

International Bioactives Conference 2026

Abstract Book



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Plenary Speakers

Professor Mary Ann Lila

Department of Food Bioprocessing and Nutrition Sciences, North Carolina State University, North Carolina Research Campus, Kannapolis NC 28081 USA

Plant Bioactives that Protect Human Health - The Call of the Wild

Abstract

Plant foods contribute to human health maintenance on two separate fronts; they are rich sources of nutrients (macro and micro) that are prerequisite for all biochemical functions at the cellular level, and dietary plants also deliver the highly interactive phytoactive molecules (bioactives) that neutralize free radicals, modulate inflammatory pathways, deliver antimicrobial benefits and bolster human immunity. Once ingested, these bioactives inhibit incidence of chronic disease in humans and promote resilience against exogenous stress factors such as pollutants, ozone, or UV radiation (immunoprotection). However, before any of this happens in the human, the plant itself has been synthesizing and accumulating bioactive compounds in its own tissues as defensive mechanisms, in response to stress triggers from the growing environment. This is why the best place to investigate the inherent bioactivities in plants is in the wild. Plants adapted to thrive in the wild environs of nature, even those at the fringe of survival, exhibit the most diversified and complex phytochemical profiles to support multiple ecological functions. Historically, tribal communities have prioritized wild indigenous plants in Traditional Ecological Knowledge and followed the lead of wild fauna (e.g. the bear, the wolf) to seek out biologically active plant resources. Brisk routine physical activity – also a routine aspect of the traditional hunter-gatherer lifestyle – serves to amplify both the bioactivity and bioavailability of plant-derived bioactives once ingested by humans. So, how do we best exploit these clues from the wilds of nature in our present-day utilization, investigation, or commercialization of bioactive plant components? First, give primary focus to plant sources that feature exceptional chemodiversity. The combination of modern genomics and metabolomics allows us to prioritize cultivars or genotypes that not only accumulate greater concentrations of bioactive phytochemicals (e.g. anthocyanin pigments, carotenoids, or glucosinolates), but are characterized by phytoactive profiles that maximize opportunities for additive and synergistic interactions that amplify biological potency. Next, combine bioactive phytochemical interventions with an exercise routine – rigorous physical exertion – to stimulate bioavailability and activity. These principles will be illustrated in our preclinical trials with racing Alaskan sled dogs challenged by wildfire pollution, and in our clinical trials with older adults exhibiting mild cognitive decline who are consuming wild blueberry interventions and engaging in habitual brisk walking bouts.

Michelle Colgrave^{1,2}

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² *Australian Research Council Centre of Excellence for Innovations in Peptide and Protein Science, School of Science, Edith Cowan University, Joondalup, WA 6027, Australia).*

Bioactive Peptides and Proteins: Using Machine Learning, Proteogenomics and Analytical Validation to Move from Discovery to Impact

Abstract

Bioactive peptides and proteins offer enormous promise for improving human and animal health, enhancing food quality, and delivering new sustainable products, yet only a small fraction of candidates progress beyond discovery. This plenary will explore how integrating machine learning, proteogenomics and rigorous analytical validation can accelerate the journey from initial discovery to tangible impact. Advances in both instrumentation and bioinformatic workflows have accelerated genome mining, proteome exploration for novel bioactives, prioritising candidates with desired functional and safety

profiles, and guide targeted experimental design. Using case studies from food and agricultural systems, this talk will illustrate a practical framework for moving bioactive peptide and protein discoveries along the translation pathway – from in silico prediction and omics discovery to validated function, product development and real-world outcomes.

Philip Yongxin Li

Department of Chemistry, The University of Hong Kong, Hong Kong

Decoding the Cryptic Chemistry of Microbiota for Drug Discovery

Abstract

The global rise of antibiotic-resistant “superbugs” demands urgent innovation in antimicrobial drug discovery. Traditional approaches are faltering, yet the human microbiota remains an underexplored reservoir of bioactive natural products. These microbial communities produce a vast array of compounds that function both as weapons in inter-microbial competition and as signals in host–microbe communication. To harness this untapped potential, we present an interdisciplinary platform that integrates deep learning, synthetic biology, and chemical biology to systematically mine the microbiota’s genetic and metabolic diversity for bioactive discovery¹. Beyond identifying novel compounds, we investigate the chemical ecology of host–microbe interactions to decode the molecular language that governs microbial behavior and resilience². By translating ecological insights into therapeutic design, we not only uncover new antibiotics but also engineer probiotic systems capable of disrupting pathogenic networks and modulating host immunity. This synergistic strategy bridges fundamental ecology with translational innovation, providing a roadmap to combat antimicrobial resistance and pioneer next-generation therapies.

Elaine Holmes

School of Medicine, Hong Kong University of Science and Technology, Hong Kong.

From Molecules to Meaning: Bioactives, Metabolism and the Future of Precision Health.

Abstract

Bioactive compounds derived from diet, the microbiome, and the environment continually interact with human metabolism, shaping health trajectories across the life course. Advances in metabolic phenotyping offer new opportunities to characterise these molecular interactions to characterize how nutrition, lifestyle, host genetics, and microbial metabolism collectively influence physiological resilience and disease susceptibility. Metabolic profiling of biofluids using high resolution spectroscopic technologies combined with AI pipelines enables the comprehensive assessment of host and microbial metabolism, which can be converted into metabolic phenotypes that provide mechanistic insights into a wide spectrum of physiological and pathological states. This lecture will explore how advances in spectroscopy, computational analytics, and artificial intelligence are transforming molecular data into clinically meaningful information using case studies from cardiometabolic diseases, pregnancy studies and dietary interventions. The journey from discovery to translation is transforming metabolic phenotyping from a powerful research tool into a cornerstone of precision health. High-resolution molecular profiling enables the identification of metabolic signatures that capture the integrated effects of bioactives, nutrition, the microbiome, genetics, and environmental exposures. Through rigorous validation, standardisation of analytical workflows, and integration with artificial intelligence and clinical data, these molecular signatures can be translated into robust diagnostic and prognostic assays that inform disease risk, patient stratification, and therapeutic response. This translational pipeline has the potential to bridge fundamental biological discovery with real-world clinical application, enabling precision interventions that move healthcare beyond disease treatment towards early detection, prevention, and optimised disease management.

Invited Keynotes

Hafiz A. R. Suleria

School of Agriculture, Food and Ecosystem Sciences, Faculty of Sciences, The University of Melbourne, Parkville 3010, VIC, Australia

Understanding Food Bioactives from Digestion to Absorption: Integrated *in Vitro*, Cellular, and *in Vivo* Porcine Models

Abstract

The biological effects of food-derived bioactive compounds depend not only on their concentrations in foods but also on their release from the food matrix, stability during gastrointestinal digestion, intestinal absorption, metabolism, and interactions with other dietary components. Bioaccessibility refers to the proportion of a compound that is released from the food matrix during digestion and becomes available for intestinal absorption, whereas bioavailability describes the proportion that is absorbed, metabolised, distributed, and ultimately available to exert physiological effects. These processes are closely linked to nutrient digestibility and may be enhanced or inhibited by interactions among bioactive compounds, macronutrients, micronutrients, and components of the gastrointestinal environment. Our research group aims to develop and apply integrated approaches to investigate the digestion, absorption, metabolism, and biological functions of food components. *In vitro* gastrointestinal digestion models provide controlled and reproducible platforms for assessing nutrient digestibility, compound stability, transformation, and bioaccessibility. Cell culture models can subsequently be used to evaluate intestinal transport, cellular uptake, metabolism, cytotoxicity, and specific biological activities. Porcine models offer greater physiological relevance because the porcine gastrointestinal tract shares important anatomical and functional characteristics with that of humans. In particular, cannulated pig models enable repeated sampling from specific regions of the gastrointestinal tract, allowing the dynamic investigation of nutrient digestion and disappearance, metabolite formation, microbial transformation, and changes in bioactive compounds. By integrating *in vitro* digestion, cell-based assays, conventional porcine studies, and cannulated pig models, our research seeks to provide a more comprehensive understanding of how food matrices and interactions among bioactive components enhance or reduce digestibility, bioaccessibility, bioavailability, and biological activity.

Ana Rodriguez-Mateos

Department of Nutritional Sciences, School of Life Course and Population Health Sciences, King's College London

Bioavailability and Beyond: Understanding Biological Responses to Dietary (Poly)phenols

Abstract

Dietary (poly)phenols have been extensively investigated for their potential to promote human health, yet marked inter-individual variability in their effects continues to challenge mechanistic understanding and clinical translation. Bioavailability is a fundamental determinant of (poly)phenol bioactivity, but its definition has evolved beyond intestinal absorption to encompass the complex interactions between foods, the gut microbiome and the host that determine exposure to bioactive metabolites. Understanding the factors that drive differences in bioavailability is therefore essential for explaining variability in biological responses and health effects.

This keynote will explore current evidence on the factors influencing the bioavailability and bioactivity of dietary (poly)phenols, highlighting how food composition, processing and bioaccessibility determine

internal exposure to bioactive metabolites, while gut microbial metabolism and host factors contribute to inter-individual variability in biological responses. Despite major advances, the relative contribution and interplay of these factors remain incompletely understood, limiting our ability to fully explain differences in health outcomes.

Improving our understanding of the factors governing (poly)phenol bioavailability and bioactivity will strengthen mechanistic evidence, improve the design and interpretation of human intervention studies, and accelerate the translation of (poly)phenol research into evidence-based dietary recommendations and future precision nutrition strategies.

Philippe Schmitt-Kopplin^{1,2,3}

¹ *Helmholtz Munich, analytical BioGeoCHemistry, Oberschleißheim, Germany,*

² *Technical University Munich TUM, analytical Food Chemistry, Weihenstephan, Freising, Germany,*

³ *Max Plank Institute for Extraterrestrial Physics, Center for Astrochemical Studies, Garching, Germany*

Food Functional Metabolomics in a Nutshell: Bioactives from Biotic and Abiotic Chemistry

Abstract

Food systems are shaped by a continuous interplay between biotic metabolism and abiotic chemical transformations, generating highly complex molecular mixtures that influence food quality, functionality, and health. Deciphering this chemical diversity requires advanced high-resolution analytical technologies combined with innovative computational approaches capable of resolving thousands of metabolites simultaneously. This presentation highlights how modern food metabolomics (Foodomics) provides unprecedented insight into the molecular composition and dynamics of complex food matrices, microbiomes, and biological systems. Through selected case studies, we illustrate how enzymatic and non-enzymatic processes jointly govern chemical evolution across the Food–Microbiome–Health continuum. Particular emphasis is placed on the discovery and characterization of bioactive compounds emerging from both biological activity and food processing chemistry. Examples from ongoing research demonstrate how untargeted high-resolution metabolomics can reveal molecular signatures, reaction pathways, and functional metabolites relevant to nutrition, food quality, and health. By integrating analytical chemistry, metabolomics, and systems-level data analysis, this talk presents food functional metabolomics as a powerful framework for understanding the origin, transformation, and biological significance of food bioactives, bridging the gap between molecular diversity, food processing, and human health.

Catherine P. Bondonno^{1,2}

¹ *Nutrition & Health Innovation Research Institute, School of Medical and Health Sciences, Edith Cowan University, Joondalup, Western Australia, Australia.*

² *Medical School, University of Western Australia, Perth, Western Australia, Australia.*

The Strange Case of Nitrate: the Dr Jekyll and My Hyde of Human Health

Abstract

Dietary nitrate occupies a controversial position in human health science. For over half a century, the nitrate content of the three major dietary sources – vegetables, meat, and water – has been legislated, regulated, and monitored because of public health concerns over cancer risk, stemming from nitrate's capacity to form carcinogenic N-nitrosamines. In contrast, a growing and compelling body of evidence indicates that dietary nitrate, particularly from vegetables, protects against cardiovascular disease and other chronic conditions, largely mediated through its conversion to nitric oxide (NO), a key signalling

molecule in vascular health. This protective evidence remains overshadowed by concern over nitrate's carcinogenic potential.

This presentation reviews the current evidence for nitrate as both a health protector and a health threat. The beneficial "Dr Jekyll" role of nitrate is examined through its effects, via the nitrate–nitrite–NO pathway, on cardiovascular disease outcomes, cognitive health, musculoskeletal health, and exercise performance, alongside emerging evidence for protection against other debilitating health outcomes. The "Mr Hyde" role is then critically examined, interrogating the long-held assumption that all dietary nitrate, irrespective of source, leads to the formation of carcinogenic N-nitrosamines, and reviewing the epidemiological evidence linking nitrate from vegetables, meat, and water to cancer risk.

Synthesising this evidence, the presentation argues that the long-standing assumption of nitrate as a uniform carcinogenic contaminant is not fully supported, replacing blanket exposure limits with an evidence-based, source-specific framework already informing drinking-water policy in Denmark and cited by regulatory and scientific agencies across 13 countries. Definitive, source-dependent studies however are still needed, particularly to resolve the unresolved frontier of N-nitrosamine formation – the next chapter in nitrate's identity story, and the key to safely harnessing nitrate's health benefits.

Rachel A. Burton, James M. Cowley, Juanita Lauer, Aaron Phillips and Matthias Salomon

School of Agriculture, Food and Wine, Adelaide University, Urrbrae, South Australia 5041, Australia.

Bioactive Bonanza: Rich Pickings in Australia's Emerging Crops

Abstract

As climate change pushes dramatic shifts in meteorological patterns and weather event frequency we have started to adopt a broader range of crops that will cope with Australia's increasingly harsh conditions. These novel or emerging crops fall outside the narrow set of plants that currently dominate our diets. Just three crops – wheat, rice and maize – supply about 50% of the world's calories, while sugarcane alone accounts for 80% of global sugar production. Not only do we need to get used to how to grow this wider range of crop types we also have to better explore the novel array of bioactive primary and secondary metabolites they offer. Some of these bioactive metabolites we already know about, others are newly described and a still significant fraction remain unknown. In many cases we lack much knowledge of the roles that these bioactives play in plants. Perhaps more intriguingly, we also don't understand how they behave when consumed as part of our diets and how they may influence downstream uses that could provide additional value streams for growers and manufacturers. Here we present new findings about the composition and behaviour of bioactive compounds from *Plantago* species, industrial hemp and agave, ranging from dietary fibres and fats, via cannabinoid metabolism through to waxes, saponins and oxalates in succulent tissues.

Yasmina Sultanbawa

Centre for Nutrition and Food Science, Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Indooroopilly, QLD, 4068, Australia.

Opportunity Crops and Bioactive Compounds: Driving Innovation for Industry Applications

Abstract

The increasing global demand for nutritious, sustainable, and functional foods has intensified interest in bioactive compounds derived from underutilised plant resources. Opportunity crops, including native and traditional food plants from diverse regions of the world, represent a rich yet largely untapped source of nutrients and phytochemicals with significant potential to address challenges in human health, food security, and sustainable agricultural development.

This keynote presentation will explore how multidisciplinary research spanning food chemistry, processing technologies, nutrition, preservation, and engineered delivery systems can transform plant biodiversity into high-value bioactive ingredients and innovative food products. It will highlight advances in the identification, characterisation, and application of natural antioxidants, antimicrobial compounds, and other health-promoting bioactives from underutilised plant resources.

The role of biodiversity stewardship, community engagement, and collaborative innovation frameworks in building resilient and sustainable food systems will also be examined. By integrating science, industry, policy, and community perspectives, opportunity crops can drive innovation across food value chains, supporting the development of sustainable, health-promoting products and more resilient food systems globally.

Munish Puri

Riddet-BSI Chair Alternative Proteins, Riddet Institute, Massey University, New Zealand.

Redefining Industrial Biotechnology: Intelligent Biomanufacturing of Future Foods and Bioactive Ingredients

Abstract

The growing demand for sustainable foods and health-promoting ingredients is reshaping industrial biotechnology through advances in precision fermentation, synthetic biology and artificial intelligence (AI). This keynote will discuss emerging strategies for engineering microbial cell factories to produce alternative proteins, omega-3 lipids and fungal-derived bioactive compounds for food, nutrition and health applications. It will highlight recent developments in systems biology, machine learning, strain engineering, and bioprocess optimisation that are enabling more efficient, scalable and sustainable manufacturing. The integration of high-throughput experimentation with digital technologies is accelerating strain development, improving process performance and enhancing product quality while shortening development timelines. The presentation will conclude by discussing the importance of interdisciplinary collaboration across academia and industry to translate scientific innovation into commercially viable biomanufacturing platforms capable of meeting the growing global demand for sustainable food and high-value bioactive ingredients.

Colin J. Barrow

Centre for Sustainable Bioproducts, Deakin University, Geelong, Australia.

High Value Bioproducts from Organic Waste to Promote a Circular Economy

Abstract

Agricultural, food and aquaculture are important contributors to the Australian economy but generates vast quantities of underutilized biomass which is often disposed of as waste or used in low value applications, with significant negative economic and environmental impacts. This waste contains many highly valuable components, which if properly processed can be utilized to produce a range of high value products.

Vegetable waste alone accounts for 277,000 tonnes of waste, which is 25% of total production and again this primarily goes to landfill or is used as low value stock feed. The cost to growers is estimated at \$155 million annually for the major vegetable crops (carrots, capsicums, cauliflower, sweet corn, cabbage, lettuce, and broccoli). There are also 90,000 tonnes of seafood processing waste annually with typically 50-60% of fish becoming by-product during processing.

A range of high value materials can be extracted and purified from organic waste, particularly phenolics, carotenoids, collagen, omega-3 lipids and various protein and carbohydrates, that have value for a range of commercial applications.

In this presentation I will discuss some of the project that Deakin University is involved with in organic waste bioprocessing to develop a circular economy, including the projects to create nutritional ingredients, functional biomaterials and medically-relevant bioproducts.

Karen J. Murphy

Allied Health & Human Performance and Alliance for Research in Exercise, Nutrition and Activity (ARENA), Adelaide University, Adelaide, Australia.

Translating Food Bioactives into Healthy Ageing Outcomes: Insights from Mediterranean Diet Intervention Trials

Abstract

With populations ageing globally, promoting healthy longevity has become a major public health priority. The Blue Zones—five regions of the world where people experience exceptional longevity and healthy ageing—provide valuable insights into the lifestyle factors associated with reduced chronic disease risk and increased lifespan. While social connectedness, physical activity, environmental influences and a strong sense of purpose are common characteristics across these populations, dietary habits are recognised as key contributors, particularly mindful eating practices and predominantly plant-based dietary patterns.

Among these, the Mediterranean diet is one of the most extensively studied and evidence-based dietary patterns, with substantial evidence supporting its role in preserving physical and cognitive function and reducing the risk of age-related chronic diseases. The Mediterranean dietary pattern is characterised by a high intake of vegetables, fruits, wholegrains, legumes, nuts, olive oil and oily fish, with moderate consumption of dairy foods and red wine, and limited intake of red meat and discretionary foods. This dietary pattern provides a diverse array of bioactive compounds, including polyphenols and monounsaturated fatty acids from olive oil and nuts, flavonoids from fruits, vegetables and red wine, carotenoids from colourful fruits and vegetables, dietary fibre from wholegrains and legumes, and long-chain omega-3 fatty acids from oily fish. Acting synergistically within the food matrix, these bioactives modulate inflammation and oxidative stress, improve endothelial and metabolic function, support gut microbial health, and contribute to the maintenance of cognitive function and healthy ageing.

