,110847, China

Aim of the study: This study aimed to investigate whether morroniside, an active compound derived from *Cornus officinalis*, protects against proteinuria in diabetic kidney disease (DKD) and to elucidate the underlying mechanism, focusing on its direct target protein, Drp1, and the regulation of Drp1 ubiquitination and proteasomal degradation. Material and methods: Sixteen-week-old db/db mice were treated with morroniside by gavage for 8 weeks. General metabolic parameters, renal function, including SCr, BUN, and cystatin C, as well as 24-h urine protein and urinary albumin-to-creatinine ratio (UACR), were assessed. Renal histopathology and fibrosis were evaluated by PAS and Sirius red staining, and glomerular ultrastructure by transmission electron microscopy. Expression of slit diaphragm proteins, including nephrin, podocin, and CD2AP, and endothelial junction proteins, including VE-cadherin and ZO-1, was measured by Western blot and immunofluorescence. To identify the direct target of morroniside, we used affinity-based chemical probes and binding assays. The direct interaction was validated by molecular docking, surface plasmon resonance, pull-down, and cellular thermal shift assays. Ubiquitination and proteasomal degradation of Drp1 were examined by cycloheximide chase, MG132 inhibition, and immunoprecipitation-ubiquitin blotting. CRISPR/Cas9-mediated knockout and overexpression of Drp1 in podocytes and glomerular endothelial cells in vitro, as well as podocyte-specific AAV-mediated Drp1 knockout in vivo, were performed to determine the dependency of morroniside's effects on Drp1. Results: Morroniside treatment significantly lowered random blood glucose and HbA1c, reduced 24-h urine protein and UACR, improved renal function, and attenuated glomerular mesangial expansion and collagen deposition. Ultrastructural analysis showed that Morroniside alleviated foot process effacement and glomerular basement membrane thickening. Molecularly, morroniside restored the expression of nephrin, podocin, CD2AP, VE-cadherin, and ZO-1, preserving the filtration barrier integrity. We identified Drp1 as the direct binding target of morroniside, with high affinity. Morroniside inhibited the ubiquitination of Drp1, prolonged its half-life, and prevented its proteasomal degradation. Knockout of Drp1 in cultured podocytes and endothelial cells completely abolished the protective effects of morroniside on cell integrity and barrier function, while Drp1 overexpression mimicked its protection. In vivo, podocyte-specific Drp1 knockout fully blocked the renoprotective actions of morroniside, including the reduction of proteinuria and the preservation of the glomerular filtration barrier. Conclusion: Morroniside ameliorates DKD proteinuria by directly targeting Drp1, inhibiting its ubiquitin-proteasome degradation, and thereby maintaining glomerular filtration barrier integrity. This work identifies a novel target and mechanistic pathway for morroniside in the treatment of DKD.

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P67: Embracing Natural Complexity: New Paradigms for Berry Puree Anthocyanin Stabilization

Xu Xie[1]*, Bin Li[1]
[1]Shenyang Agricultural University, College of Food Science, Shenyang, China

Berry processing often overlooks the inherent complexity of raw materials, favouring excessive processing into clarified juices. Such over-processing diminishes the berries' original flavour and nutritional quality. This report aims to challenge the conventional mindset of ‘over-processing’ by proposing a new processing paradigm that embraces complexity. We systematically elucidate how non-thermal processing combined with mesothermal treatment strategies can be adapted to the complex food matrix of berry puree. Content focuses on resolving the unclear dynamics of anthocyanins in whole berry puree within authentic systems, revealing key regulatory mechanisms for nutrients like anthocyanins during Medium-temperature processed conditions: through a multidimensional synergistic effect of ‘release-synthesis-degradation-protection’, maximising the retention and enrichment of bioactive compounds such as anthocyanins within the puree, while validating the stabilisation patterns of endogenous pectin. Ultimately, it elucidates how this novel paradigm achieves a transition from ‘simple sterilisation’ to ‘multidimensional steady-state regulation’. Furthermore, considering current global nutritional trends and consumer demand for authentic ingredients and minimal processing, we propose three innovative principles for berry processing to embrace the complexity of berry raw materials: (1) harnessing the inherent chemical, physical, biological, and nutritional potential of berries; (2) integrating optimal processing techniques capable of addressing berry complexity; (3) developing high-quality berry products aligned with clean label and minimal processing standards. Adherence to these principles will facilitate the development of technologies transforming raw materials into healthier, more sustainable berry products.