This presentation will synthesise evidence from Mediterranean diet intervention and population studies, including emerging Australian research, to illustrate how Mediterranean diet intervention research is informing the translation of food bioactives into evidence-based strategies for healthy ageing.

Xuyu Liu^{1,2}

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From Kitchen to Bench to Bedside: Investigating the Antithrombotic Potential of Brassica Vegetable-Derived Antiplatelet Agents

Abstract

A wide range of dietary phytochemicals has been shown to modulate the activities of kinases, ubiquitin-conjugating enzymes, and transcription factors, providing long-lasting impacts on immune responses, neural plasticity, and cardiovascular health. Many of these bioactives contain electrophilic functional groups that enable covalent modification of cysteine residues within proteins. Such diet-induced covalent modifications have been associated with chemopreventive actions and, more recently, with reduced risks of thrombosis and stroke. Despite these findings, the effects of dietary electrophile-induced protein modifications on blood function remain largely unexplored.

In our recent investigation, we profiled the effects of dietary electrophiles extracted from different vegetables on platelet function. This analysis revealed distinct antiplatelet selectivity profiles among naturally occurring isothiocyanates derived from broccoli. Notably, these compounds attenuated platelet responses to ADP without affecting thrombin-mediated activation. Using proteomic mapping and

knockout animal models, we identified protein disulfide isomerase A6 (PDIA6)⁵ and protein tyrosine kinase 2 beta (Pyk2) as key targets. Importantly, using mouse models of thrombosis and tail bleeding, we demonstrated that selective inhibition of PDIA6 or Pyk2 enhanced stroke treatment outcomes *in vivo* without increasing bleeding risk.

Our findings reveal a new avenue for thrombosis and stroke prevention inspired by diet-induced protein modifications, potentially offering safer and more effective therapeutic options through personalised vegetable-based diets.

Miranda Miroso

Department of Food Science, University of Otago, Dunedin, New Zealand.

Translating Bioactives from the Circular Food Economy

Abstract

Extracting high-value bioactives from agri-food side-streams offers strong circular economy potential, yet bridging the gap between lab discovery and market adoption presents complex challenges. While functional efficacy is crucial, successful translation depends equally on broader system factors, including supply chain economics, regulatory landscapes, and consumer perception. This presentation explores the socio-technical and cultural dynamics surrounding upcycled bioactives, highlighting potential bottlenecks and opportunities within the food pipeline. By framing bioactive translation as a human ecosystem, we examine how transdisciplinary approaches can better align scientific innovation with consumer trust and meaningful societal impact.

Karen Charlton

School of Health Sciences, University of Newcastle and Nutrition and Metabolic Health Research Program, Hunter Medical Research Institute, New Lambton.

Navigating the Regulatory Landscape for Food Bioactives

Abstract

The growing global interest in food bioactives presents significant opportunities for improving population health, supporting sustainable food systems and creating new value chains from underutilised natural resources. In Australia, this opportunity is particularly evident in the increasing research and commercial interest in native and Indigenous plants, many of which contain unique phytochemicals, polyphenols, peptides, fibres, and other bioactive compounds with potential health-promoting properties. However, translating promising bioactivity into market-ready products requires navigating a complex regulatory landscape that sits at the intersection of food, complementary medicines, pharmaceuticals, and Indigenous knowledge governance.

This presentation will examine the regulatory considerations underpinning the development and commercialisation of food bioactives, with a primary focus on the Australian context. It will explore how regulators distinguish between foods, functional foods, supplements, complementary medicines, and therapeutic goods, and how claims relating to physiological effects, disease risk reduction, and treatment can alter regulatory pathways. Particular attention will be given to the evidentiary requirements needed to substantiate bioactivity, including mechanistic, pre-clinical, clinical, and real-world evidence, and the challenges associated with translating emerging scientific findings into legally defensible health claims.

The roles of Food Standards Australia New Zealand (FSANZ) and the Therapeutic Goods Administration (TGA) will be considered, alongside emerging policy frameworks relating to Indigenous data sovereignty, benefit sharing, and ethical engagement with Aboriginal and Torres Strait Islander communities. Case studies involving Australian native species will illustrate both the opportunities and challenges associated

with commercialising bioactive-rich products while respecting cultural knowledge and ensuring equitable participation and benefit sharing.

Within a broader international context, regulatory models adopted by organisations such as the European Food Safety Authority (EFSA), the United States Department of Agriculture (USDA), and the U.S. Food and Drug Administration (FDA) will be discussed. Differing approaches to health claim substantiation, novel food assessment, dietary supplement regulation, and the integration of nutrition, agriculture, and public health objectives will be considered. Lessons from these jurisdictions highlight the importance of harmonised evidence frameworks, transparent risk assessment processes, and clear regulatory pathways that encourage innovation while protecting consumers.

Jayashree Arcot

Food and Health, School of Chemical Engineering, University of New South Wales, Sydney, NSW 2033, Australia.

Bioactives in Foods: Their Interactions, Bioaccessibility and Bioavailability can Influence their Bioactivity.

Abstract

Bioactives are classified according to their chemical structure, source and their bioactivity. They are generally classified into polyphenols, flavonoids, terpenoids, organosulphur compounds, carotenoids, fatty acids, prebiotics, polysaccharides, phytoestrogens and synthetic bioactive compounds. Their effects on human health can be positive or negative depending on their bioaccessibility, bioavailability and functions. The combination of bioactive compounds could result in changes in biological properties and bioavailability of the compounds. A number of phytochemical mixtures and food combinations provide synergistic effects on inhibiting oxidation, inflammation and cancer cell proliferation.

The combinations of different pure bioactive compounds or their extracts from food sources can equally enhance the benefits conferred by individual bioactive compounds. There are multiple phytochemicals in a single fruit or vegetable. We consume many vegetables in a single meal or fruits in desserts or drinks. Concurrently consumed bioactive compounds may affect the intestinal absorption of each other. The interactions of phytochemicals may enhance or reduce the bioavailability of a given compound, depending on the facilitation/competition for cellular uptake and transportation taking place between them. This paper will provide examples of bioaccessibility studies using in vitro cell 2D culture techniques to show these interactions as well as provide a case for studies using 3D organoids for such studies.

Andrew Holmes

Charles Perkins Centre, School of Life and Environmental Sciences, The University of Sydney, Australia.

Promises and Pitfalls for Precision Nutrition

Abstract

Arguably the major health issues in the modern world are chronic diseases with complex etiology that have a strong environmental component. There is now a wealth of evidence that our food environment and our gut microbiome are significant factors for many aspects of our physiology that underpin these diseases. Such understanding has inspired efforts to translate this into healthcare through so-called precision nutrition. Use of deep phenotyping via multi-omic platforms coupled with machine learning to enable ‘targeted’ interventions. A major challenge is that even for specific, defined nutrient interventions outcomes are variable and the underlying mechanisms leading to effects are not well understood. We postulate that poor conceptualization of the system remains a challenge for modelling the interaction between diet components and microbiome processes in both the etiology of, and intervention in, nutrition-

related chronic diseases. I will discuss the potential for improving predictive capacity via definition of the ecological mechanisms that constrain the human and microbiome response to intervention in a range of diseases.

Kamal Dua ^{1,2}

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Emerging Next-Generation Bioactive Therapeutics for Lung Diseases through the Integration of Phytomedicine, Biology and Advanced Drug Delivery Systems

Abstract

Chronic respiratory diseases, including asthma, chronic obstructive pulmonary disease (COPD), cystic fibrosis (CF), and respiratory infections, remain among the leading causes of morbidity and mortality worldwide. The growing burden of these conditions, driven by population ageing, environmental exposures, smoking, and emerging infectious diseases, highlights the urgent need for innovative therapeutic strategies that move beyond conventional treatment approaches. Despite significant advances in understanding the molecular and immunological mechanisms underlying pulmonary diseases, many critical questions remain regarding host–pathogen interactions, inflammatory pathways, disease heterogeneity, and the translation of promising discoveries into effective clinical interventions.

This presentation will showcase our team's translational research focused on developing next-generation bioactive therapeutics for respiratory diseases by integrating phytomedicine, biological sciences, and advanced drug delivery technologies. Our work explores the therapeutic potential of plant-derived bioactives and other novel biological interventions, supported by mechanistic studies that elucidate their anti-inflammatory, anti-oxidant and immunomodulatory properties. To enhance therapeutic efficacy, bioavailability, and targeted pulmonary delivery, these bioactives are incorporated into advanced delivery platforms, including nanoparticle-based systems, designed to achieve controlled drug release while minimising systemic adverse effects.

A key component of this translational framework is the validation and standardisation of advanced biological methodologies to ensure robust, reproducible, and clinically meaningful outcomes. Integrating validated biological models with rational formulation design provides a strong foundation for accelerating the development of safe and effective respiratory therapeutics.

By bridging discoveries in phytomedicine and biology with innovative drug delivery systems, this presentation will highlight how multidisciplinary research is facilitating the translation of emerging bioactive therapeutics from laboratory discovery towards clinical application. These advances offer exciting opportunities for developing more precise, effective, and patient-centred therapies for chronic inflammatory and infectious lung diseases, exemplifying the journey from discovery to translation.

¹ *Biochemistry and Molecular Biology*

² *Great Lakes Bioenergy Research Center*

Michigan State University, East Lansing, MI, USA.

Inspired by Nature's Principles: Discovery and Portability of Terpene Biosynthesis

Abstract

The immense chemical diversity of the mint family (*Lamiaceae*) is awarding our field a cookbook with a spectrum of high-value bioproducts extending far beyond culinary herbs. Recreating nature's recipes in the lab revealed fascinating innovations, including their structure and organization, local adaptation and evolution of formulas over generations, and lastly fusion, presenting previously inaccessible flavors. Examples highlight a dynamic composition of biosynthetic gene clusters at a timescale matching recent speciation and C₂₀ diterpene diversification. In the older buttercup (*Ranunculaceae*) family, we detected a single enzymatic conversion, sufficient for merging the two otherwise insulated chemistries of diterpenes and alkaloids, characteristic for the family. This event has spawned hybrid terpenoid products with most outstanding therapeutic potential. Carrying the hallmark of bioactives, terpenes and terpenoid bioproducts are attractive targets for applications in agriculture, the pharmaceutical industry and as nutraceuticals. Consequently, scaling of production is emerging as the next hurdle of the field. For this, portability of the biotechnology to production-oriented, or -optimized systems will require the development of technology at unprecedented resolution and a careful look at the interpretation of the recipes. Again, we can find inspiration in nature's organized kitchen, such as cellular compartments to keep enzymatic reactions separated (prep stations), dedicated sequestration for safe storage of bioactives and volatiles (pantry), and organ- or cell-specific recipes ensuring time- and location-controlled execution (head-chef oversight). Ultimately, adopting and tuning the natural logistics can enable the next generation of biosustainable and chassis-agnostic engineering.

Ingenie Bio, Sydney, Australia.

Lessons from Integrating Machine Learning into the Bioactive Discovery Pipeline

Abstract

Nature has provided us with a wealth of bioactive molecules, yet the journey from natural hits to optimised leads remains slow, costly and resource-intensive. Machine learning offers efficient strategies for navigating biochemical space and reducing the experimental burden through more informed, evidence-based candidate selection, provided we remain honest about its limitations. This talk presents frameworks and lessons learned from confronting three fundamental challenges in the bioactive discovery pipeline.

Where should we look? We explored data-driven bioprospecting, integrating scientific literature, taxonomic databases, and ethnobotanical knowledge to identify venomous ants and cyclotide-rich plants associated with traditional medicine across multiple Mexican states, illustrating how heterogeneous data sources can guide field collections.

What should we prioritise? We developed and applied predictive models over large chemical databases, including the discovery of marine natural products for neurodegeneration, antimicrobial peptides with reduced haemotoxicity, and scorpion toxins relevant to human envenomation.

How much should we trust what we find? Drawing from several post hoc analyses, we showed that training data distributions - more than model complexity - shape predictive behaviour, and discuss practical approaches to assessing bias, quantifying limitations, and resisting self-reinforcing discovery loops.

Oral Presentations

Electrospun Multi-Encapsulation of Vitamin A for Edible 3D Printing and Personalised Nutrition

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²*Agriculture and Food, CSIRO, Werribee, Australia.* ³*Bega Group, Tatura, Australia*

Abstract

Vitamin A is an essential micronutrient with widespread global deficiency; however, its incorporation into food systems is hindered by its sensitivity to light, heat, and oxygen. This study presents a novel multi-encapsulation strategy designed to enhance the stability and delivery of vitamin A for food applications, particularly among emerging personalised nutrition platforms.

An oil-in-water emulsion containing retinyl palmitate was formulated using Tween 80 as a stabiliser and subsequently embedded within a pullulan-based matrix. Electrospinning was used to process the system and make fibrous scaffolds that effectively trapped emulsion droplets in a microstructured network. The stability and protection of vitamin A within this architecture were evaluated under simulated gastric conditions and compared with conventional drying techniques, including freeze drying and spray drying.

The resulting electrospun fibre-emulsion composites can be further incorporated into pumpkin- and bean-based pastes to develop extrusion-based 3D printing inks. The rheological characterisation and printability assessments of the 3D printing ink material demonstrated improved viscoelastic behaviour and filament fidelity, enabling the successful fabrication of stable 3D structures. The printed products complied with international dysphagia

diet standards, highlighting their suitability for texture-modified nutritional applications.

Overall, this work demonstrates a novel approach to stabilising vitamin A through combined emulsification and electrospinning, while enabling its integration into 3D-printed edible systems. This strategy offers significant potential for the development of personalised nutrient delivery platforms using bioactive-loaded food matrices.

AI-guided discovery of multifunctional bioactive peptides from edible rhizomes and root vegetables

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⁵*Factors Group Australia, Sydney, Australia*

Abstract

Chronic inflammation underpins a wide spectrum of diseases, including metabolic syndrome, neurodegenerative disorders, and autoimmune conditions. While conventional therapies predominantly target downstream inflammatory pathways, food-derived bioactive peptides are gaining attention as natural modulators of inflammation. This study investigates edible rhizomes and root vegetables, specifically ginger, sweet potato, purple carrot, and red radish, as underexplored sources of anti-inflammatory peptides with potential functional and therapeutic relevance.

Proteins were extracted and hydrolysed using food-grade bacterial proteases, applied individually and in combination to maximise

peptide yield and diversity. LC-MS/MS identified 10,049 unique peptides, subsequently screened using AI-guided prediction models based on quantitative structure–activity and property relationships (QSAR/QSPR) to assess potential bioactivities. This computational prioritisation reduced the dataset to 36 high-confidence anti-inflammatory peptide candidates, of which 7 were selected for in vitro validation.

Four peptides demonstrated anti-inflammatory activity through modulation of key inflammatory mediators, including nitric oxide production and oxidative stress pathways. All 7 peptides also exhibited antidiabetic potential, while 2 peptides showed cardioprotective potential, including one with ACE inhibitory activity comparable to Captopril.

Future work will integrate deep mutational scanning to evaluate optimised peptide variants with enhanced target affinity, potency, and stability. This multidisciplinary workflow integrating food science, peptidomics, bioinformatics, and computational biology provides an efficient strategy for prioritising bioactive peptide candidates and reducing experimental screening burden. By linking traditional plant-based knowledge with modern AI-guided discovery, this study highlights edible rhizomes and root vegetables as sustainable sources of multifunctional bioactive peptide candidates for future applications in chronic inflammatory and metabolic disorders.

Pre-immunized NK Cell-Derived Exosomes as Bioactive Messengers for Transferring Antigen-Specific Memory-like Anti-tumor Immunity

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Abstract

Natural killer cells can acquire memory-like functional properties, offering new opportunities for cancer immunotherapy. Exosomes are nanoscale bioactive extracellular vesicles that

mediate intercellular communication by transferring proteins, nucleic acids and membrane-associated signals. This study investigated whether exosomes derived from pre-immunized NK cells could transfer antigen-specific memory-like anti-tumor activity to naïve NK cells. NK cells were co-cultured with fluorescently labelled MCF-7 breast cancer cells to establish a pre-immunization model. Fluorescence microscopy and flow cytometry showed evident membrane material exchange between NK cells and target tumor cells during recognition and cytotoxic interaction, suggesting acquisition of tumor-associated antigenic information. Exosomes were isolated from the culture supernatant of pre-immunized NK cells by ultracentrifugation and characterized by nanoparticle sizing, zeta potential analysis and Western blotting for CD63 and CD81. Treatment with pre-immunized NK cell-derived exosomes significantly reshaped the phenotype of naïve NK cells, with increased expression of memory-associated markers CD25, CD57 and NKG2C, together with modulation of the activating receptor NKG2D and inhibitory receptor NKG2A. Cell cycle and apoptosis analyses indicated that exosome treatment did not compromise NK cell homeostasis. Functionally, exosome-conditioned NK cells showed selectively enhanced cytotoxicity against homologous MCF-7 cells, whereas no comparable enhancement was observed against heterologous A549 cells. In an estrogen-supported MCF-7 xenograft model, exosome-conditioned NK cells exhibited enhanced tumor suppression, increased NK cell infiltration, promoted tumor cell apoptosis and reduced proliferative activity. These findings identify pre-immunized NK cell-derived exosomes as bioactive messengers capable of transferring antigen-specific memory-like anti-tumor immunity, supporting an exosome-based immune modulation strategy for precision cancer therapy.

From Leaf to Bioactive: Optimising Processing of *Vernonia amygdalina* (Bitter Leaf) for Functional Tea Development

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Abstract

Vernonia amygdalina, an underutilised African medicinal plant, is gaining increasing attention for its rich nutritional profile and bioactive potential. In the context of sustainable functional food development, understanding how processing influences bioactive composition and antioxidant activity is critical for optimising plant-based beverages such as functional teas.

This ongoing study investigates the impact of processing methods—dehydration (40, 50, and 60 °C), freeze-drying, and steam blanching—on the antioxidant capacity, bioactive composition, and nutrient profile of *V. amygdalina* leaves cultivated at Western Sydney University (Hawkesbury campus). Comparative analyses were conducted against commercially available teas (peppermint, lemon balm, raspberry, and ginkgo; n = 19). Phytochemical, proximate, and mineral analyses were performed, with mineral composition determined using XRF, while antioxidant activity of methanolic extracts was evaluated using ABTS and DPPH assays.

V. amygdalina demonstrated superior nutritional value, with higher protein (21.22–21.87%) and ash content (8.30–8.60%) compared to commercial teas (protein 12.41–18.70%).

Essential minerals, including Ca (16–21 mg/g), K (8–9 mg/g), and Zn (0.05–0.08 mg/g), were well retained across processing treatments. Notably, samples processed at 50 °C exhibited the highest antioxidant activity ($IC_{50} = 10.80 \times 10^2$ µg/mL, ABTS), indicating an optimal balance between bioactive preservation and processing conditions.

These preliminary findings highlight that targeted processing optimisation enhances antioxidant functionality and nutrient retention, positioning *V. amygdalina* as a promising candidate for the development of sustainable, bioactive-rich functional teas.

Bridging ethnobotany and biotechnology: pharmaceutical and industrial bioactives from a single *Microbacterium* endophyte

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Abstract

Endophytes of medicinal plants are underexplored sources of bioactive specialised metabolites, yet only a small fraction have been functionally linked to biosynthetic gene clusters (BGCs). The continued global burden of tuberculosis (1.23 million deaths in 2024) and rising demand for sustainable microbial production of natural antioxidants and pigments motivate systematic exploration of such strains. Here we report the genome-guided discovery and functional characterisation of two distinct classes of specialised metabolites from *Microbacterium* sp. SD1, an endophyte of *Andrographis paniculata*, a herb traditionally used in Indonesia to treat tuberculosis-associated symptoms.

Comparative genome mining across 1,034 publicly available *Microbacterium* genomes placed SD1 within the genus and identified two prioritised BGCs: a type III polyketide synthase (T3PKS) cluster and a carotenoid-associated terpene cluster designated *mtp*. Both were heterologously expressed in *Escherichia coli*

BL21 (DE3) and characterised by LC–HRMS/MS, feature-based molecular networking and SIRIUS-based in silico annotation. The T3PKS pathway yielded a family of 19 related features, including alkylresorcinol-like scaffolds, with semi-preparative fractions showing selective activity against Gram-positive bacteria and *Mycobacterium smegmatis*, one fraction maintained >90% inhibition at 37.5 µg/mL. The *mtp* pathway produced multiple pigmented metabolites, including a candidate cyclic C50 carotenoid (C₅₀H₇₂O₂; *m/z* 705.559, [M + H]⁺) spectrally distinct from sarcinaxanthin, with fractions displaying measurable ABTS and DPPH radical scavenging activity.

These outcomes bridge ethnobotanical knowledge and modern biotechnology, demonstrating that an endophyte can encode pathways relevant to antimicrobial discovery and sustainable production of high-value bioactive ingredients, and establish a transferable pipeline for ethnobotanically informed strain collections.

Impact of nutrient-dense spinach-enriched bread on postprandial glycaemia, satiety and sensory acceptance: A randomised controlled crossover trial in healthy adults

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Abstract

The declining intake of plant-based foods contributes to the rising global burden of diet-related health problems. Incorporating sustainable vegetables into staple foods may improve nutrient intake, provided formulations maintain acceptable sensory qualities. Spinach (*Spinacia oleracea*) is a nutrient-rich functional

ingredient, but it is highly perishable due to its high water content. This study evaluated the nutritional composition, sensory acceptance, appetite regulation, and postprandial glycaemic and insulinaemic responses of spinach-enriched bread compared with white bread in healthy adults. A single-blinded, randomised crossover trial was conducted in 15 healthy adults (mean age 28.8 ± 7.0 years; BMI 28.0 ± 7.8 kg/m²). Participants consumed either white bread (106 g) or spinach-enriched bread containing 20% (w/w) spinach (111 g; equivalent to 21.8 g blended spinach and 50 g available carbohydrates) following an overnight fast, with a one-week washout between treatments. Compared with white bread, spinach-enriched bread contained higher total polyphenols (+60.6 mg/100 g), fibre (+28%), folate (+58%), calcium (+78%), iron (+90%), and potassium (+2.1-fold), while maintaining similar sensory acceptance for appearance, taste, texture, and aroma (*p* > 0.05). Appetite scores increased 3 h after white bread consumption (*p* < 0.01) but not after spinach bread intake, suggesting a delayed appetite response. Peak glucose concentration, glucose AUC, and insulin AUC did not differ significantly between treatments; however, spinach bread delayed insulin C_{max} by 30 min, indicating altered early insulin dynamics. Overall, spinach-enriched bread improved nutritional quality without compromising sensory acceptance and may modestly influence appetite and insulin responses, supporting sustainable nutrition strategies.

Promoting Bioactive-Rich foods in Culturally and Linguistically Diverse Populations

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Abstract

Background: Plant foods are key sources of bioactive compounds linked to reduced chronic disease risk, yet intake of fruits and vegetables remains suboptimal in many culturally and linguistically diverse (CALD) populations. Health promotion strategies often overlook how cultural practices, food access, and trust influence engagement with bioactive-rich foods. **Objective:** This study synthesises evidence on interventions designed to increase fruit and vegetable intake among CALD populations, with a view to informing culturally appropriate approaches to promoting bioactive-rich diets. **Method:** A systematic review of 32 studies targeting CALD populations was conducted. Cultural adaptation was analysed using the Kreuter's framework. **Results:** Nearly all studies reported at least one positive outcome, with 66% showing increased fruit and vegetable intake. Improvements were also observed in knowledge, attitudes, and dietary diversity. Interventions that incorporated multiple culturally tailored strategies, particularly linguistic, sociocultural, and community-engaged approaches, were more effective than those relying on single adaptations. Programs combining education with practical, experience-based components were consistently associated with stronger outcomes. **Conclusion:** Promoting bioactive-rich diets in CALD populations requires more than general nutrition education. Approaches that embed bioactives within culturally meaningful foods and practices, and that actively involve communities in design and delivery, are more likely to achieve meaningful and sustained dietary change.

Fermentation Enhances the Bioaccessibility of Xanthophylls and the Prebiotic Potential of Vegetables

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Abstract

Lutein and zeaxanthin are xanthophyll carotenoids that play an important role in maintaining eye health and must be obtained from dietary sources, as humans cannot synthesise them *de novo*. However, their concentrations in foods are generally low, and their bioaccessibility is strongly influenced by food matrix and processing methods. This study evaluated the effects of spontaneous and controlled fermentation on the bioaccessibility of lutein and zeaxanthin in kale and corn, two food sources containing measurable levels of these compounds. In addition, the prebiotic potential of the fermented products was assessed by colonic fermentation of the samples with faecal inoculum using a RoboGut model.

Lutein and zeaxanthin contents increased by 30–50% in kale and corn after five days of spontaneous fermentation. Similarly, cellular uptake of those compounds increased by 35% and 38% in kale and corn, respectively. The consistent increase in lutein and zeaxanthin during the controlled fermentation of kale and corn by *Weissella confusa* and *Lactiplantibacillus plantarum*, respectively, further supports the potential of fermentation to enhance xanthophyll content in plant foods. During colonic fermentation, kale samples exhibited a higher abundance of *Bifidobacterium* spp. than corn samples. Furthermore, fermented kale and corn samples showed higher abundances of *Bifidobacterium* spp. compared with their respective raw samples. In all samples, acetate was the predominant short-chain fatty acid, followed by propionate and butyrate. These findings demonstrate that fermentation is an effective strategy for enhancing the bioaccessibility of xanthophylls and improving the prebiotic potential of vegetables.

More than food, not quite drug: stress-testing pharmacological models of bioactive compounds

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Abstract

Bioactive compounds in plant foods are often studied and translated through a pharmacological logic: one compound, one target, one mechanism, one dose–response relationship, one marketable claim. This model has generated genuine mechanistic insight, and its assumptions are embedded in many evidentiary standards, regulatory frameworks, and commercial pathways shaping bioactive research. However, the fit becomes less secure when applied to compounds consumed in complex food matrices, transformed by cooking and storage, metabolised by gut microbiota, and expressed differently across bodies, diets, and ecological contexts. Unlike small-molecule therapeutics, dietary bioactives often act through low-dose, cumulative, pluripotent, synergistic, and context-sensitive effects rather than acute, isolated, and linear mechanisms. This paper stress-tests the pharmacological model against emerging evidence on bioavailability, food-matrix interactions, microbial metabolism, and systems-level function. In critiquing the structuring expectation that health-relevant compounds can be isolated, standardised, dosed, and commercialised as discrete agent–target relationships, this paper asks what pharmacological models make visible, and what they risk obscuring, when bioactives are treated primarily as extractable agents rather than relational compounds. I argue that the health relevance of bioactives may be better understood through frameworks that foreground coevolutionary relationships between plants and mammals, dietary diversity, culinary transformation, agrobiodiversity, and ecological resilience. From this perspective, bioactives are not simply natural drugs awaiting extraction, but compounds whose functions emerge through interactions among plant stress responses, food

systems, microbial ecologies, and host physiology. Reframing bioactives in this way has implications for experimental design, regulatory translation, product development, and the responsibilities of market claims.

From Beany to Meaty: Co-Fermentation of Textured Soy Protein for Meat Analogues

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Abstract

The potential of textured soy protein (TSP) in meat analogues was investigated by co-fermentation with *Lactiplantibacillus plantarum* and *Aspergillus oryzae*. The TSP was fermented at 50% and 70% moisture conditions over 168 h at 24-h intervals. The effect of co-fermentation on pH, microbial growth, colour, water-holding capacity (WHC), oil-holding capacity (OHC), texture, free amino acid (FAA) composition, and volatile flavour profiles. *L. plantarum* dominated at both moisture conditions, while fungal growth was favoured at 50% moisture. The 50% moisture condition produced textural properties comparable to meat and commercial plant-based meat analogues during 72–120 h of fermentation. A total of 12 free amino acids and 35 volatile compounds were identified throughout co-fermentation. Umami-related amino acids, particularly glutamic acid and aspartic acid, exhibited the highest taste activity values (TAV > 1), indicating their major contribution to taste perception. During early fermentation (24–48 h), both moisture conditions were dominated by 1-hexanol, 1-octen-3-ol, and 2-pentylfuran, contributing green, grassy, beany notes. 50% moisture showed increased concentrations of pyrazines, including methyl pyrazine, 2,5-dimethylpyrazine, and 2-ethyl-6-methylpyrazine, corresponding to roasted, nutty, cocoa-like, and meat-like aroma characteristics during mid-fermentation (72–120 h), samples fermented at. In contrast, 70% moisture favoured esters, acetic acid, and guaiacol, producing fruity, fermented, acidic,

and smoky aroma notes. Overall, co-fermentation at 50% moisture effectively improved flavour and textural characteristics, demonstrating its potential as a clean-label strategy to produce plant-based meat analogues (PBMA).

Modelling phytochemical intestinal absorption to enable functional fingerprinting of complex plant extracts

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Abstract

The efficacy of dietary phytochemicals is often limited by poor and highly variable intestinal absorption, constraining their translation into functional food applications. Optimal bio-efficacy requires synchronisation between the time required to reach maximal plasma concentration (T_{max}) and periods of elevated oxidative stress and inflammation. This study presents a statistical model to predict intestinal absorption of phytochemicals based on published human intervention studies. The model predicts T_{max} based on molecular mass and lipophilicity and demonstrates strong performance across diverse phytochemical classes. To extend its application, we introduce a novel approach for characterising the absorption behaviour of complex phytochemical mixtures present in plant extracts. Chemical profiles of plant extracts were obtained using liquid chromatography-mass spectrometry, and molecular features of individual components were used to predict their T_{max} , generating an absorption-based “functional fingerprint”. This approach enables the assessment of temporal bioavailability profiles for uncharacterised plant extracts and provides a new tool for designing bioactive mixtures aligned with physiological demand. To further strengthen biological relevance, current work is integrating

mechanistic validation using advanced cell culture systems within the newly established BioCell Core, a cutting-edge cell culture research supported by a \$1.56 M strategic investment. These models will extend beyond intestinal systems to include hepatic and immune cell models, enabling investigation of key mechanisms such as cellular metabolism, oxidative stress modulation, and inflammatory responses. This integrated approach supports bioactive research and enables the rational design of functional foods tailored to specific health outcomes.

Synergistic Anti-Inflammatory Effects of Celery Seed and botanical extracts: Bioactivity-Guided Identification and Optimisation of Multi-Herb Combinations

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Abstract

Chronic inflammatory conditions remain a major global health burden, driving interest in bioactive-rich herbal medicines with improved efficacy and safety. This study investigated the anti-inflammatory activity and synergistic interactions of extracts from *Apium graveolens* (celery seed), *Curcuma longa* (turmeric), *Zingiber officinale* (ginger), and *Boswellia serrata*. Using bioassay-guided fractionation, chemical characterisation, and *in vitro* macrophage models, we identified active constituents and optimised multi-herb combinations.

Fractionation of celery seed extract revealed Fraction 8 as the most bioactive, with subsequent isolation identifying senkyunolide A as the principal active compound. Quantitative analysis showed that supercritical celery

extracts contained substantially higher levels of key phthalides, correlating with enhanced biological activity.

Anti-inflammatory activity was evaluated via nitric oxide (NO) and interleukin-6 (IL-6) inhibition assays. Synergistic effects were observed for combinations of ginger–turmeric, celery–turmeric, and celery–ginger. Optimal ratios varied by endpoint: for NO inhibition, ginger: turmeric (23:1), celery: turmeric (5:7), and celery: ginger (1:8) produced the strongest synergy, while IL-6 assays identified different but consistent synergistic trends.

These findings demonstrate that both phytochemical composition and extract ratios critically influence bioactivity, supporting the concept of rationally designed multi-component herbal formulations. Notably, synergy was not observed in NF-κB assays, indicating pathway-specific effects.

This work provides a framework for translating traditional herbal knowledge into evidence-based bioactive products, with implications for quality control, formulation optimisation, and future clinical development. Further studies are warranted to elucidate mechanisms, evaluate in vivo efficacy, and support industrial application.

The Comparative Analysis of Various Ionizing Bioburden Reduction Methods for Medicinal Cannabis

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Abstract

Dried medicinal cannabis flower is a chemically complex bioactive product in which microbial safety must be achieved without weakening the cannabinoid, terpene and moisture-related

attributes that support therapeutic consistency. This research evaluated Gamma irradiation, X-ray irradiation and Cold Plasma as bioburden reduction modalities, using a staged design that linked minimum effective dose (MED) establishment, standardised immediate comparison and 12-month real-time stability assessment. Dried flower samples were assessed for total aerobic microbial count (TAMC), total yeast and mould count (TYMC), cannabinoids, total and individual terpenes, loss on drying (LOD) and water activity (a_w). Dose escalation established practical MED ranges for Gamma and X-ray irradiation and a Cold Plasma operating condition, after which modalities were compared under harmonised packaging, environmental and analytical conditions. Gamma and X-ray achieved the most consistent microbiological control, reducing or maintaining TAMC and TYMC at or near reporting thresholds. Major cannabinoid potency, including total THC, was generally more robust than terpene and moisture-related endpoints, although storage was associated with total THC decline and CBN formation, consistent with cannabinoid degradation. Terpenes showed clearer modality-dependent behaviour, with X-ray demonstrating the most favourable 12-month terpene retention. Cold Plasma showed promise as a non-ionising alternative but displayed greater process-configuration dependence and a microbiological excursion requiring further validation. Overall, the findings show that bioburden reduction for dried medicinal cannabis should not be selected on microbial efficacy alone. Modality choice should integrate microbiological control, cannabinoid stability, terpene preservation, LOD and a_w to support product quality, patient safety and regulatory-aligned process justification.

Kakadu Plum Extract Disrupts Proliferation and Metastatic Hallmarks of Lung Cancer

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Abstract

Background: Lung cancer remains one of the leading causes of cancer-related mortality worldwide, with limited therapeutic options and significant treatment-associated toxicity, driving interest in novel bioactive compounds from natural sources such as medicinal plants. The Australian native Kakadu plum (*Terminalia ferdinandiana*) is recognized as one of the richest natural sources of vitamin C and contains diverse polyphenolic compounds with potential anticancer activity; however, its effects on lung cancer progression remain insufficiently characterized.

Aim: This study aimed to investigate the anti-proliferative and anti-migratory effects of Kakadu plum ethanolic extracts on human lung adenocarcinoma A549 cells in vitro.

Methods: Kakadu plum fruits were extracted using hydroethanolic solvent systems to obtain crude polyphenol-rich fractions. A549 cells were cultured under standard conditions and treated with graded concentrations of the extract. Cell proliferation was assessed using MTT and colony formation assays, while cell migration was evaluated using scratch wound healing and transwell migration assays. Mechanistic insights were explored through Human XL protein array profiling and quantitative real-time PCR analysis of gene expression.

Results: Kakadu plum extracts significantly reduced proliferation and migration of A549 cells in a dose-dependent manner. Proteomic and transcriptomic analyses revealed

modulation of key oncogenic proteins and genes associated with lung cancer progression.

Conclusion: These findings suggest that Kakadu plum extract exerts anti-lung cancer activity, mediated through suppression of oncogenic signaling pathways. These results support development of Kakadu plum-derived compounds as therapeutic candidates for lung cancer management. Future work focus on translating these findings into nanoformulated delivery systems to enhance bioavailability and efficacy.

Rapid Targeted Analysis of Hydrolyzed Plant Polysaccharides by DREAMTIME NMR Spectroscopy

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Abstract

Monosaccharide profiling of plant-derived food matrices by conventional ¹H NMR is severely limited by spectral overlap that obscures minor components and complicates structural assignments. While chromatographic methods such as HPAEC-PAD provide excellent resolution, their workflows limit suitability for rapid analytical screening and high-throughput analysis. Here, a selective DREAMTIME NMR strategy is applied to detect individual monosaccharides in acid-hydrolyzed extracts of apple, beetroot, and carrot without chromatographic separation. Using ¹H-¹H COSY-guided selection, frequency-selective excitation and J-editing are used to isolate diagnostic spin systems from highly congested

carbohydrate regions (δ 3.0–5.5 ppm). This enables targeted detection of arabinose, fucose, fructose, galacturonic acid, glucose, and xylose directly from crude hydrolysates. Parallel HPAEC-PAD analysis confirms both identity and relative abundance, showing strong qualitative agreement with the DREAMTIME-derived NMR fingerprints. This approach provides a rapid NMR-based strategy for targeted metabolite screening in complex food matrices relevant to food quality assessment, authenticity verification, and nutritional analysis.

Unravelling a butyrate-linked gut-brain axis in Machado Joseph Disease

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Abstract

Machado Joseph disease (MJD) is a progressive neurodegenerative ataxia with no effective treatments, and Australia has one of the highest prevalences worldwide. Growing evidence implicates the gut microbiome and its metabolites, particularly short-chain fatty acids (SCFAs), in neurodegeneration. Here, we define, for the first time, a gut-brain axis in MJD and evaluate butyrate-enhancing interventions with bioactive potential.

Using a transgenic MJD mouse model, we show that gut microbiome alterations precede neurological decline. Early reductions in butyrate-producing bacteria emerged before motor symptoms appeared, and loss of these taxa positively correlated with later symptom severity, linking early microbiome dysbiosis to disease progression. MJD mice also displayed faster gut transit before motor onset, with further acceleration over time, supporting a temporal sequence in which microbiome changes first, followed by altered gut function, then motor impairment.