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P68: Synergistic Effects of Hyperoside and Salvianolic Acid B on Ameliorating Metabolic Dysfunction-associated Steatotic Liver Disease through FXR/NPC1L1-Mediated Lipid Homeostasis Regulation

Yaxing Li*, Songsong Wang[1]
[1]School of Pharmaceutical Sciences & Institute of Materia Medica, Shandong First MedicalUniversity & Shandong Academy of Medical Sciences, Jinan 250017, P.R. China

Metabolic dysfunction-associated steatotic liver disease (MASLD) is one of the most prevalent chronic liver diseases worldwide. Its incidence continues to rise with the increasing prevalence of obesity and metabolic disorders, and it may further progress to metabolic dysfunction-associated steatohepatitis, liver fibrosis, and hepatocellular carcinoma[1,2]. Currently, effective specific therapeutic drugs for MASLD remain limited, and multi-target combination interventions have gradually emerged as a promising strategy for the treatment of complex metabolic diseases. The combination of Salvianolic acid B (Sal B) and Hyperoside (Hyp) has been shown to ameliorate MASLD; however, the underlying synergistic mechanisms remain unclear. This study aimed to investigate the molecular mechanisms underlying the combined therapeutic effects of Sal B and Hyp against MASLD.Previous studies demonstrated that Hyp improves hepatic lipid accumulation in MASLD rats by activating the farnesoid X receptor (FXR) signaling pathway and regulating cholesterol metabolism as well as bile acid (BAs) synthesis and excretion[3]. Further investigations revealed that Sal B suppresses the expression of Niemann-Pick C1-like protein 1 (NPC1L1), a key intestinal cholesterol transporter, thereby reducing intestinal absorption of exogenous cholesterol and reabsorption of biliary cholesterol, ultimately disrupting the enterohepatic circulation of cholesterol[4,5]. Combined treatment with Sal B and Hyp restored lipid homeostasis in MASLD through multiple mechanisms. Specifically, the combination activated FXR signaling, regulated bile acid metabolism mediated by cholesterol 7α-hydroxylase (CYP7A1) and cholesterol 27α-hydroxylase (CYP27A1), and activated peroxisome proliferator-activated receptor α (PPARα) to promote fatty acid β-oxidation. Meanwhile, inhibition of NPC1L1 enhanced fecal cholesterol excretion and reduced intestinal lipid reabsorption. Collectively, Sal B and Hyp synergistically alleviated hepatic steatosis and lipotoxicity by restoring abnormal lipid metabolism in MASLD. This study elucidates the potential molecular mechanisms underlying the synergistic effects of Sal B and Hyp in the treatment of MASLD and provides new theoretical insights into multi-target combination therapy strategies based on FXR/NPC1L1-mediated gut–liver axis regulation.

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P69: Sequential Physical Field Pretreatment Modulates Tilapia Soup Quality: A Multi-Omics Investigation of Processing Order to Flavor and Nutrition

Jiaxuan Huang[1], Qiaoli Zhao[1]*, Di Huang[1], Zhuo Wang[1,2], Ziru Dai[3], Saiyi Zhong[1,2]*
[1]College of Food Science and Technology, Guangdong Ocean University, Zhanjiang 524088, China
[2]Shenzhen Research Institute, Guangdong Ocean University, Shenzhen, 518108, China
[3] College of Food Engineering, Beibu Gulf University, Qinzhou, 535011, China

Traditional tilapia soup production faces critical bottlenecks: low soluble solids release from fish tissue into broth, insufficient nutrient leaching, and severe flavor loss. Although individual physical treatments enhance soup quality, the sequential effects of distinct physical fields remain poorly characterized. This study investigated the effects of two physical field processing sequences (colloid milling followed by ultrasonication, CMUFS, and ultrasonication followed by colloid milling, UCMFS) on the microstructure, nutritional composition, flavor profile, and overall quality of tilapia soup, using untargeted metabolomics, volatilomics, electronic sensor technology, and correlation network analysis. Results showed that the CMUFS group produced smaller droplets ($D_{4,3}$=16.51 μm) and a more stable suspension, yet exhibited lower total hydrolyzed amino acid content (284.9 mg/100 mL) and a poorer amino acid score (13.4). This was attributed to initial shear-induced protein aggregation that could not be fully disrupted by subsequent ultrasonication, entrapping nutrients within dense matrices. Conversely, UCMFS achieved a higher amino acid score (24.9, 86% improvement) and richer flavor richness (electronic tongue richness value of 0.663), despite larger droplets ($D_{4,3}$=28.77 μm) and reduced stability. The sequence of ultrasonication followed by colloid milling avoids shear-induced protein aggregation, achieves thorough dispersion of the material, and reduces damage to the protein conformation caused by the shearing, enhancing substrate availability for Maillard reactions and lipid oxidation pathways. Metabolomics analysis identified 15 differential metabolites involved in lipid and amino acid metabolism, confirming UCMFS improves both nutritional value and flavor quality. These findings provide a theoretical basis for sequence-guided quality regulation of aquatic soup production.

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P70: Machine Learning-Driven Multimodal Optimization of Selenium Biotransformation and Flavor Profiling in Fermented Apple-Yacon Functional Beverages

Tao Guan[1], Jue Gong[1], Jiaxi Lin[1], Chella Perumal Palanisamy[2], Jinjin Pei[1], A.M. Abd El-Aty[3,4]
[1]College of Food Science and Technology, Guangdong Ocean University, Guangdong Provincial Key Laboratory of Aquatic Product Processing and Safety, Guangdong Province Engineering Laboratory for Marine Biological Products, Guangdong Provincial Engineering Technology Research Center of Seafood, Guangdong Provincial Engineering Technology Research Center of Prefabricated Seafood Processing and Quality Control, Zhanjiang 524088, China
[2]Department of Dermatology, Saveetha Medical College and Hospital, Saveetha Institute of Medical and Technical Sciences (SIMATS), Chennai, 602105, India
[3]Department of Pharmacology, Faculty of Veterinary Medicine, Cairo University, Giza 12211, Egypt
[4]Department of Medical Pharmacology, Faculty of Medicine, Atatürk University, Erzurum 25240, Türkiye

The market demand for selenium-enriched functional beverages is growing rapidly owing to the physiological activities of selenium, including antioxidant capacity and immune regulation. Inorganic selenium suffers from low bioavailability and exhibits toxicity at high dosages, while organic selenium biosynthesized via lactic acid bacteria boasts superior safety and absorption efficiency. Yacon is rich in prebiotic components such as fructooligosaccharides and polyphenols, and co-fermentation with apples can optimize fermentation substrates and flavor profiles. Nevertheless, most existing studies merely optimize selenium conversion efficiency as a single indicator, lacking an integrated multi-objective optimization system that synergizes multimodal data of selenium speciation, bioactive compounds and volatile flavors.
In this study, *Lactiplantibacillus plantarum* YKX was adopted as the fermentation strain to develop selenium-enriched fermented apple-yacon beverages. Response Surface Methodology (RSM) was combined with the XGBoost machine learning algorithm to realize multi-objective precise fermentation optimization. Electronic nose and Headspace-Gas Chromatography-Ion Mobility Spectrometry (HS-GC-IMS) were employed to characterize dynamic flavor evolution throughout fermentation. A comprehensive quality prediction model for the beverage was established by integrating multimodal data of chemical compositions, sensory evaluation and volatile flavors, and interpretable artificial intelligence tools including SHAP and PDP were utilized to reveal the mechanism of key processing parameters.
Multi-round optimization via single-factor experiments, RSM and XGBoost yielded the optimal fermentation parameters: apple-to-yacon raw material ratio of 1:2.2, enzyme dosage of 0.65 g/L, and fermentation temperature of 34.8 °C. Under these conditions, the beverage contained 149.42 mg/100 mL crude polysaccharides and 1.250 mg/mL flavonoids, with a selenium biotransformation rate of 89.78% and a comprehensive quality index of 83.2. A total of 68 signal peaks were detected by HS-GC-IMS, among which 52 volatile flavor compounds were identified, dominated by alcohols, acids and esters. The total content of esters showed an extremely strong positive correlation with sensory scores (r=0.91), acting as the core flavor substances that improve beverage palatability. SHAP analysis verified that fermentation temperature was the primary processing factor affecting comprehensive quality. Correlation heatmaps indicated that polysaccharide metabolism simultaneously facilitates the synthesis of ester flavors, achieving coordinated improvement of nutritional properties and flavor quality. The time-series LSTM model identified the golden conversion window for selenium biotransformation ranging from 12 h to 24 h of

fermentation.