Targeted metabolomics revealed significantly reduced butyrate in faeces and brain tissue of

MJD mice, motivating a systematic comparison of butyrogenic interventions: inulin, resistant starch, probiotics, tributyrin and the α -glucosidase inhibitor acarbose. Acarbose was the most effective at elevating circulating butyrate. In transgenic MJD mice, acarbose improved motor performance, increased *Bifidobacterium* abundance in the gut, reduced neuronal protein aggregates, and was associated with decreased expression of the mutant ataxin-3 gene.

Collectively, these findings (i) establish an early butyrate-linked microbiome signature in MJD, (ii) demonstrate a stepwise progression from gut dysbiosis to functional gut changes to motor symptoms, and (iii) highlight acarbose-mediated butyrate enhancement as a promising bioactive strategy for gut-targeted intervention in MJD.

Metabolomic Characterisation of Baby Spinach Phenolics Transformation During Gastrointestinal Digestion and Microbiome-Mediated Metabolism

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Abstract

Gastrointestinal digestion and colonic fermentation determine phenolic transformation and reciprocal microbiome modulation, thereby influencing the generation of gut-derived metabolites that support epithelial integrity, inflammatory regulation, and metabolic homeostasis. Baby spinach phenolics possess antioxidant and microbiome-modulating potential; however, their functional efficacy is constrained by storage-induced degradation and limited gastrointestinal bioaccessibility. This study investigated phenolic transformation in fresh and stored baby spinach (at 4 °C and 25 °C) during simulated gastrointestinal digestion and subsequent colonic fermentation. Standardised in vitro digestion revealed limited phenolic bioaccessibility (10–15%), with storage at 25 °C accelerating oxidative degradation and reducing antioxidant capacity. Storage at 25 °C reduced

TPC from approximately 465 to 265 µg GAE/g and decreased antioxidant activity by nearly 30%, whereas refrigerated storage (4 °C) better preserved phenolic stability and antioxidant capacity throughout the storage period. LC–MS/MS–based untargeted metabolomics characterised digestion-driven structural remodelling and identified diverse colonic metabolites generated during human faecal fermentation. Despite storage-induced alterations in precursor phenolics, 16S rRNA sequencing revealed microbiome-relative microbial stability, with fermentation time exerting a stronger influence on community assembly than storage conditions. Microbial metabolism produced shared downstream metabolites, particularly phenylpropionic and flavonoid-derived intermediates. These results suggest that storage modifies phenolic availability during digestion, while gut microbial metabolism sustains the production of functionally relevant metabolites.

The Use of Green Solvents to Obtain Bioactive-rich Extracts from Broccoli Leaves

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Abstract

Bioeconomy is a system that uses renewable biological resources to generate value while reducing waste and environmental impacts. Within agri-food systems, the valorisation of underutilised biomass can contribute to a circular bioeconomy by converting low-value by-products into sources of high-value bioactive compounds. Broccoli leaves represent approximately 47% of crop biomass and 78% of associated waste, yet remain an underutilised source of phenolic acids, flavonoids and glucosinolates.

Natural Deep Eutectic Solvents (NADES) offer a promising approach for this valorisation,

providing alternative extraction media based on naturally derived components and supporting greener processing. In this study, ten choline chloride- and betaine-based NADES were synthesised and characterised according to their physicochemical properties, biocompatibility and extraction performance.

Among the systems evaluated, Bet:Glucose1:1, Bet:Urea1:2, and Bet:Glycerol1:2 were identified as top-performing systems. When assessed against conventional solvents, Bet:Glu1:1 yielded the highest phenolic content, and Bet:Gly1:2 produced the highest total flavonoid content, exceeding those obtained with water, 80% ethanol, and 80% methanol. Untargeted metabolomics revealed distinct phytochemical fingerprints across the NADES, with selective enrichment of phenolic acids, flavonoids, coumarins, and terpenes. These compositional differences were reflected in the antioxidant assays, with NADES-based extracts exhibiting up to 72.3% greater antioxidant activity than conventional solvent extracts.

In an environmental assessment (AGREE) NADES-based workflow scored 0.66 compared with 0.50 for conventional solvents, supporting its improved overall sustainability. These findings demonstrate the potential of NADES-based extraction as a sustainable strategy for broccoli leaf valorisation within a circular bioeconomy.

Challenges and Opportunities in Translating *Leptospermum* Bioactives into Functional Products

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Abstract

The growing demand for natural health-promoting ingredients has increased interest in plant-derived bioactives for applications in functional foods, nutraceuticals, cosmetics, and pharmaceuticals. Among Australian native flora, *Leptospermum* species, including *Leptospermum petersonii* and *Leptospermum polygalifolium*, are recognised as valuable sources of bioactive compounds with reported

antimicrobial, antioxidant, anti-inflammatory, and other therapeutic properties. These attributes highlight their potential for the development of innovative functional products. Despite this potential, the successful translation of *Leptospermum* bioactives to commercially viable products remains challenging. Major barriers include the complexity and natural variability of bioactive constituents resulting from genetic diversity, environmental conditions, geographic location, and harvest timing. Achieving product standardisation and batch-to-batch consistency is further complicated by the influence of extraction, processing, and storage conditions on bioactive composition, stability, and efficacy. Additional challenges relate to the ethical and legal considerations associated with the utilisation of native plant resources. These include obtaining appropriate consent, establishing equitable benefit-sharing arrangements with Indigenous communities. Regulatory approval also presents significant hurdles, as generating the safety, quality, and efficacy data required for compliance with Therapeutic Goods Administration (TGA) and international regulatory frameworks can be both costly and time-consuming. Furthermore, establishing sustainable and scalable sources of plant material is essential for long-term commercial viability. Addressing these challenges will require genuine partnerships with Indigenous communities alongside advances in cultivation, analytical chemistry, extraction, and formulation technologies. These innovations can improve product consistency, support sustainable production, strengthen scientific validation, and facilitate regulatory approval, ultimately accelerating the development of commercially viable *Leptospermum*-based functional products.

Promising, Not (Yet) Proven: Balancing Evidence and Enthusiasm when Communicating Bioactive Research.

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Australia.*

Abstract

Bioactive research routinely uncovers exciting findings – a compound that inhibits a pathogen, reduces inflammation, or modulates the gut microbiota in a pre-clinical model. Translating these findings for broader audiences, however, poses a persistent challenge: how do we convey genuine enthusiasm for emerging results while accurately representing the strengths, and limits, of the underlying evidence? A single promising laboratory finding can be extrapolated into far broader claims of efficacy than the evidence supports, with real consequences for public trust, consumer decision-making, and scientific credibility.

Drawing on my own research in bioactive honey, superbugs, and the gut microbiome, this talk explores where the gap between evidence and belief tends to emerge. It considers what responsible communication of emerging bioactive research can look like in practice, conveying nuance and uncertainty while still preserving scientific enthusiasm.

From Fed to Free-Living: Integration of Dietary Biomarkers and Metabolomics into Precision Nutrition

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Abstract

Metabolomics can provide greater insight into dietary intake and the mechanisms in which diet may influence health outcomes, thus helping us advance precision nutrition at a population and individual level. Therefore, this proof-of-concept study aimed to test the reproducibility of dietary metabolomic signatures generated in a controlled dietary feeding intervention where all food was provided against an independent sample of free-living individuals who received 6-

months of medical nutrition therapy (MNT). Plasma metabolomic signatures were constructed from 43 metabolites representing a 'healthy' and 'unhealthy' dietary pattern using data from a randomised controlled crossover feeding study. These dietary metabolomic signatures were used to map changes in diet-derived plasma metabolites over 6-months in an independent sample of rural adults (n=11) screened as at elevated-cardiovascular disease risk who received MNT. Mixed-effect models were used to evaluate change in metabolites and dietary intake across the MNT intervention. Principal component analysis (PCA) and partial least squares discriminant analysis (PLS-DA) plots were used to compare metabolite profiles between both studies. Plasma Ethylmalonate

and Glycosyl-N-stearoyl-sphingosine (d18:1/18:0) significantly reduced at both 3- and 6-months. Ethylmalonate was associated with intake of grains and both Ethylmalonate and Glycosyl-N-stearoyl-sphingosine (d18:1/18:0) were associated with changes in cardiometabolic outcomes (triglycerides, total cholesterol and LDL-cholesterol). Across the MNT intervention self-reported diet quality significantly improved by approximately 13% from baseline. PCA and PLS-DA plots showed that plasma metabolite signatures at 3- and 6-months aligned more closely with the 'healthy' dietary pattern signature. These findings are promising for the advancement of precision nutrition and the inclusion of metabolomic signatures that are representative of diet quality.

Lightening Talks

Understanding Fat, Protein and Carbohydrate Rearrangement of Plant-Based Milk Alternatives in Coffee

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Abstract

Plant-based drinks continue to play a significant role as an alternative to dairy milk for lactose-intolerant individuals, those who enjoy coffee-milk drinks and those changing their lifestyle because of health reasons. Therefore, plant-based drinks' manufacturers strive to formulate milk alternatives which can withstand the acidic coffee environment and mimic the behaviour and taste of the much-preferred dairy milk. Despite these efforts, there is evidence of milk

alternatives separating when heated or poured into coffee. These undesirable behaviours depend on how well their major molecular components (fat, protein and carbohydrate) interact with the coffee environment. In this work, we present the molecular arrangement of fat, protein and carbohydrate in plant-based drinks comparing with bovine milk, with and without coffee. We have compared the structural features of these components using spectroscopy (small-angle x-ray scattering, dynamic light scattering, Fourier transform, laser diffraction x-ray diffraction and x-ray fluorescence) and chromatography (gas chromatography-mass spectrometry and size-exclusion chromatography) to determine molecular arrangements. In milk alternatives, two kinds of particles exist: protein-fat and protein-fat-carbohydrate, while in bovine milk protein-fat-carbohydrate particles are more evenly distributed. When oat milk is mixed with coffee, protein and calcium are sedimented. These results provide a foundation to improve milk alternatives' formulation for consumer satisfaction.

Understanding the Digestibility of Meat Fat Analogues: Implications for Nutraceuticals Absorption

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Abstract

The world population is increasing exponentially and is expected to reach approximately 9.2 billion people by 2040, which is leading to global food insecurity. To overcome the challenges of feeding the global population in an environmentally friendly manner, alternative meats and milks have been developed as a nutritional alternative to animal proteins and fats, with an array of products present in market. However, while extensive research has been conducted on protein digestion of these analogues, the digestion and absorption of fats remain unexplored, despite their crucial role in nutritional quality, sensory properties, and beneficial health impacts. Plant-sourced fats, which vary in saturation levels and structures (including emulsified or non-emulsified), impact the fats absorption, digestion kinetics of fats as well as bioavailability of fat-soluble vitamins and micronutrients. In light of this, the focus of this study was to understand how plant and microbial fat analogues are digested in the gastrointestinal tract (GIT), in contrast the meat fats. An advanced in-vitro model of lipid digestion was used to simulate the enzymatic environment of the GIT, which allowed for probing of unique insights into the role of fat structure on lipase-mediated digestion. Further, the solubilization of essential micronutrients and vitamins during lipid digestion was investigated to predict potential changes in micronutrient/vitamin absorption following

consumption of alternate fat analogues versus meat fats. Ultimately, the findings derived from this research aid in identifying nutritional differences of plant and microbial fats and help direct the future development of alternate fat analogues.

Functional Characterisation of Polyunsaturated Fatty Acids and Their Metabolites at GPR55 Receptor Using the TRUPATH Assay

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Abstract

Polyunsaturated fatty acids (PUFAs) and their bioactive metabolites are key lipid mediators implicated in inflammation, metabolism, and neuronal signalling. They have been proposed to interact with non-classical cannabinoid-related receptors such as GPR55. However, their direct functional activity at this receptor remains incompletely characterised. In this study, we assessed the effects of omega-3 (EPA and DHA), omega-6 PUFAs (γ -LA), and their ethanolamide and glycerol ester derivatives on human GPR55 expressed in HEK-293 Flp-In T-REx cells using the TRUPATH Ga13-based BRET assay.

The endogenous ligand lysophosphatidylinositol (LPI) and the synthetic agonist ML-184 elicited robust, concentration-dependent activation of GPR55, with pEC_{50} values of 5.87 ± 0.15 and 6.53 ± 0.11 , and E_{max} values of 3.34 ± 0.20 and 3.81 ± 0.11 , respectively. The agonist effects of LPI were blocked by the GPR55 inhibitor, ML-193. In contrast, PUFAs did not activate or inhibit GPR55, however, several PUFA-derived metabolites, including DHEA, γ -LEA, AEA, 2-AG, 2-AG ether, and 2-LG, reduced LPI-induced GPR55 signalling.

Collectively, these findings demonstrate that PUFAs are not directly involved in GPR55 activation of the Ga13 signalling pathway, whereas specific PUFA-derived metabolites can negatively modulate receptor signalling. These

results support a role for lipid metabolism in regulating GPR55 activity and suggest that PUFA metabolites may contribute to the physiological control of this receptor.

Anticancer properties of fucoidan and its potential molecular targets

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Abstract

Fucoidan is a sulphated polysaccharide derived from the cell walls of brown seaweeds that has been widely studied for its diverse biological activities, including anticancer effects. Previous studies suggest that variations in monosaccharide composition and sulphation patterns influence the biological activity of fucoidan through interactions with multiple cellular targets and signalling pathways. While molecular regulators and signalling pathways such as Bax, Bcl-2, and Wnt/ β -catenin are implicated in fucoidan-mediated apoptosis, proliferation, and cell cycle regulation, our understanding of the structural features of fucoidan and its precise molecular targets remains limited. Therefore, this study aimed to characterise fucoidan extracted from *Turbinaria decurrens* and evaluate its anticancer activity against colorectal cancer (CRC) cells. Fucoidan was extracted from *T. decurrens*, purified, characterised, and tested against SW480, HT29, and HCT116 colorectal cancer cells by evaluating cytotoxicity, migration, colony formation, cell cycle distribution, and apoptotic induction. Finally, multi-omics approaches, including proteomic and metabolomic analyses, were applied to investigate the molecular targets and mechanisms underlying fucoidan

activity. The fucoidan selected for anticancer testing had a molecular weight of 74.5 kDa, sulphate content of 33.4 %, monosaccharides dominated by fucose and galactose, with α -L-(1 $\rightarrow$ 3) Fucp and α -(1 $\rightarrow$ 4)-Fucp linkages identified as major structural features. Fucoidan exhibited significant cytotoxicity in all CRC cell lines and inhibited cell migration at 250 μ g/mL. At 500 μ g/mL, fucoidan induced G0/G1 phase arrest in HT29 and HCT116 cells, but not in SW480 cells. Ongoing multi-omics integration aims to identify molecular targets underlying fucoidan-mediated anticancer activity.

Liposomal encapsulated curcumin attenuates lung cancer proliferation, migration and apoptosis

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Abstract

Lung cancer is one of the most diagnosed types of cancer worldwide, accounting to one fifth of cancer-related deaths. The high prevalence of lung cancer (LC) is due to various factors such as environmental pollution or lifestyle factors such as cigarette smoking. Non-small cell lung cancer (NSCLC) is the most diagnosed type of lung cancer. Despite the availability of several lines of treatment for NSCLC, including surgery, chemotherapy, radiotherapy, immunotherapy, and combinations of these, this disease still has very low survival rate, highlighting the urgent need to develop novel therapeutics. Phytochemicals, or plant-derived bioactives are a promising source of biologically active compounds. Among these, curcumin is particularly relevant due to its wide range of anticancer, antioxidant, and anti-inflammatory

activity. However, its poor solubility causes low bioavailability, severely limiting its clinical application. Encapsulation of curcumin in nanoparticle-based delivery systems such as liposomes holds promise to overcome this limitation. In the present study, we demonstrate promising *in vitro* anticancer effect of curcumin-loaded liposomes (PlexoZome®) on A549 human lung adenocarcinoma cells. The study reveals how liposomal curcumin functionally suppresses the proliferation, migration, and colony formation of these cells whilst also drastically reducing the expression of multiple cancer marker proteins. This work provides foundational data for the development of a curcumin-based nano formulation to be used as therapy for NSCLC.

Applying discovery proteomics coupled with *in-silico* data mining to understand the bioactive potential of *Cucumis sativus* (Lebanese cucumber) tissue extracts

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Abstract

The *Cucurbitaceae* family includes nutritionally and economically important crops, such as melons, cucumbers, and pumpkins. Cucumbers are among the top 10 vegetables by production and industrial value in Western Australia.

Beyond their nutritional benefits, many *Cucurbitaceae* fruits offer potential health benefits, including antioxidant, antidiabetic, antihypertensive, and antimicrobial properties. However, research has largely focused on secondary metabolites, with limited understanding of bioactive peptides (BPs) bioactive peptides (BPs), particularly beyond seeds. This study investigated the tissue-specific distribution of BPs in Lebanese cucumber (seed, peel, and flesh) using multiple extraction conditions and integrated *in-silico* and *in-vitro* validation. Proteins were extracted using alkaline, acidic, and chaotropic solvents, followed by liquid chromatography-tandem mass spectrometry (LC-MS/MS) with data-dependent acquisition combined with database searching and *in-silico* data mining. Urea extraction yielded the highest number of proteins at a 1% false discovery rate, with normalised counts (based on the size of the *Cucumis sativus* proteome) of 2.55, 3.45, and 3.45 for flesh, peel, and seed, respectively. The detected proteins were primarily enriched for functions related to small-molecule metabolic process, oxoacid metabolic process, and protein translation, as determined by Gene Ontology overrepresentation analysis. *In-silico* bioactive motif mapping of tryptic peptides against a curated bioactive database (>80% similarity) revealed a high prevalence of antioxidant motifs, which was supported by DPPH-based *in-vitro* functional validation. These studies provide a comprehensive tissue-resolved protein and peptide resource for *Cucumis sativus* and highlight the potential to valorise processing by-products into nutraceutical ingredients, contributing to waste management and added economic value.

Antimicrobial Activity of *Hericium erinaceus* (Bull.) Persoon Extracts Against Neurodegeneration-Associated Bacterial Pathogens: Bioactive Profiling and Cultivation Optimisation

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Abstract

Hericium erinaceus (HE), commonly known as Lion's Mane mushroom, is a bioactive rich traditional medicinal fungus with well-documented anti-inflammatory, neurotrophic, and immunomodulatory properties. Emerging evidence indicates specific bacterial species as potential triggers of neuroinflammatory and neurodegenerative conditions, positioning antimicrobial bioactives as a promising avenue for neuroprotective intervention. This study investigated the antimicrobial activity of HE extracts against neurodegeneration-associated five bacterial pathogens: *Acinetobacter baylyi*, *Pseudomonas aeruginosa*, *Streptococcus pyogenes*, *Klebsiella pneumoniae*, and *Proteus mirabilis*.