Three prediction models, namely Random Forest, XGBoost and RSM, were compared, and the Random Forest model achieved the optimal fitting performance (R^2=0.927, RMSE=2.345), which verified the necessity of integrating multimodal data for comprehensive beverage quality assessment. This study innovatively applied machine learning coupled with multimodal data fusion to the development of selenium-enriched fermented fruit and vegetable beverages for the first time, elucidated the internal correlation between selenium biotransformation and dynamic flavor changes, and constructed an interpretable AI framework for precision fermentation. It provides theoretical basis and technical references for the intelligent and standardized production of selenium-enriched functional fruit and vegetable beverages.

P71: Fractionation and Effect-Directed Analyses of Antioxidants from Crude Extracts of Plant Species from the Genus *Fallopia*

Irena Vovk[1]*, Vesna Glavnik[1], Živa Vipotnik[1], Maja Bensa[2], Simona Strgulc Krajšek[3]
[1]Laboratory for Food Chemistry, National Institute of Chemistry, Ljubljana, Slovenia
[2]Research Institute of Faculty of Health Sciences, Faculty of Health Sciences, University of Ljubljana, Ljubljana, Slovenia
[3]Department of Biology, Biotechnical Faculty, University of Ljubljana, Ljubljana, Slovenia

The aim of this study was to investigate antioxidants in the following invasive alien plant species from the genus *Fallopia*: Japanese knotweed (*Fallopia japonica* Houtt.), giant knotweed (*Fallopia sachalinensis* Ronse Decr.), Bohemian knotweed (*Fallopia bohemica* J. Chrtek & A. Chrtková) J.P. Bailey), as well as Russian-vine (*Fallopia baldschuanica* (Regel) Holub) and Chinese knotweed (*Fallopia multiflora* (Thunb.) Haraldson). Different plant parts (e.g., leaves, rhizomes) of these plant species were collected in several localities from different phytogeographical regions of Slovenia. Methods used were based on high-performance thin-layer chromatography (HPTLC) combined with effect-directed analysis (EDA), image analysis and densitometry and flash column chromatography. Analyses of antioxidants in crude extracts of collected plant materials obtained by ultrasound-assisted extraction (UAE), and supercritical fluid extraction (SFE with supercritical carbon dioxide followed by SFE with supercritical water) were performed by combining HPTLC and EDA. In vitro antioxidant analyses were performed on the developed HPTLC silica gel plates by post-chromatographic application of 2,2-diphenyl-1-picrylhydrazyl (DPPH•) reagent. Antioxidants, as quenchers of free radicals, were observed as bright bands on a purple background. Evaluation of the HPTLC profiles obtained by HPTLC-DPPH•-image analysis and HPTLC-DPPH•-densitometry in fluorescence mode (FLD) confirmed differences between the crude extracts of plant materials from the different plant parts of the same plant species, different plant species as well as different years on the same location and different locations. Additionally, fractionation of antioxidants from the SFE extract obtained from leaves of Bohemian knotweed using supercritical water was performed by flash column chromatography using a diol column. Evaluation of fractions by HPTLC-DPPH•-image analysis showed diverse antioxidant activities of the fractions.