HE mycelium was cultivated under controlled laboratory conditions with cultivation optimised through mechanical agitation during incubation, achieving a 1700% increase in mycelium yield compared to static methods. Sequential solvent extraction was performed using five solvents: hexane, chloroform, ethyl acetate, methanol, and water, to capture the bioactive compounds across a range of polarities. Antimicrobial activity was evaluated, at concentration ranging from 4.2 to 50.4 mg/ml using standard microbial assays, with all extracts demonstrating moderate inhibitory activity against tested strains.

Toxicity assessment using *Artemia franciscana* nauplii lethality assays demonstrated 0% lethality at concentrations above 1000 µg/mL, classifying HE as non-toxic. Non-targeted LC-MS analysis identified a range of potential bioactive compounds across all extracts, with elution profiles consistent with their respective polarity.

These findings demonstrate that HE extracts possess antimicrobial activity against bacterial species implicated in neurodegeneration supporting a potential mechanistic link between its bioactive constituents and neuroprotective pathways. Therefore, this study demonstrates HE can be a potential candidate for neurological

health applications and further studies will be conducted to gather more evidence.

Maternal sugarcane-derived polyphenol supplementation programme the foetus via neonatal salicylate- and lipid-associated metabolome shifts

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Abstract

Maternal nutrition during gestation can influence offspring metabolism. We evaluated neonatal metabolomic changes in Holstein calves following maternal supplementation with a sugarcane-derived polyphenol extract (Polygain®) during gestation. A total of 120 pregnant Holstein cows at 5 months ±7 days of gestation were allocated into control and treatment groups. Treatment cows received a sugarcane-derived polyphenol extract at a dose of 50 g/day/animal from mid-gestation until parturition. After calving, 48 female calves (20 control and 28 treatment) born to these cows were selected and grouped according to maternal treatment. Birthweight was recorded for all calves, and blood samples were collected for serum biochemical and plasma untargeted metabolomic profiling using GC-MS. Data were analysed using multivariate statistics, univariate testing with false discovery rate correction, random forest, receiver operating characteristic and pathway enrichment. Serum biochemistry and birthweight did not differ significantly between groups. However, multivariate analyses demonstrated clear separation between groups. Salicylic acid and phosphoric acid were consistently higher in treatment calves (P<

0.05). Several fatty acids including elaidic, oleic, palmitic and palmitoleic acids contributed strongly to group separation. Random forest and ROC analyses identified salicylic acid (AUC=0.96) and several unsaturated fatty acids (AUCs ≥ 0.90) as top discriminators. Pathway enrichment analyses showed treatment-associated alterations in glyoxylate and dicarboxylate metabolism, TCA cycle and multiple amino-acid and carbohydrate pathways. Maternal supplementation of polyphenol induced neonatal metabolic remodelling characterised by salicylate and lipid-related signatures supporting potential foetal programming effects. Further work should assess implications for growth, immunity and later-life metabolic effects.

Cardiovascular-Relevant Bioactivity Profiling of Native Australian Acacia Species: Antioxidant, Phenolic and Anti-Inflammatory Properties.

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Abstract

Cardiovascular disease in Australia is strongly shaped by lifestyle factors and disproportionately affects Aboriginal and Torres Strait Islander peoples, highlighting the need for culturally appropriate, innovative treatments. *Acacia* species are rich in polyphenols and other bioactive metabolites, yet their cardiovascular properties remain poorly defined- despite traditional use. Because oxidative-stress and chronic inflammation drive endothelial dysfunction and cardiovascular disease, antioxidant and anti-inflammatory assays provide a crucial foundation for assessing potential cardioprotective activity.

Nineteen *Acacia* species were ethanol-extracted and HPLC profiled to generate comparative

phytochemical fingerprints. Antioxidant activity was assessed using DPPH assays, total phenolics quantified via the Folin-Ciocalteu method, and anti-inflammatory activity evaluated through nitric-oxide inhibition in LPS-stimulated macrophages, with IL-6 and TNF- α assays planned for further characterisation.

The extracts showed substantial chemical diversity, with HPLC profiles revealing distinct phenolic and flavonoid signatures. Several species demonstrated strong antioxidant activity, with DPPH inhibition positively linked to total phenolic content. Multiple extracts significantly reduced NO production in activated macrophages, and selected species are expected to suppress IL-6 and TNF- α , indicating broad anti-inflammatory potential. These findings highlight species-specific bioactivity and suggest that certain *Acacia* taxa contain compounds capable of modulating oxidative and inflammatory pathways relevant to cardiovascular health.

This study provides one of the first comparative bioactivity assessments across numerous Australian *Acacia* species and supports their potential as sources of cardioprotective bioactives. Future work will incorporate endothelial cell assays and ACE inhibition testing to strengthen cardiovascular relevance and identify lead species for deeper investigation.

Tryptamine derived Pictet–Spengler metabolites in Australian Acacia species: spontaneous or enzymatic origin?

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Abstract

Acacia (Fabaceae) is the most spacious genus of flowering plants in Australia, with over 1000 species recognised. The biosynthesis of alkaloids in *Acacia* is of emerging interest, especially following a clinical trial which described the psychopharmaceutical effects of *N,N*-dimethyltryptamine derived from *Acacia acuminata*. Pictet–Spenglerase (P-S) enzymes catalyse the condensation of β -arylethylamines with aldehydes or ketones, to form nitrogen containing heterocycles including tetrahydroisoquinoline and tetrahydro- β -carboline. This study collected branchlets of 73 *Acacia* species from the Botanic Gardens of Sydney. The steady-state concentration of tryptamine and the corresponding P-S product 1-methyl-1,2,3,4-tetrahydro- β -carboline (1MeTH β C) was studied by LC-MS/MS.

Tryptamine was detected in 60 species, whilst 1MeTH β C was detected in 25 species; with an approximate detection limit of 0.1 μ g/g. Distributions for both compounds were positively skewed. Enzymatic synthesis might be required to account for the high concentration of 1MeTH β C observed in some species, with the highest level in this study at 1.68 ± 0.13 mg/g (dry weight basis). However, a weak positive correlation was observed between the two metabolites, 0.438711 (Pearson R). This positive correlation does not exclude the possibility that the presence of 1MeTH β C was the result of a concentration-dependant spontaneous reaction with acetaldehyde, rather than enzymatic reaction; especially for species with low yields. Artefactual formation of 1MeTH β C during sample preparation was evaluated by spiking synthetic tryptamine onto *Acacia oraria*, a species negative for both metabolites. Further studies of *Acacia* should investigate alternate biogenic amines and carbonyl substrates of the putative Pictet–Spenglerase, before attempting isotope-assisted metabolic flux analysis.

Poster Presentations

Vibrational Spectroscopy for Protein Quantification in Plant-Based Milk Alternatives: A Comparative Evaluation of Raman and ATR-FTIR Approaches

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Abstract

The rapid growth of the plant-based milk alternatives (PBMA) market demands fast, reliable, and minimally invasive analytical tools for protein quantification in quality control settings. Vibrational spectroscopy methods offer label-free approaches based on protein-specific molecular vibrations, yet their applicability to complex food matrices has not been fully evaluated. This study compares Raman spectroscopy and attenuated total reflectance Fourier transform infrared (ATR-FTIR) spectroscopy for protein quantification in commercial oat, almond, soy, and bovine milk samples, benchmarked against nitrogen-based elemental analysis.

Raman spectroscopy demonstrated excellent analytical performance in purified protein systems, with calibration curves yielding strong linearity ($R^2 = 0.998$). However, when applied to PBMA, fluorescence interference from the complex food matrices severely compromised spectral quality, rendering quantitative analysis impractical for routine use.

ATR-FTIR spectroscopy overcame these limitations. With appropriate selection of analysis parameters, excellent linearity was achieved ($R^2 = 0.997$). FTIR-predicted protein values for soy and bovine milk fell within approximately 5–7% of both manufacturer label claims and elemental analysis estimates, while almond milk predictions agreed within approximately 14% of elemental analysis values. Blind testing further confirmed the accuracy of the calibration model.

These findings position ATR-FTIR spectroscopy as a highly promising tool for industrial protein quantification in plant-based foods, combining rapid analysis, minimal sample preparation, and robust performance across diverse matrices. Future investigation of surface-enhanced Raman spectroscopy (SERS) may extend the applicability of Raman-based methods to complex food systems.

Plant-derived bioactive peptides as novel candidates for metabolic syndrome and neuroprotective applications

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Abstract

Chronic metabolic diseases and neurodegenerative disorders are major global health challenges influenced by dietary factors. Plant-derived bioactive peptides have emerged as promising and sustainable candidates as nutraceutical or functional food applications. This study evaluated the *in vitro* bioactivity of five novel peptides derived from sunflower seeds, eucalyptus leaves, ginkgo leaves, and jujube fruit. Peptides were identified following enzymatic hydrolysis, using LC-MS/MS, and *in silico* bioactivity prediction, then synthesised for experimental validation.

The peptides were screened for antioxidant capacity (ORAC assay), antihypertensive activity through angiotensin-converting enzyme (ACE) inhibition, antidiabetic activity via α -amylase and α -glucosidase inhibition, and neuroprotective potential using monoamine oxidase (MAO) and acetylcholinesterase (AChE) inhibition assays.

Two peptides demonstrated particularly strong bioactivity profiles. A sunflower-derived peptide showed significant inhibition of α -amylase ($IC_{50} = 6.06 \mu M$), α -glucosidase ($IC_{50} = 53.93 \mu M$), and ACE ($IC_{50} = 53.32 \mu M$), indicating multifunctional cardiometabolic potential. A eucalyptus-derived peptide exhibited potent antidiabetic activity, with IC_{50} values of 5.23 μM and 49.08 μM against amylase and glucosidase, respectively.

These findings highlight the potential of plant-derived peptides as multifunctional bioactive ingredients for metabolic health applications and support further investigation of their cardiometabolic and broader neuroprotective potential.

Smart iron-targeting therapeutics: chelation strategies and microbiome modulating delivery systems

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Abstract

Iron plays a vital role in cellular function, immune regulation, and metabolic processes, yet iron deficiency remains one of the world's most widespread nutritional disorders. Current iron supplements often suffer from poor bioavailability, gastrointestinal side effects, oxidative stress, and disruption of the gut microbiome due to uncontrolled iron release.

This project aims to develop smart iron-targeting therapeutics based on nanoporous delivery platforms, chelation strategies, and microbiome-modulating systems. Mesoporous silica nanoparticles and iron-based metal-organic frameworks (MOFs) are being investigated as potential carriers for ferric phosphate (FePO₄) delivery. The materials are being characterised using X-ray diffraction (XRD), nitrogen adsorption-desorption analysis, scanning electron microscopy (SEM), transmission electron microscopy (TEM), dynamic light scattering (DLS), zeta potential analysis, X-ray fluorescence (XRF), and X-ray photoelectron spectroscopy (XPS) to evaluate mesoporous structure, morphology, pore properties, colloidal behaviour, surface chemistry, and iron incorporation.

Future studies will incorporate chelators, polymer coatings, and probiotics such as *Lactobacillus plantarum* to improve iron solubility, minimise oxidative stress, support gut microbiota, and enable controlled intestinal release. This work aims to establish safer, microbiome-friendly, and controlled iron-delivery platforms with improved therapeutic efficiency and iron homeostasis.

Elucidating Cancer-related Epigenetic Targets of *Passiflora edulis* via Computational Approaches

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Abstract

Multiple evidence has demonstrated the significant roles of epigenetic changes in the progression of cancer cells. Consequently, there exists compelling therapeutic potential in targeting proteins involved in these mechanisms. This study employs network pharmacology to investigate the functions of bioactive compounds from *Passiflora edulis* and their molecular mechanisms in cancer epigenetics, aiming to elucidate the intricate relationships among cancer targets. Active metabolites of *P. edulis* and their associated target genes were obtained from the Natural Product Activity and Species Source (NPASS) and Swiss Target Prediction databases. Disease-associated targets were obtained from the GeneCards platform. Core targets were selected by a protein-protein interaction (PPI) network, followed by extensive GO and KEGG enrichment studies. Molecular docking and molecular dynamics simulations were utilised to unveil the interactions between hub genes and bioactive compounds. Thirty-five intersecting targets between cancer epigenetics and *P. edulis* were discovered, with ESR1, EGFR, GSK3B, PTGS2, ESR2, CYP19A1, CCNB1, CDK1, MAOA, and MAOB designated as hub genes. GO and KEGG pathway analysis indicated that these compounds are integral to cancer-related processes, including the cell cycle, cell proliferation, and apoptosis. Molecular docking of hub genes reveals favourable binding interactions with apigenin, genistein, and flavanone, with Vina Scores equivalent to reference inhibitors. The active metabolites of *P. edulis* may possess therapeutic capacity in cancer epigenetic mechanisms through targets including ESR1, ESR2, and MAOB. The regulatory mechanisms are probably linked to multiple critical pathways in cancer progression. Focusing on critical nodes within this network may provide a multifaceted therapeutic approach for cancer treatment.

R-phycoerythrin-derived peptides from the red seaweed *Halymenia dilatata* with antidiabetic and antihypertensive potential

Mst Sharmin Sultana Shimu

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Abstract

Naturally occurring proteins and peptides from macroalgae are increasingly recognised as valuable sources of bioactive compounds with potential applications to human health, functional foods, and therapeutics. Red macroalgae (*Rhodophyta*) are particularly rich in phycobiliproteins, which are widely used as natural colourants and fluorescent biomarkers. Among these, R-phycoerythrin (R-PE) is often a dominant phycobiliprotein in red seaweeds and has attracted growing interest due to its potential bioactive properties. However, R-PE derived from the genus *Halymenia* remains largely unexplored.

This study investigated the bioactive potential of R-PE protein and derived peptides from *Halymenia dilatata* for antidiabetic and antihypertensive applications. LC-MS/MS analysis was used to identify peptides from four enzymatic hydrolysates prepared from crude R-PE extracts. Following *in silico* bioactivity screening, three peptides were selected for further evaluation. Among these, P-1 (VGGTGPLDEWGIA)_(R-PE) exhibited the strongest α -amylase inhibitory activity, with an IC₅₀ value of 0.176 mg/mL, comparable to that of the reference drug acarbose (0.161 mg/mL), indicating potential antidiabetic properties. P-1 also demonstrated the highest ACE inhibitory activity (67.7%) with an IC₅₀ of 0.435mg/mL, indicating potential antihypertensive properties. In addition, purified R-PE protein exhibited strong antioxidant activity across four biochemical assays.

This study highlights the bioactive potential of R-PE and its derived peptides from *Halymenia dilatata* for antidiabetic, antihypertensive, and antioxidant applications. Further structural characterization and *in vivo* studies are needed to better understand their biological activity and mechanisms of action.

Bioactive effects of Aqueous Leaf Extract of Bitter Leaf (*Vernonia amygdalina*) and black cumin on Blood Glucose, lipid profile, and pancreatic cell regeneration in Alloxan Induced Type-1 Diabetic Mice

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Abstract

Plants of the genus *Vernonia* are rich in several bioactive compounds that provide significant antioxidant, anti-inflammatory, and antimicrobial properties, making them valuable in both traditional and preclinical medicines. The antidiabetic effects of the leaf extract of *Vernonia amygdalina* and the seed extract of black cumin were investigated using alloxan-induced diabetic mice. There were six groups of mice, and each group comprised five mice. The groups of mice represented a control group, a diabetic control group, and the other four groups treated with *Vernonia*, black cumin, *Vernonia* with black cumin, and amyral[®]. The leaf extracts of *Vernonia amygdalina*, the seed extract of black cumin, and *Vernonia* with black cumin extract had hypoglycemic effects on all the groups of diabetic mice. The treatments reduced fasting blood sugar (FBS) levels of the mice over eight weeks. The hypoglycemic effect of *Vernonia amygdalina* leaf extract reduced the mean FBS level comparable with the Amyral[®] treated group. The biochemical analysis showed that the aqueous leaf extract significantly reduced blood glucose and increased body weight. The lipid profile of Cholesterol, Triglyceride, HDL, and LDL was found to be better than usual ($p > 0.05$). The histopathological study revealed that the *Vernonia*-treated group and the *Vernonia* with black cumin-treated group worked together, and that pancreatic cells may regenerate or repair, thereby regenerating islet cells in alloxan-induced diabetic mice. Our results suggest that *Vernonia* leaf extract may contain bioactive compounds to induce insulin production and regulate glucose utilization to maintain normal pancreatic cell function.

Assessment of Oxidative Behaviour in Polyunsaturated Fatty Acid (PUFA)-rich Oils Using Spectroscopic Techniques and Multivariate Analysis

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Abstract

There is a growing need for rapid and robust analytical methods to assess the authenticity and quality of natural products in the bioactive sector. Lipid oxidation significantly affects the nutritional value, safety, and shelf life of edible oils, leading to secondary oxidation products such as peroxides, aldehydes, and ketones. Therefore, early detection and monitoring of oxidation are essential to maintain product integrity, consumer safety, and brand reputation. This research aims to develop a rapid analytical platform for detecting adulterants and assessing lipid oxidation and oxidative stability in natural edible oils. A non-destructive and reagent-free approach was applied using Fourier-transform infrared (FTIR) and Raman spectroscopy combined with multivariate data analysis to evaluate oxidative degradation in three PUFA-rich oils: borage oil (BO), evening primrose oil (EPO), and fish oil (FO). Raman spectroscopy assessed the degree of unsaturation through key vibrational markers, while FTIR detected functional group changes during oxidation. Thermal oxidation at 50 °C simulated realistic storage conditions, and molecular changes were monitored over time. Spectral data were analysed using chemometric classification models, including partial least squares-discriminant analysis (PLS-DA), random forest (RF), and support vector machine (SVM). Among these, SVM achieved the highest classification accuracy in distinguishing oxidised (OX) from non-oxidised (NOX) samples. Overall, this study demonstrates an accurate, rapid, and sustainable platform for detecting lipid oxidation in PUFA-rich oils. This approach offers strong potential for industrial quality assurance by reducing analysis time, cost, sample preparation, and reagent use, while supporting oil quality, authenticity assessment, regulatory compliance, and consumer confidence.

Investigation of Plasma Membrane Protein Remodeling and Tight Junction Alterations in Carcinoma through Integrated Synthetic Probe and Nanoparticle Design Targeting CLDN and EGFR

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Abstract

Tight junction (TJ) proteins, including claudins and occludins, undergo dysregulated remodeling during epithelial carcinogenesis, while EGFR overactivation further compromises membrane integrity. Despite co-

implication in cancer progression, their membrane axis remains mechanistically unresolved in most cancers. Anti-EGFR-Au nanoparticles are novel tools for real-time membrane-level EGFR enrichment and analysis. Synthetic probes have also been previously used for precision targeting of EGFR and other membrane-bound proteins, such as claudins, that are intrinsically difficult to detect and analyze.

Our study will investigate the TJ-EGFR interactome by using functionalized nanoparticles and synthetic probes to facilitate the prognosis and treatment of carcinoma cells. So far, we have functionalized the nanoparticles through the EDC/NHS-activated gold nanoparticles coated with anti-EGFR antibodies. The nanoparticles have been characterized by FTIR, UV-Vis, DLS, TEM, SEM, and EDS analyses.