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P72: Soluble Dietary Fiber from *Piper sarmentosum* Roxb. Leaves Modulates Gut Microbiota-Derived Cis-11-Eicosenoic Acid to Regulate Lipid Metabolism

Yangyang Wang[1], Jianbo Xiao[2], Hui Wang[1]*, Hui Cao[1,2]
[1]College of Food Science and Technology, Guangdong Ocean University, Guangdong Provincial Key Laboratory of Aquatic Product Processing and Safety, Guangdong Province Engineering Laboratory for Marine Biological Products, Zhanjiang 524088, China
[2]Universidade de Vigo, Nutrition and Bromatology Group, Department of Analytical and Food Chemistry, Faculty of Science, 32004 Ourense, Spain

Obesity represents a critical global health challenge, significantly elevating risks for major chronic diseases. This underscores the urgent necessity to develop innovative prevention and therapeutic interventions. While *Piper sarmentosum* Roxb. has demonstrated antidiabetic and antihypertensive properties, its anti-obesity effects and underlying mechanisms remain largely uncharacterized[1]. This study aimed to evaluate the anti-obesity effects of soluble dietary fiber from *Piper sarmentosum* Roxb. leaves (PSDF) and elucidate its molecular basis. PSDF was characterized as an acidic dietary fiber, predominantly composed of galacturonic acid (55.64%), galactose (21.74%), and arabinose (11.97%), exhibiting a triple-helical conformation and high thermal stability. In diet-induced obese mice, six weeks of PSDF administration significantly ameliorated glucose and lipid metabolic disorders ($p < 0.05$), an effect associated with modulation of gut microbiota[2]. Untargeted metabolomics identified cis-11-eicosenoic acid (GA) as a key metabolite. In a 3T3-L1 single-cell model, GA treatment did not affect adipocyte differentiation. However, in a co-culture model of 3T3-L1 adipocytes and RAW264.7 macrophages, GA significantly downregulated pro-inflammatory cytokines (IL-1β, TNF-α) and SREBF1 expression, while upregulating anti-inflammatory markers (IL-4, IL-10) and fatty acid oxidation genes (CPT1A, PGC-1α). These results initially suggested that GA may exert anti-obesity effects primarily through modulating inflammation-associated lipid metabolism pathways. Fecal microbiota transplantation (FMT) confirmed both GA elevation and anti-adiposity effects were microbiota-dependent[3]. These findings demonstrated PSDF alleviated lipid accumulation by modulating a gut microbiota-adipose axis centered on GA production, thereby improving inflammation-mediated lipid metabolism. This newly elucidated microbiota-GA axis establishes a theoretical basis for developing PSDF-based soluble dietary fibers into microbiota-focused anti-obesity nutraceuticals.

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P73: Divergent Polyphenol Transformations in *Oenanthe javanica* Induced by Dry-Heat and Moist-Heat Processing as Revealed by UPLC-Q-TOF-MS/MS

Fuying Wang[1,2], Haolin Zhang[1,2], Hui Cao[1,2]*
[1]College of Food Science and Technology, Guangdong Ocean University, Guangdong Provincial Key Laboratory of Aquatic Product Processing and Safety, Guangdong Province Engineering Laboratory for Marine Biological Products, Guangdong Provincial Engineering Technology Research Center of Seafood, Guangdong Provincial Engineering Technology Research Center of Prefabricated Seafood Processing and Quality Control, Zhanjiang 524088, China
[2]Collaborative Innovation Center of Seafood Deep Processing, Dalian Polytechnic University, Dalian 116034, China

Oenanthe javanica is a characteristic aquatic vegetable rich in polyphenols. Thermal processing is the most common preparation method, yet the transformation of polyphenols and their functional responses under different heating environments remain unclear. In this study, microscopic observation, UPLC-MS/MS, and multivariate statistical analysis were combined to investigate the dynamic changes in polyphenols and antioxidant activity of *O. javanica* stems and leaves during dry-heat roasting and moist-heat boiling. Thermal processing disrupted the tissue microstructure, promoting the release of free and partially bound polyphenols. A total of 31 major polyphenols were identified, including flavonoid glycosides, flavonoid aglycones, chlorogenic acid, ferulic acid, caffeic acid, and related phenolic acid derivatives. The leaves contained a greater diversity and abundance of polyphenols than the stems. During dry-heat processing, leaf polyphenols exhibited a sequential pattern of release followed by degradation, while antioxidant activity remained relatively stable. In contrast, moist-heat processing promoted the migration of polyphenols into the cooking water, resulting in reduced antioxidant capacity in the leaves. The antioxidant activity of the cooking water changed synchronously with polyphenol release and degradation. In the stems, most phenolic acids increased during dry-heat treatment, whereas under moist heat they first increased and then declined. Changes in antioxidant activity of both stems and leaves were strongly correlated with alterations in polyphenol composition. Mechanistically, flavonoid glycosides were deglycosylated into aglycones and subsequently transformed into simple phenolic acids, while complex phenolic acids underwent isomerization, ester hydrolysis, and thermal degradation. These findings reveal the medium-dependent transformation of polyphenols and its association with antioxidant activity, providing a scientific basis for improving the functional quality of thermally processed vegetables.