The analysis confirmed protein conjugation and successful surface modification. The TEM analysis also revealed a distinct protein corona surrounding AuNP cores, confirming effective antibody conjugation by imaging. Concurrently, various cell cultures have been subjected to proteomics analyses to establish the workflow for incorporating the new nanoparticles and probes.

The long-term goal of Tight junctions, Claudins, EGFR, Nanoparticles, Probes, Carcinoma Tight junctions, Claudins, EGFR, Nanoparticles, Probes, Carcinoma the combined use of these new tools should shed new light on the endogenous activities of these membrane proteins for finding potentially new fluorescent biosensors and therapeutic payloads, enabling real-time visualization of TJ alterations alongside receptor-level perturbation.

Quercetin Nanoemulsion Ameliorates Key Hallmarks of Lung Cancer

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Abstract

Lung cancer is a leading cause of mortality worldwide, with current treatments facing challenges such as adverse effects, limited targeting and resistance. Quercetin, a naturally occurring and abundantly available flavonoid in the global flora, exhibits promising anti-inflammatory and anti-cancer

properties. However, its clinical application is limited by poor bioavailability and stability. Nanotechnology offers a solution to enhance the delivery and efficacy of quercetin. In this study, an optimised nanoemulsion of quercetin was developed and its anti-cancer effects against non-small cell lung cancer (NSCLC) were evaluated in the human adenocarcinoma cell line (A549), comparing its effects with the Quercetin pure drug (QPD) at varying concentrations. QNE in comparison to QPD was found to significantly inhibit key cancer hallmarks like cell proliferation, migration and colony formation in the functional assays and downregulated the expression of numerous oncogenic proteins and genes that are associated with angiogenesis, metastasis and uncontrolled cell growth, ultimately facilitating cancer progression. The anticancer potential of Quercetin was further examined through computational approaches involving network analysis and molecular docking that further supported its potential as an anti-cancer agent, correlating *in vitro* and *in silico* data. The enhanced anti-cancer activity of QNE compared to QPD suggests that nanoemulsion based delivery of quercetin is attributing to its effective therapeutic efficacy, highlighting its potential against lung cancer. However, expedited studies, particularly *in vivo* animal models, are essential to fully assess its therapeutic potential and safety profile.

What you feed matters: Dietary fibre source drives distinct canine gut microbiome responses

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Abstract

Dietary fibre (DF) plays key roles in host physiology, including stool bulking, glycaemic regulation, and satiety, but its most significant impact is mediated by the gut microbiome. Arriving in the colon undigested, DF is anaerobically fermented by resident microbes, producing short-chain fatty acids (SCFAs) that have known benefits to host health. Different fibres selectively enrich distinct bacterial populations, resulting in differential microbial shifts and SCFA profiles. While fibre supplementation is increasingly incorporated into commercial canine diets, research characterising fibre-specific effects on the canine gut microbiome remains limited.

This study assessed the impact of three DFs – inulin, apple pomace, and PetBiome (a commercial fibre supplement) – on canine gut microbial community composition and diversity using an *in vitro* gut microbiome model system. The INFOGEST 2.0 simulated gastrointestinal digestion protocol was followed for each fibre. The digests were anaerobically cultured for 48 hours with ten individual canine faecal communities. Fibre fermentation induced distinct community shifts relative to the control. Alpha diversity was significantly reduced by inulin and increased by apple pomace. Inulin significantly reduced ASVs assigned to *Bacteroides* and *Fusobacterium*, while apple pomace and PetBiome enriched *Fusobacterium* ASVs. *Prevotella* ASVs were enriched by all fibres, and an apple pomace-specific increase in a *Phascolarctobacterium* ASV was observed. These results highlight DF as a bioactive that drives distinct microbial community shifts in the canine gut, with fibre type determining the nature and direction of those shifts – a critical consideration for evidence-based canine dietary fibre selection. SCFA profiling is underway to characterise the associated metabolic outputs.

In-depth characterisation of Australian seaweed-derived polysaccharide and protein extracts: advancing analytical specification for complex marine biopolymers

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Abstract

This study addresses a critical gap in marine biopolymer research: the limited analytical repeatability in chemical and biological tests, method depth, and comparable datasets for seaweed-derived polysaccharides and proteins. These shortcomings hinder the development of reliable specifications and the linking of molecular features to functional properties. Such connections are essential for advancing the food, pharmaceutical, material, and other translational applications of seaweed polysaccharides.

Here, we present an in-depth characterisation of polysaccharide-rich and protein-rich fractions from an Australian *Ulva* species, aiming to strengthen analytical confidence and support specification-building for complex marine biopolymers. Robust analytical techniques were employed, including WST-1 dye assays for carbohydrate quantification, Qubit™ assays for protein content, and 1,9-Dimethyl-Methylene Blue (DMMB) derivatisation combined with elemental analysis for sulfation assessment. Protein profiling was performed using SDS-PAGE, amino acid analysis, and proteomics, while polysaccharide structure was elucidated via HPAEC-PAD monosaccharide analysis and 2D-NMR for glycosidic linkages. Physical properties, including molecular weight distribution, viscosity, and gelation behaviour, were evaluated using GPC-MDS and rheometer.

Results revealed distinct compositional and physicochemical differences between the fractions, demonstrating the level of analytical rigour required to characterise seaweed macromolecules comprehensively. This work contributes to improved methodological standards and data reliability in seaweed biopolymer research, ultimately facilitating the development of important real-world applications.

Targeting Lung Cancer Hallmarks with Marine Algae

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Abstract

Lung cancer is the leading cause of cancer-related mortality worldwide, accounting for approximately 18% of all cancer deaths in 2020. Non-small cell lung cancer represents approximately 85% of cases and carries a poor five-year survival rate, due to late-stage presentation and limitations of conventional therapies, including chemoresistance and damage to healthy tissue. These challenges highlight an urgent need for safer and more targeted therapeutic alternatives. Marine algae have emerged as a promising source of bioactive phytochemicals; *Sargassum aquifolium* and *Kappaphycus alvarezii* containing key compounds including fucoxanthin,

astaxanthin, and laminarin, known to target multiple hallmarks of cancer. This study evaluated the anticancer potential of aqueous and ethanolic extracts of both algal species against human lung carcinoma epithelial (A549) cells using MTT, scratch wound, Boyden chamber, and colony formation assays. Both extracts reduced A549 cell viability in a concentration-dependent manner. In the scratch wound assay, the untreated control exhibited approximately 40% wound closure after 24 hours, whereas *S. aquifolium* aqueous extract at 75 µg/mL reduced closure to ~15% ($p < 0.01$), and both *S. aquifolium* ethanolic and *K. alvarezii* aqueous extracts reduced closure to ~20% ($p < 0.05$). Colony formation was most suppressed by *S. aquifolium* aqueous extract ($p < 0.0001$), with *K. alvarezii* aqueous extract producing a partial but significant reduction. Boyden chamber assays confirmed significant inhibition of transwell migration with *S. aquifolium* aqueous extract ($p < 0.05$). These findings support the therapeutic promise of marine algae, with future work to focus on protein array and gene expression analyses to elucidate underlying molecular mechanisms.

Extraction and Characterisation of Fibre-Bound Phenolic Acids from Selected Dietary Fibre Matrices

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Abstract

Dietary fibers are increasingly recognized as carriers of bioactive compounds, particularly fiber-bound phenolic acids, which are associated with plant cell wall structures and may influence health beyond conventional fiber functions. Unlike free phenolics, fiber-bound phenolic acids are often less bioaccessible in the upper gastrointestinal tract and may reach the colon, where they may be released through microbial fermentation.

Previous studies in cereal matrices, particularly wheat bran and oats, have demonstrated that fiber structure strongly influences the abundance, extractability, and accessibility of bound phenolic compounds. In wheat, phenolic acids such as ferulic acid are commonly ester-linked to arabinoxylans, whereas oat matrices exhibit distinct phenolic profiles associated with differences in fiber composition. However, considerably less is known regarding fiber-bound phenolic acids in non-cereal dietary fibers.

Building upon evidence from cereal-based systems,

this study investigates the extraction and characterization of fiber-bound phenolic acids from selected dietary fibers with contrasting physicochemical structures, including pectin- and inulin-based matrices. Extraction approaches are being evaluated to optimize recovery of bound phenolic compounds while preserving analytical integrity for downstream characterization. Particular attention is given to understanding how fiber type and structural properties may influence the potential for phenolic acid release.

Improved characterization of fiber-bound phenolic acids across diverse dietary fiber matrices may expand the current understanding of dietary fiber functionality and inform future nutritional strategies targeting gut and metabolic health.

Green Extraction of Bioactives from Broccoli Leaf Waste Using NADES

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Abstract

Agri-food systems generate substantial underutilised plant biomass. Broccoli leaves represent approximately 47% of crop biomass and 85% of post-harvest waste despite their significant bioactive content. By-products valorisation aligns with circular bioeconomy principles and the United Nations Sustainable Development Goals. Concurrently, Natural Deep Eutectic Solvents (NADES), green alternatives to conventional solvents due to low toxicity and biodegradability, have emerged, promoting more targeted recovery of plant compounds from food waste enabled by their physicochemical properties.

In this study, ten choline chloride (ChChl)- and betaine (Bet)-based NADES were synthesised and characterised for pH, viscosity, density, polarity, FTIR profile, and cytotoxicity. ChChl-based systems were more acidic than Bet-based NADES. Overall, NADES viscosity ranged between 6.29 and 20.78mm²/s, with high biocompatibility toward Caco-2 cells (EC₅₀: 7,485-190,000 mg/L). Bet:Glucose_{1:1} achieved the highest total phenolic content (TPC: 10.5mg GAE/g DW) and Bet:Urea_{1:2} the highest total flavonoid content (TFC: 1.3mg QE/g DW). The three systems that performed best (Bet:Glucose_{1:1}, Bet:Glycerol_{1:2}, and Bet:Urea_{1:2}) were compared with water, 80% methanol, and 80% ethanol. Bet:Glucose_{1:1} yielded

the highest TPC (14.0mg GAE/mL), exceeding conventional solvents by up to 41.4%, and showed higher antioxidant activity (ABTS: 708.5; FRAP: 1154.3; ORAC: 1602.2μM TE/mL), surpassing the best conventional solvent by up to 72.3%. Untargeted metabolomics revealed selective enrichment of phenolic acids, flavonoids, glucosinolates, indoles, coumarins, and terpenes by NADES, while conventional solvents favoured carbohydrate extraction. These findings support NADES as sustainable, scalable tools for broccoli leaf valorisation, with promising applications in functional food, nutraceutical, and cosmetic product development.

Integrating Evidence Synthesis, Chemometrics and Formulation Science to Advance Bioactive Translation

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Abstract

Bioactive compounds from natural and plant-derived sources have considerable potential for disease prevention, immune modulation and therapeutic applications. However, their translation into effective products is often limited by inconsistent evidence, chemical complexity, poor stability, low bioavailability and challenges in delivery. This presentation introduces an integrated translational framework that combines systematic review and evidence synthesis, analytical characterisation, chemometric modelling and formulation development to support the robust evaluation and application of bioactives.

The talk will discuss how systematic review methodology can be used to critically assess formulation design, biological outcomes and clinically relevant biomarkers, as demonstrated through recent work on nutritional bioactives, blood fatty acid profiles and inflammatory outcomes (Khabir et al., 2026). It will then highlight the importance of analytical and data-driven approaches, including chromatographic and spectroscopic techniques, for characterising bioactive composition and monitoring stability and purity. Chemometric modelling further supports the interpretation of complex analytical datasets by enabling classification, pattern recognition and prediction of compositional or

functional changes, particularly in chemically complex lipid-rich systems (Ahadi et al., 2026).

Formulation development is also a key translational step for improving the stability, compatibility, release behaviour and bioavailability of selected bioactives. Using topical and dermal delivery as representative application platforms, this presentation will examine how formulation composition and delivery system design can influence bioactive performance, including penetration and delivery across skin-relevant barriers (Khabir et al., 2023). Overall, this integrated approach supports evidence-based, data-driven and formulation-informed decision-making, helping progress bioactives from discovery and characterisation toward clinical, industrial and commercial translation.

The Role of the Matrix Around Bioactive Molecules: Curcumin in Turmeric Matrix

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Abstract

Curcumin is a primary bioactive polyphenol present in turmeric (*Curcuma longa*), which is highly unstable in its isolated form. It is sold as a chemical that needs to be stored at -20°C and away from light while turmeric is displayed on illuminated retail shelves and kept in kitchen cabinets in households. So why does the curcumin in turmeric appear to survive conditions that would rapidly degrade the pure compound? This study explores that contradiction and what the native turmeric matrix might be doing to protect it.

This study investigates the role of the turmeric matrix in protecting curcumin from degradation under conditions that simulate real-world storage. We subjected both whole turmeric and isolated curcumin to accelerated thermal stress and controlled photodegradation. Degradation was tracked using liquid chromatography–mass spectrometry (LC-MS), allowing us to compare how curcumin degrades in its natural matrix versus in isolation. Microscopy is additionally being used to probe the structural features of the matrix that may physically shield curcumin from degradation.

LC-MS data indicate that curcumin within the intact turmeric matrix is substantially more resistant to both thermal and photodegradation compared to the isolated compound under equivalent conditions,

consistent with a protective function of the surrounding matrix. Microscopy findings are anticipated to provide further mechanistic insight into this phenomenon. These findings highlight that the food matrix is not merely a passive carrier of bioactive molecules, it may actively govern their stability, with real implications about storage, processing, and the bioavailability of curcumin in food systems.

Are Precision-Fermented Caseins Functionally Equivalent? Phosphoproteomic and Peptidomic Insights into αS1-Casein

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Abstract

The commercial scale-up of precision fermentation (PF) as a platform for animal-free dairy proteins requires rigorous molecular characterization of recombinant caseins. However, whether these proteins faithfully reproduce the post-translational modification (PTM) landscape and bioactive peptide potential of native caseins remains unclear. Here, we characterized monomeric (CF AS1) and tandem fusion (CF AS1-AS1) αS1-casein constructs produced by PF, alongside a bovine reference, using integrated phosphoproteomics, simulated gastrointestinal digestion (SGID), and LC-MS/MS peptidomics. Both PF constructs preserved canonical phosphoserine clusters characteristic of native αS1-casein and exhibited non-canonical tyrosine phosphorylation events (Y109, Y119) absent in the mammary-derived reference, reflecting differences in the recombinant kinase environment. SGID revealed construct-dependent peptide repertoires, with the fusion construct generating the largest unique peptide output (n = 38) compared with CF AS1 (n = 15) and the bovine reference (n = 25). Bioinformatic screening identified the database-validated ACE-inhibitory sequence YKVPQL exclusively as its phosphorylated form, pY-KVPQL, in PF-derived hydrolysates. This PTM-dependent phosphorylation alters the charge environment of the ACE-binding motif and is being investigated by molecular docking to evaluate its effect on inhibitory potency. These findings

demonstrate that precision-fermented α S1-casein preserves key phosphorylation features of native caseins while generating distinct peptide repertoires and PTM-dependent bioactive peptide variants with potential implications for bioactivity.

Anti hyperglycaemic effect of fruit extract of Aegle Marmelos in combination with nanoparticles in Streptozotocin induced diabetic mice.

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Abstract

Diabetes mellitus is a metabolic disorder causing a great economic burden globally. It is extremely important to construct an inexpensive and reliable treatment having no side effects. This study demonstrates the use of Aegle Marmelos fruit extract as herbal medicine, Magnesium oxide nanoparticle, Copper nanoparticle and DNA-loaded chitosan nanoparticle as nanomedicine, individually as well as combined anti-hyperglycemic effect. All treatments were compared with commercially available medicine. Maximum reduction in blood glucose levels (BGLs) was shown by 5mg/kg DNA-loaded chitosan nanoparticles (74.2 ± 0.95) and their combination with Aegle Marmelos fruit extract (500mg/kg) (60 ± 2.72) as compared to standard drug - Glucophage (500mg/kg) ($43.6 \pm$). Body weight analysis was also observed in experimental mice. Maximum decrease of body weight observed was of 3.95g by DNA-loaded chitosan nanoparticle (5mg/kg) while increase in body weight was observed in positive control. The results suggest that (5mg/kg) DNA-loaded chitosan nanoparticles and their combination with Aegle Marmelos fruit extract could be a potent anti-diabetic agent.

How are bioactives portrayed in the media?

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Abstract

Bioactive compounds are increasingly promoted as substances that enhance health, despite ongoing scientific debate about their dietary significance and regulation. This study examines how knowledge about bioactive compounds moves from scientific research into public discourse through an analysis of 907 newspaper articles published in Australia and New

Zealand between 2008 and 2026. This media analysis investigates how bioactive knowledge is communicated and how it interacts with, reshapes, or sidelines traditional understandings of food and health. Four key themes emerged: First, molecularisation framed food primarily through its chemical constituents, reducing complex foods to measurable compounds such as antioxidants, polyphenols, and probiotics. Second, innovation framing presented bioactives as technological solutions to challenges in health, sustainability, and agriculture, transforming biological materials into sources of economic value and commercial opportunity. Third, wellness moralisation encouraged individuals to optimise their health through bioactive-rich foods, reinforcing neoliberal ideals of personal responsibility despite uncertainty surrounding many health claims. Finally, media reporting revealed a notable cultural absence, with Indigenous and relational food knowledges frequently overlooked. For example, in coverage of native species such as Gumby Gumby, which was often valued for its commercial bioactive potential rather than its cultural significance. These findings demonstrate how media coverage contributes to a process of universal nutritionalism, privileging molecular, market-oriented, and individualised understandings of food while marginalising cultural and historical connections. The study contributes to debates on nutritionism, biopolitics, and the medicalisation of the Anthropocene by legitimising certain forms of expertise making food system increasingly understood through the lens of bioactive value.

Co-designing Bioactives Communication with Young Adults: Bridging Science, Practice, and Everyday Food Choices

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Abstract

Background: For young adults, eating practices are shaped by everyday constraints such as cost, time, habits, and trust in information sources. Objective:

This study aims to design, implement and evaluate a co-design approach to bioactives communication with young adults, with a focus on aligning scientific knowledge with everyday food practices. Method: The study is currently in the design and development phase. It is structured as an online intervention for young adults, covering key topics around plant bioactives, including how they interact with the body, bioavailability, cooking and preparation practices, sustainability, and the relationships between food and culture. Participatory workshops are being conducted with a Young Adult Advisory Group, which are used to refine content, language, and delivery, and to ensure that the intervention reflects participants' lived experiences, priorities, and constraints. Preliminary insights: Early observations suggest that young adults engage more readily with practical, actionable guidance, such as what to eat and how to prepare it, than with abstract nutritional concepts. Scientific explanations are valued when clearly linked to everyday decisions. Trust is emerging as a central issue, particularly in navigating conflicting messages across social media, marketing, and health advice. Conclusion: This work highlights the importance of involving young adults in the design of bioactives communication from the outset. A co-design approach has the potential to produce more relevant and credible strategies, better connecting scientific evidence with lived experience and supporting healthier and more sustainable dietary practices.

Source-specific nitrate and nitrite intake and the incidence of chronic kidney disease in the Danish Diet, Cancer, and Health Cohort*

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*Also oral presentation

Abstract

Background: Nitrate and nitrite from plant sources may benefit renal function through nitric oxide conversion, whereas intake from animal-sourced foods (naturally occurring and additive-derived) and drinking water may promote renal damage via N-nitrosamine-mediated oxidative stress.

Objective: To investigate associations between source-specific nitrate and nitrite intakes from plants, vegetables, animal foods, and drinking water, and incident chronic kidney disease (CKD) in the Danish Diet, Cancer, and Health cohort.

Methods: Dietary nitrate and nitrite intakes were estimated from food frequency questionnaires using the Nitr-Navigator database. Drinking-water nitrate intake was derived from national monitoring data. Associations with incident CKD were examined using restricted cubic spline-based multivariable Cox models. Analyses were stratified by smoking and intakes of vitamins C and E, folate, and polyphenols, hypothesised modifiers of N-nitrosamine formation.

Results: During 25 years of follow-up (median [IQR]: 24 [21, 25]), 2,793 CKD cases were identified among 54,691 participants. Higher plant-sourced nitrate and nitrite intakes were associated with a lower CKD rate [HR_{Q5vsQ1} (95% CI): 0.90 (0.80, 1.01) for nitrate; 0.85 (0.76, 0.95) for nitrite], with similar findings for vegetables [0.88 (0.79, 0.99); 0.87 (0.78, 0.98)]. Nitrite from additive-permitted meats was associated with a higher risk of CKD [HR (95% CI): 1.11 (1.02, 1.20)]. Higher CKD rates were also observed with higher tap-water nitrate intake [HR_{Q5vsQ1} (95% CI): 1.35 (1.21, 1.52)] and higher drinking-water nitrate concentrations [1.15 (1.03, 1.30)].

Conclusions: Findings support increasing plant-based foods, particularly nitrate-rich leafy vegetables, and limiting processed meats. Drinking-water nitrate may contribute to CKD risk and warrants further investigation.

Comparative metabolomic and chemometric analysis of wild and commercially cultivated yams in Australia

Olumide fawale, Oladipupo Adiamo, Michael Netzel, Olufemi Akinsanmi, Henrietta Marie, Yasmina Sultanbawa

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Abstract

In this study, phenolic metabolites were identified and correlated with organic acids, antioxidant activity, vitamin C, and carotenoids. Untargeted and targeted metabolite profiling using UPLC-QTOF/MS, combined with PLS-DA models, was used to compare two *Dioscorea* species – *D. alata* (*Da*), and *D. bulbifera* (*Db*) obtained from wild bushland (*wDa* and *wDb*) and three accessions of commercially cultivated *D. alata* (*cDa-A*, *cDa-B* and *cDa-C*). Metabolic-chemometric analysis showed N1, N10-Dicoumaroylspermidine discriminated the *cDa-A* from the other three clusters. The highest procyanidins B5 (706.7 mg/kg) and C1 (76.3 mg/kg) were found in *cDa-C*, while alatanin E (13.8 mg/kg), alatanin C (287 mg/kg), alatanin G (48.4 mg/kg), and alatanin F (22.6 mg/kg) were found in *cDa-B*. Carotenoid levels varied significantly ($p \leq 0.05$), with *wDa* (8.7 mg/100g DW) having the highest trans- β -carotene and *wDb* (278.9 mg/100g DW) the highest total carotenoid content. Vitamin C (39.2 mg/100g DW), total phenolic content (15.2 mg GAE/g DW) and antioxidant capacity determined by DPPH (89.0 μ M TE/g DW), ABTS (377.8 μ M TE/g DW) and FRAP (16.4 μ mol Fe²⁺/g DW), were highest in *cDa-C*. The results from this study will support the yams breeding programs aimed at producing high-quality varieties with favourable nutritional profiles. These findings enhance the understanding of biochemical relationships among the yam species and provide valuable insight to support future breeding strategies and biofortification programs aimed at producing high-quality varieties with favourable nutritional profiles

Phytochemical Characterisation of Australian Acacia Longifolia Clade Species and Comparative Psychoactive Botanicals Using LC–MS and Preparative LC

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Abstract

Amid Australia's substantial mental health burden, there is growing interest in natural psychedelics within psychedelic-assisted therapy due to their potential to deliver rapid and durable improvements in treatment-resistant conditions. While N,N-dimethyltryptamine (DMT) is recognised as a principal psychoactive constituent in several botanical species, additional plant-derived alkaloids may contribute to an “entourage effect,” potentially influencing pharmacokinetics, subjective experience, and therapeutic outcomes.

This study describes the development of analytical workflows for the phytochemical characterisation of Australian Acacia species, with a primary focus on members of the eastern Australian Acacia longifolia clade due to reports of elevated DMT content in several species. Selected comparator species, including Mimosa hostilis, Banisteriopsis caapi, and Peganum harmala, are also being investigated. Plant extracts are analysed using liquid chromatography-mass spectrometry (LC-MS) to generate quantitative data, compare metabolite profiles between species, and identify compounds of interest. Fractionation approaches incorporating liquid-liquid partitioning, strong cation exchange solid-phase extraction, and preparative liquid chromatography are used to isolate target constituents for subsequent structural and biological investigation.

Preliminary LC-MS analyses have demonstrated substantial variation in chemical composition both within and between species, including differences in alkaloid abundance and the detection of numerous compounds that remain uncharacterised. While DMT is often the primary focus of research into these species, these findings suggest the surrounding phytochemical matrix may be more complex than DMT content alone would suggest.

These workflows will support future investigations into serotonergic receptor interactions and monoamine oxidase (MAO) inhibition, with particular interest in the pharmacological contribution of co-occurring metabolites within DMT-containing extracts.

Cannabidiol Modulates Phosphate/Calcium-Induced Calcification and Smooth Muscle Cell Phenotype in Human Aortic Smooth Muscle Cells

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Abstract

Vascular calcification is a clinically significant process associated with ageing, atherosclerosis and chronic kidney disease, involving phenotypic transition of vascular smooth muscle cells from a contractile to an osteogenic-like state. Cannabidiol (CBD), a non-intoxicating cannabinoid, has been widely investigated as a bioactive compound with anti-inflammatory and cardiovascular effects; however, its direct impact on vascular calcification remains unclear. This study evaluated whether CBD modulates phosphate/calcium-induced calcification and smooth muscle cell phenotype in primary human aortic smooth muscle cells (HASMCs).

Primary HASMCs were cultured under calcifying conditions using inorganic phosphate and calcium chloride for up to 7 days, with or without CBD treatment. Calcium deposition was assessed by Alizarin Red S staining followed by cetylpyridinium chloride extraction, while cell viability was measured using Alamar Blue. Phenotypic marker expression was examined by Western blotting, focusing on the contractile marker SM22 α .

Phosphate/calcium treatment induced robust calcification in primary HASMCs and was associated with reduced cell viability and phenotypic modulation. Under calcifying conditions, CBD treatment further promoted calcification-associated morphological changes and significantly reduced SM22 α expression, suggesting enhanced loss of the contractile smooth muscle phenotype.

Overall, this study highlights the importance of evaluating the vascular effects of bioactive compounds in disease-relevant human cell models and suggests that CBD may have complex, context-specific effects on vascular calcification.

Therapeutic effectiveness of LipiSpense technology-containing Berberine in Lung Cancer

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Abstract

Berberine is a naturally derived isoquinoline alkaloid with reported anticancer and anti-inflammatory activity; however, its biological application is limited by poor aqueous solubility, low oral bioavailability, and suboptimal cellular exposure. BioBerb, a LipiSpense-enhanced berberine formulation, has been developed to improve berberine dispersion and may enhance its biological activity *in vitro*. This study investigates the effects of BioBerb treatment on A549 human lung adenocarcinoma cells using cell viability, proliferation, migration, and molecular signalling.

A549 cells were treated with BioBerb and assessed using MTT assays to determine cell viability. Long-term proliferative capacity was evaluated using colony formation assays. Scratch wound healing and cell migration assays were performed to examine the influence of BioBerb on cellular motility and wound closure. To explore potential mechanisms of action, RNA was extracted for gene expression array analysis, and protein array analysis was conducted to identify treatment-associated changes in oncogenic signalling pathways.

Our findings suggest that BioBerb produces promising anti-cancer effects in A549 cells, with evidence indicating treatment-associated inhibition of cell proliferation, and migration. qPCR and oncogenic protein array analyses revealed the key gene and protein modulated by BioBerb treatment, including those potentially involved in cell growth, metastasis, survival, apoptosis, and epithelial–mesenchymal transition. Collectively, this study provides an initial *in vitro* evaluation of LipiSpense-enhanced berberine in a lung cancer cell model and supports further investigation into its anticancer potential and underlying mechanisms of action.

Harnessing Protein-ligand Interactions by Mono-fluorination of (-) Balanol for Enhanced Selectivity Towards AGC Protein Kinases

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Abstract

Fluorinated analogues of natural products are emerging as important scaffolds in drug discovery. (-)-Balanol, a bioactive derived from a fungus, is a potent ATP mimic of protein kinase A (PKA), PKB/Akt and PKC of the AGC protein kinases but exhibits limited selectivity across the superfamily of kinases.

The three 'fragments' of balanol viz; benzamide, benzophenone, and azepane mimic adenosine, triphosphate, and ribose subsite in the catalytic pocket respectively. The intrinsic dynamics of proteins is increasingly being recognised as a key factor for the development of drug leads with selectivity. Imatinib, the drug for chronic myelogenous leukaemia provides the first example of conformation selection upon binding to Abl-Bcl protein. The drug exhibits high efficacy and selectivity by binding to a non-phosphorylated, inactive conformation of the protein. Inspired by the recognition of conformational entropy in protein-ligand binding, in this work, fluorine was used as a conformation tuning motif for (-)-balanol as a model system, in order to exploit discrete conformational differences within highly homologous catalytic sites of PKA, protein kinase B (PKB/Akt) and C (PKC) of the kinase family. A series of four new balanoids were accessed involving total synthesis.

The bioactivity profiling results showed a six-hundred-fold selectivity gains upon mono-fluorination on the triphosphate subsite mimic in one balanoid towards archetypical PKA knocking out all the protein kinase B/Akt isozymes. The results can serve as a guide for determining the optimal fluorine position in the development of next generation of more selective balanol analogues.

Fresh Produce Bioactives: Connecting Plant Compounds, Food Practices and Public Health

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Abstract

Fresh produce bioactives are naturally occurring compounds in plant foods that may support vascular health, immune function, metabolic regulation, gut microbial activity, and healthy ageing. Their function is shaped by plant stress responses, cultivation conditions, storage, processing, cooking, food matrices, microbial metabolism, and the social practices through which people select, prepare, and eat food. This poster presents an overview of a multidisciplinary research program that connects laboratory science with food practices, public communication, and health translation. The Fresh Produce Bioactives project brings together natural scientists, social researchers, and communication specialists to examine how bioactive knowledge is produced, interpreted, and applied. Key streams of work include Bioactive Master Files synthesising evidence on foods such as onion and broccoli; media analysis of how bioactives are represented in public discourse; citizen food ethnography exploring shopping, cooking, eating, and communication practices; and behaviour-change work informed by COM-B and Behaviour Change Wheel frameworks. Following compounds from cultivation through storage, preparation, eating, microbiome metabolism, and health outcomes, this project embraces a systems view of bioactives. This approach foregrounds four practical messages: whole foods matter, diversity matters, cooking practices matter, and cultivation practices matter. A simple public-facing rule of thumb is to aim for 30 or more different plant foods each week. By linking molecular pathways to kitchen tables, the project supports clearer communication, better research translation, and more sustainable food systems.

Regulating Bioactives: Towards a New Framework for Evidence-Proportionate Oversight and Whole of Government Implementation

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Abstract

The rapid advancement of bioactive science has outpaced the regulatory frameworks designed to govern it. Compounds with well-characterised antioxidant, anti-inflammatory, and neuroprotective mechanisms increasingly occupy a grey zone between food standards and therapeutic goods regulation — simultaneously evidenced, commercially viable, and regulatorily stranded.

This presentation diagnoses three structural fault lines in current frameworks: single-agency thinking that cannot accommodate dose-dependent, food-derived compounds; evidentiary standards modelled on pharmaceutical RCTs that disadvantage mechanistic and epidemiological data; and a claims architecture that perversely rewards vagueness over rigour. Together, these failures have produced a consumer trust crisis — with survey data indicating the majority of consumers cannot distinguish regulated health claims from marketing, and a significant proportion of products making claims unsupported by approved registers.

Drawing on the Australian regulatory landscape — including the jurisdictional boundaries of FSANZ, TGA, DAFF, and the ACCC — this presentation proposes four core reform principles: evidence-proportionate approval pathways; spectrum-based classification replacing binary food/medicine categories; a tiered, consumer-intelligible claims framework; and coordinated multi-agency jurisdiction reviews with mutual recognition provisions. A whole-of-government Bioactives Coordination Hub model is proposed as the structural mechanism for implementation.

These reforms are presented not as aspirational but as operationally necessary: the science of bioactives is translation-ready, and the regulatory architecture must evolve to match.

Oral Delivery of Food Bioactive Compounds*

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*Also oral presentation

Abstract

The effective oral delivery of food bioactive compounds is challenging because many bioactives are susceptible to thermal processing, environmental stresses and gastrointestinal degradation. Encapsulation can improve their stability, but effective delivery also requires controlled release and preservation of bioaccessibility during gastrointestinal digestion. This presentation highlights the development of food-compatible delivery systems for protecting and delivering bioactive compounds through oral administration.

Our work initially focused on enzyme delivery using food-compatible metal–organic frameworks (MOFs). A rapid room-temperature synthesis approach was developed to improve enzyme stability, while defect engineering enabled control over gastrointestinal release. Encapsulation substantially improved phytase thermal stability, increasing residual activity after heat treatment from 4% to 95%, while more than 80% of the encapsulated enzyme was released under simulated gastrointestinal conditions. Spray-drying strategies were subsequently explored to facilitate the production of MOF-based bioactive powders and improve their scalability.

The approach is further being extended to oil-soluble food bioactives, including vitamins A and E and β -carotene. Emulsion-assisted spray drying is being engineered to address key formulation challenges, including encapsulation efficiency, powder yield, oil leakage and gastrointestinal release. Overall, this work demonstrates how food-compatible material and particle engineering can be combined to protect bioactive compounds during processing and digestion while enabling controlled gastrointestinal delivery and improved bioaccessibility.

Characterising Illawarra Plum Bioactives via Lactic Acid Bacterial Fermentation; In Vitro Digestion and Targeted Metabolomics

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Abstract

Background: Illawarra plum (IP; *Podocarpus elatus*) is an Indigenous Australian fruit recognised for its distinctive antioxidant profile. However, most antioxidants found in fruits, including IP, exhibit limited bioavailability. Previous studies suggest that lactic acid bacterial fermentation (LABF) can enhance antioxidant bioavailability and confer probiotic benefits. Despite increasing commercial interest, the effects of LABF and *in vitro* digestion on the bioaccessibility of IP antioxidants remain poorly understood.

Methods: IP fermentation was optimised using a mathematical model with IP puree concentration (PC; w/v), bacterial concentration (BC; v/v), and time (T; h) as factors, and antioxidant activity as the response, measured by the standard CUPRAC antioxidant assay. Optimally fermented IP puree was subjected to *in vitro* digestion using the standardised INFOGEST protocol, and phenolic bioaccessibility was quantified at the gastric (G120) and intestinal (I60 and I120) phases by a targeted LC-MS approach. Both G120 and I60 digesta of fermented IP were also tested for antiproliferative activity against AGS gastric adenocarcinoma cells.

Results: Each factor combination used to model IP fermentation showed enhanced antioxidant activity in the fermented puree compared to its unfermented counterpart. The optimal factors for IP fermentation were 5.32% PC, 1% BC, and T 16 h. Lower bioaccessibility was observed for some antioxidants, indicating matrix-specific release. Dose-dependent antiproliferative activity was observed for digesta against the AGS cells. Overall, LABF was found to enhance the antioxidant activity of IP; however, the reduced bioaccessibility of antioxidant compounds warrants further investigation using advanced gastrointestinal models that more closely simulate human digestion.

Preliminary Evaluation of Davidson's Plum and Illawarra Plum Extracts in Intestinal and Hepatic Cell Models

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Abstract

Background: Metabolic syndrome constitutes an increasing global health issue, characterised by interconnected metabolic irregularities that increase the risk of type 2 diabetes (T2D) and cardiovascular diseases (CVD). Despite recent advances in therapeutic approaches, many standard treatments are expensive and associated with adverse effects, highlighting the need for adjunct therapies from natural sources. Rich in nutrients and secondary metabolites, Australian native fruits have been an essential source of food and medicine for Indigenous Australians for millennia. However, their biological activities in relation to metabolic and gut health remain relatively underexplored.

Methods: The current study investigated the preliminary cellular effects of extracts from Davidson's plum (DP; *Davidsonia pruriens*) and Illawarra plum (IP; *Podocarpus elatus*) to determine appropriate concentrations for future bioactivity studies. Aqueous, 70% ethanol and 100% ethanol extracts of DP and IP were evaluated in human HepG2 liver and Caco-2 intestinal epithelial models. Cells were exposed to a range of extract concentrations, and cell viability was assessed using the resazurin-based Alamar Blue assay.

Results: Preliminary findings indicated that both DP and IP extracts generally maintained cellular viability across the investigated concentration ranges, although responses varied according to fruit, extraction solvent, and cell model. Aqueous extracts were generally well tolerated, whereas ethanolic extracts exhibited greater variability and, in some cases, reductions in cell viability. These findings established preliminary cytocompatibility profiles and appropriate concentration ranges for subsequent mechanistic studies investigating the potential

bioactivity of DP and IP in metabolic syndrome, particularly pathways relevant to T2D and gut health.

Synergistic Inhibition of Triple-Negative Breast Cancer Cells by Gut Microbial Metabolites: A Mechanistic Investigation

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Abstract

Objective: This study aimed to evaluate synergistic interactions between gut microbial metabolites and determine their potential to enhance the anticancer activity of standard chemotherapies against MDA-MB-231 triple-negative breast cancer (TNBC) cells *in vitro*.

Methods: The antiproliferative effects of three gut microbial metabolites- sodium butyrate (NaB), sodium propionate (NaP), and urolithin B (UB), alone and in combination, were assessed using the Alamar Blue assay. Synergistic interactions between metabolites and with docetaxel (D), capecitabine (C), and doxorubicin (DOX) were quantified using the combination index (CI) model. Mechanisms underlying treatment responses were investigated through reactive oxygen species (ROS), apoptosis and cell-cycle analyses, complemented by LC-MS-based proteomic profiling and pathway enrichment analysis.