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P74: A Comprehensive Review of Luteolin: Sources, Chemistry, Bioavailability And Pharmacological Properties, as Well as Health Benefits

Xiaodong Ge[1], Ligen Chen[1], Chao Zhao[2], Rong Shao[1], Wei Xu[1]*
[1]College of Marine and Bioengineering, Yancheng Institute of Technology, Yancheng, 224051, China
[2]College of Marine Sciences, Fujian Agriculture and Forestry University, Fuzhou 350002, China

Plant-derived flavonoids are frequently proposed as accessible agents for chronic disease prevention and adjunctive management[1-3]. Luteolin (3′,4′,5,7-tetrahydroxyflavone) is widely distributed in edible and medicinal plants and is often cited for favorable safety and nutritional attributes; however, its therapeutic application remains constrained, most notably by limited bioavailability and an immature clinical evidence base[4,5]. This review aimed to synthesize current knowledge on luteolin's sources and chemical features, summarize the evidence supporting its pharmacological activities and potential health benefits across major chronic disease contexts, and evaluate formulation strategies intended to overcome bioavailability barriers. We integrated and critically organize published findings on luteolin's natural sources, synthesis and physicochemical properties, absorption/bioavailability considerations, reported biological activities, and delivery approaches, with emphasis on how formulation choices may influence exposure and applicability. Accumulating studies describe luteolin as a potent antioxidant and anti-inflammatory compound with additional neuroprotective potential, and suggest possible roles in the prevention and management of diabetes, obesity, and cancer. Nonetheless, these proposed benefits are repeatedly tempered by poor oral bioavailability and variability in delivery and study designs. To address this, multiple delivery forms have been reported, including capsules, solid dispersions, co-crystals, inclusion complexes, and nanotechnology-based formulations. Current literature supports luteolin as a promising multi-functional bioactive compound, but definitive therapeutic positioning requires better exposure-response characterization and more rigorous translational studies. Future work should prioritize standardized bioavailability assessment, formulation comparisons with clinically relevant endpoints, and well-designed human studies to define efficacy, safety margins, and appropriate use scenarios.

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P75: Epigallocatechin Gallate Overcomes Trastuzumab Resistance in HER2-Positive Breast Cancer through GLUT2-Mediated Metabolic Reprogramming and Anti-Angiogenic Effects

Chen LiChing[1], Ho YuanSoon[2]*
[1]Department of Biological Science & Technology, College of Life Sciences, China Medical University, Taichung, Taiwan
[2]Institute of Biochemistry and Molecular Biology, College of Life Sciences, China Medical University, Taichung, Taiwan

This study investigates the therapeutic potential of epigallocatechin gallate (EGCG) in overcoming trastuzumab resistance in HER2-positive breast cancer through metabolic reprogramming. GLUT2 expression was significantly upregulated in trastuzumab-resistant HCC1954 cells, indicating enhanced glycolytic adaptation. EGCG treatment (10 μM, 24 h) reduced GLUT2 expression and dose-dependently suppressed glycolytic capacity, with stronger effects in resistant cells.
Long-term EGCG exposure (P5–P15) markedly inhibited cell migration and tumorigenicity. Xenograft models using EGCG-treated cells showed over 50% tumor growth suppression ($p<0.0001$), accompanied by reduced Ki-67, CD105, and GLUT2 expression. Despite enhanced GLUT2–HER2 interaction observed by IF and FRET, EGCG did not affect trastuzumab binding, suggesting a metabolism-driven mechanism independent of HER2 targeting.
Additionally, EGCG demonstrated potent anti-tumor activity in TNBC patient-derived xenograft models, achieving over 60% tumor growth inhibition ($p<0.01$). Overall, EGCG exerts broad anti-cancer effects by suppressing glycolysis, proliferation, angiogenesis, and migration across breast cancer subtypes.