Results: All three metabolites and their combinations exhibited antiproliferative activity against MDA-MB-231 cells and demonstrated promising synergistic interactions with D+C and D+DOX combinations (CI<1). Mechanistic analyses demonstrated treatment-associated induction of oxidative stress, apoptosis and alterations in cell-cycle progression. Proteomic analyses further revealed treatment-specific molecular responses, including enrichment of pathways associated with cell-cycle regulation, cellular stress and cancer-related signalling. Notably, metabolite treatments also altered proteins involved across multiple stages of mRNA regulation, including mRNA processing, spliceosomal and alternative splicing, 3'-end processing, and mRNA metabolism and turnover.

Conclusions: Gut microbial metabolites exert multifaceted anticancer effects in TNBC cells and can synergistically enhance responses to standard chemotherapies. The identification of proteomic changes involving cell-cycle and post-transcriptional mRNA regulatory processes provides new mechanistic insight into microbiome-derived metabolites as potential adjuncts to TNBC therapy.

From Mapping to Micelles: Unveiling Multispecies Casein Phosphorylation Profiles and the Impact of Calcium Phosphate on Digestion of Artificial Casein Micelles

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Abstract

Milk proteins, particularly caseins (CNs) play an integral role in nutrition and functionality. Casein phosphorylation is essential for binding calcium phosphate nanoclusters and forming casein micelles. Comprehensive characterization of casein phosphorylation remains analytically challenging due to heterogeneous phosphorylation states, sub-stoichiometric abundance and poor detectability of highly phosphorylated isoforms. Conventional phosphoproteomics approaches typically require phosphopeptide enrichment increasing workflow complexity, cost and potential analytical variability. Understanding how these casein-mineral interactions control micellar structure and digestibility is important for engineering functional, sustainable animal-free dairy alternatives.

We developed a rapid and reliable liquid chromatography-tandem mass spectrometry (LC-MS/MS) method for characterization of casein phosphorylation in a single injection without phosphopeptide enrichment. This method was applied to map casein phosphorylation profiles in cow, camel, goat, sheep and human milk. Followed by formulation of Artificial casein micelles (ACMs) with varying calcium phosphate to achieve α values 0.5, 0.7, 1.0; where α represents the fraction of bound phospho-caseins. ACMs were characterized for particle size distribution, rheological properties and digestion kinetics.

The LC-MS/MS workflow successfully captured the broad phosphorylation of casein phosphorylation across mammalian species in a single injection

without phosphopeptide enrichment. The method resolved multiple phosphorylation states for individual peptides ranging from unphosphorylated (0P) to penta-phosphorylated (5P) in bovine, and up to hexa-phosphorylated (6P) in non-bovine milk. Variations in mineral composition influenced micellar assembly, size distribution, gelation and digestive behaviour. These findings support the design of sustainable and functional dairy alternatives with tailored properties, enabling development of application-specific products for diverse industrial applications.

Exploring the constituent plants of an Ayurvedic formulation for activity against cancer and modulating the gut microbiota.

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Abstract

Background: Phytochemicals, as multifunctional, multitarget agents, are promising leads in drug research that warrant thorough exploration. An Ayurvedic formulation, *Varanadi Kashayam*, contains 16 constituent plants, some of which have been reported in the literature for potential anticancer activity, such as *Plumbago zeylanica* and *Terminalia chebula*. The formulation is cited in the Ayurvedic text *Ashtangahridayam* for its ability to modulate metabolism and may also influence the gut microbiome. Accordingly, the phytochemicals from the constituent plants were explored in the literature for their potential anticancer activity and effects on the gut microbiota.

Method: A systematic search was conducted in Google Scholar and PubMed for phytochemicals from these plants reported to exhibit anticancer activity in cellular or in vivo models. The resulting

phytochemicals were also assessed for reported effects on the gut microbiome.

Results: Ten plants were included in the most research articles, and 62 molecules from these plants were reported to have anticancer activity. Furthermore, a study using HRMS analysis of *Varanadi Kashayam* also identified its key phytochemicals. Cross-checking these lists identified six phytochemicals present in the formulation, all of which have been reported to influence the gut microbiome in the current literature.

Conclusion: *Varanadi Kashayam*, a polyherbal Ayurvedic formulation, contains active compounds with a bidirectional mode of action, exerting anticancer effects and influencing the gut microbiome. Further preclinical, mechanistic and clinical studies are necessary to validate these findings.

Unique antimicrobial properties of Australian stingless bee honey

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Abstract

Australian stingless bee honeys represent a unique and largely untapped natural resource with remarkable antimicrobial potential. We evaluated honey from *Tetragonula carbonaria*, *T. hockingsi*, and *Austroplebeia australis* against human bacterial and fungal pathogens. All samples inhibited growth, with *Trichophyton interdigitale* most sensitive (MIC 4–9% [wt/wt]), followed by *Staphylococcus aureus* (9–11%), *Escherichia coli* (10–13%), and *Cryptococcus neoformans* (24–34%). Heat treatment (80°C, 30 min) removed hydrogen peroxide, yet *T. carbonaria* and *T. hockingsi* retained substantial non-peroxide activity, a rare property outside of medicinal Manuka honey. Strikingly, hydrogen peroxide production in stingless bee honey was sustained for over six days in some samples, and *T. carbonaria* honey retained activity after 18 years of storage. Chemical and proteomic analyses revealed diverse proteins, phenolics, flavonoids, and antioxidants, indicating multifactorial mechanisms underpinning antimicrobial efficacy. These findings highlight stingless bee honeys as distinctive, durable, and heat-stable antimicrobials with strong translational potential for therapeutics, wound care, and combating drug-resistant infections, offering a potential native Australian analogue to the world-renowned medicinal Manuka honey.

An *Acetilactobacillus*-Dominated Larval Food Microbiome Reveals a Potential Source of Bioactive Metabolites in Australian Stingless Bees

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Abstract

Tetragonula carbonaria is one of the most widely managed species of native stingless bees in Australia. They play an important role as pollinators of both native plants and economically significant crops, so protecting these bees is crucial. The microbial communities of *T. carbonaria* larval food, made from a mixture of pollen, nectar, and bee secretions, remain completely uncharacterised despite being potentially vital for larval health. Stingless bee species from other parts of the world are known to rely on bacteria in their hive products to produce antimicrobials against hive pathogens and preserve pollen through fermentation.

Our study characterised the bacterial community present in larval food and pollen from 30 managed *T. carbonaria* colonies across the east coast of Australia. 16S amplicon sequencing revealed the larval food microbiomes were consistently dominated by *Acetilactobacillus*, ranging from 79%-99% in colonies across Sydney, Byron Bay, and the Atherton Tablelands.

Comparisons of ASV beta diversity and phylogenetic analyses of *Acetilactobacillus* ASVs revealed distinct regional clustering, with Atherton Tablelands-associated strains separated from those identified in the other regions. These findings suggest geographic structuring of *Acetilactobacillus* populations and a potential specialised association between these bacteria and *T. carbonaria*. *Acetilactobacillus* has recently been found in Brazilian stingless bee honey, but its ecological and functional roles remain poorly understood. Further characterisation of the metabolites produced by these bacteria may provide insights into their contributions to larval development, microbial defence, and hive health, while identifying novel bioactive compounds of ecological and medical significance.

Zombie Fungi: Exploring Australian Entomopathogenic Fungi and their Bioactive Metabolites

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Abstract

Entomopathogenic fungi (EPF) are parasitic microorganisms with the ability to infect and kill insects. During infection, fungal hyphae proliferate throughout the body cavity of the insect, producing secondary metabolites that disrupt physiological processes, change host behaviour, and deter opportunistic microbes. Common EPFs include the caterpillar fungus *Ophiocordyceps sinensis*, used in traditional Chinese medicine to enhance kidney function, *Ophiocordyceps unilateralis*, known for their unique ‘zombification’ of host-ant behaviour, and *Beauveria bassiana*, which is used as an environmentally friendly biopesticide.

The increasing prevalence of antimicrobial resistance worldwide, coupled with a dwindling pipeline of new antimicrobial agents, poses a significant threat to public health. The ESKAPE pathogens have been identified as critical multidrug-resistant bacteria for which effective new therapies are urgently needed. Due to their interactions with other opportunistic microbes that compete for nutrients from the environment, EPFs are a valuable, untapped source for new antimicrobial drug candidates. This project aims to explore a unique collection of Australian EPF strains through their cultivation, isolation of secondary metabolites, and investigation of their antibiotic, antifungal, cytotoxic, and antiparasitic bioactivities.

Performance and nutrient quality of black soldier fly (*Hermetia illucens*) larvae reared on agro-industrial waste streams for aquafeed applications

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Abstract

Growth of the aquaculture industry is limited by sustainable feedstock availability highlighting the need for alternatives. Black soldier fly (*Hermetia illucens*, BSF) larvae can meet nutritional requirements of aquaculture species while potentially enhancing health. This study evaluated BSF larval growth and composition to determine suitability of BSF biomass reared on agro-industrial waste streams as a sustainable feedstock for aquafeed. Initially, BSF larvae were reared on abundant, underutilized waste streams—spent brewery grains (SBG), cauliflower offcuts (CAO) and spent coffee grounds (SCG). SCG was ineffective as an individual substrate, but SBG and CAO were promising with BSF larval yields of 8.91 g and 12.29 g, survival rates of 79.67% and 82.5%, and development times of 27 and 33 days, respectively. SBG-reared larvae contained higher protein (37.51%) and lipid (48.31%) than CAO-reared larvae (33.87% protein; 41.23% lipid), whereas ash was lower in SBG larvae (5.18%) compared to CAO (17.1%). Subsequently, SBG and CAO were combined at 1:3, 1:1, 3:1 ratios. The 1:3 SBG:CAO substrate showed low larval survival (less than 10%), while 1:1 and 3:1 SBG:CAO substrates displayed higher survival (71.83% and 87.5%, respectively) and high yields (13.95 g and 16.41 g, respectively). Protein contents of larvae reared on 1:1 and 3:1 SBG:CAO substrates were 41.44% and 40.63%, lipid contents were 37.16% and 38.92% while ash contents were 7.74% and 5.70%, respectively. Out of the substrates tested, 1:1 and 3:1 SBG:CAO substrates were most suitable for BSF larvae for aquafeed applications due to higher yields and protein contents.

Comparison of Different Packaging Processes on Bioactives Changes of Australian Jackfruit during Storage

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Abstract

Jackfruit (*Artocarpus heterophyllus* Lam.) is one of the biggest tropical fruits that has gained increasing attention in recent years because of its versatility, unique texture and nutritional value. The encouragement of developing jackfruit industry in Australia brings the demand increases of this fruit. However, post-harvest loss of jackfruit is a barrier to nourish the jackfruit industry. Effective post-harvest technology, including storage, and packaging

strategies, is essential to mitigate this large amount loss. It is worthy to point out that fruit pre-cutting causes the quality change by increased oxidative stress, including the contaminated by microorganisms, texture change, browning and phytochemicals loss. This study aims to explore the two different packaging methods, modified atmosphere packaging (MAP) and vacuum packaging (VP), to extend the shelf-life for jackfruit while maintain the quality of jackfruit.

Phytochemical changes were evaluated by measuring total phenolic content (TPC), total flavonoids content (TFC), and four antioxidant assays, which are DPPH, ABTS, FRAP, and FICA. Over five weeks of storage, TPC decreased in all packaging treatments, and storage time has a significant effect on TPC for jackfruit samples ($p < 0.01$). TFC showed similar trend with TPC. DPPH showed decreased tendency with different pattern. FRAP and ABTS showed similar trend with DPPH, while FICA had the slightly decline during the storage, but with some fluctuation at week 3 and 4. This study demonstrates the potential of packaging processes to influence quality preservation of fresh-cut jackfruit during storage and provides insights for reducing postharvest losses in the Australian jackfruit industry.

Concentration dependence of laminarin conformation in solution: An NMR spectroscopy study

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Abstract

The bioactivities and physicochemical properties of polysaccharides are found to be closely associated with their structural characteristics and conformations. Meanwhile, it is well recognized that physical and structural properties of polysaccharides depend strongly on their concentration in solution, i.e. polysaccharides adopt extended linear chains below the critical overlap concentration but aggregate at higher concentrations. Studies of concentration dependent properties of polysaccharides provide means for improving in food texture. In the present study, we report the PGSE NMR measurements of laminarin in D₂O over a wide concentration range. 1D ¹H spectra of laminarin show minor chemical shift perturbation, as a function of its concentration, for protons of base-unit. Experimentally measured

translational diffusion coefficients of laminarin over the concentration range suggest sequential events of conformation change upon the increase of concentration: (1) at concentration below 1.0 mM, laminarin exists in linear form, (2) laminarin starts to coil up when concentration increases above 1.0 mM, as evident by an increase in translational diffusion coefficient, (3) subsequently, its translational diffusion coefficient decreases when concentration reaches 5 mM, and eventually diffuses slower than that in its linear form, consistent with an increase in molecular mass as a result of self-entanglement. This study represents the first investigation of the chain conformational changes of laminarin in an aqueous solution and reveals its coil-like structure. The insights obtained here may also be applicable to other polysaccharides. From a structural perspective, these findings provide a useful basis for the further development and application of polysaccharides with concentration guidance.

Phenolic and prebiotic bioactives in Australian honey alleviates DSS-induced colitis

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Abstract

Inflammation of the gastrointestinal tract can arise from bacterial or viral infection, immune dysfunction, or disruption to the homeostatic relationship between the gut microbiota and host immunity. Inflammatory Bowel Diseases (IBDs) are characterised by chronic intestinal inflammation and long-term gut inflammation has well-documented detrimental effects on overall health, with links to cardiovascular, neurological, and hepatic disease. Non-invasive, palatable treatment options are therefore highly sought after. Australian honey is a rich source of bioactive phenolic compounds that confer antioxidant capacity, with profile and concentration variation by floral source. This variation suggests that specific floral types may carry greater anti-inflammatory potential, thus establishing the need to investigate in vivo effects. Honey possesses oligosaccharide components with prebiotic activity, and oral administration of Australian honey as part of a healthy diet has been shown to increase key beneficial bacteria, which in turn suppress colonisation by potentially pathogenic taxa. The bioactivity of the phenolic compounds and oligosaccharides in honey are therefore plausible contributors to resolving gut inflammation.

This work assesses the anti-inflammatory and prebiotic effects of orally administered Australian honey in a DSS-induced colitis model, to evaluate its potential as a preventative or therapeutic measure in gut disease states. Australian honey altered several aspects of DSS-induced intestinal injury, most notably reduced histopathological markers of colitis, increased anti-inflammatory immune cell populations in the mesenteric lymph nodes, and shifts in key taxonomic abundances. These findings suggest that bioactive components in Australian honey act to alleviate gut inflammation, supporting its potential as a bioactive-rich intervention for intestinal disease.

Non-digestible bioactive components in honey drive prebiotic effects across dietary contexts

Kathleen Schell, Erin Shanahan, Nural Cokcetin

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Abstract

The gut microbiota plays a critical role in human health, with dysbiosis associated with gut inflammation and numerous chronic conditions. Consequently, there is growing interest in manipulating the microbiota through dietary interventions such as prebiotics. Honey has a long history of therapeutic use, and emerging evidence suggests certain honeys have prebiotic activity. These effects may be driven by non-digestible oligosaccharides. Australian honey has demonstrated in vitro antibacterial activity against gut pathogens and growth-promoting effects on probiotic bacteria, despite compositional variation between floral sources.

This study assessed the in vivo prebiotic potential of Australian honey in mice under two dietary contexts: standard chow (healthy) and Western high-fat (unhealthy) diets. Gut microbiota composition was compared between baseline, untreated, inulin-supplemented, honey-supplemented, and ‘artificial honey’ groups, with artificial honey comprising simple sugars to distinguish simple sugar-driven effects from those of non-digestible and bioactive components.

Australian honey demonstrated prebiotic activity, promoting beneficial bacteria, particularly Lactobacillaceae and Muribaculaceae. These effects were not replicated by artificial honey, supporting a role for honey components beyond simple sugars. Under the Western diet, honey did not restore depleted Lactobacillaceae or suppress potential

pathobionts, but promoted other commensal bacteria associated with complex carbohydrate metabolism, including species of emerging probiotic interest. Collectively, these findings demonstrate the prebiotic potential of Australian honey across dietary contexts, with microbiota-modulating and indirect pathogen-suppressive effects most pronounced within a metabolically stable gut environment.

Comparative Characterization of Australian Fetta Cheese: Physicochemical Properties, Antioxidant and Anti-Inflammatory Activities

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Abstract

This study investigated and compared the physicochemical properties, antioxidant activity, anti-inflammatory activity, and amino acid profiles of Fetta cheese produced in Australia by five brands: DODONI, RIVERINA, Woolworths, EMPORIUM, and Lemnos. Cheese samples were homogenised in Milli-Q water and centrifuged at 4,700 rpm for 20 min at 4 °C. Following centrifugation, the upper fat layer was removed, and the samples were separated into water-soluble extracts (WSEs) and water-insoluble extracts (WISs). The WSE from each cheese sample was further fractionated according to molecular weight using molecular weight cut-off (MWCO) membranes of 10, 30, and 100 kDa, yielding three molecular-weight fractions: 1-10 kDa, 10-30 kDa, and 30-100 kDa. The WSEs and WISs were subsequently freeze-dried for further analysis. The antioxidant activity of the freeze-dried fractions was evaluated using DPPH, FRAP, ABTS radical-scavenging, ferrous ion-chelating activity (FICA), reducing power activity (RPA), and total antioxidant capacity assays. The results showed that the 1-10 kDa WSE fraction exhibited the highest antioxidant activity among the molecular-weight fractions, whereas the WIS fractions exhibited comparatively very low antioxidant activity. In addition, the WSE fractions from all Fetta cheese samples demonstrated significant anti-inflammatory activity. These findings suggest that low-molecular-weight water-soluble components of Fetta cheese may contribute substantially to its antioxidant and anti-inflammatory activities, highlighting their potential as sources of bioactive compounds.

Ultrasonic-Assisted Extraction and LC-ESI-QTOF-MS/MS based Characterization of Red Beetroot Phenolic Compounds for Enhanced Antioxidant Profile using Response Surface Methodology: A Box Behnken Design Approach

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Abstract

Optimization of extraction parameters of bioactive compounds is of cardinal importance for controlled extraction and maximization of phytochemicals in the final extract for their subsequent use in food formulations, nutraceuticals and cosmetics. Conventional extraction methods may not produce high extract yields and ever-changing composition of crude extracts and require high extraction time to obtain commercially viable extracts. Hence, ultrasonication is sought as an alternative technique to couple with conventional extraction approaches to reduce the extraction time and improved extract yields. In this context, this research is planned to optimize the extraction parameters include ethanol concentration in binary solvent system, sonication amplitude, sonication time and solvent to solid ratio for maximum extraction of phenolic compounds from fresh red beetroot. The Box-Behnken Design approach was used to minimize the experimental runs to analyze the data using Response Surface Method. High regression coefficient (R^2) values showed that the model was able to explain the variance in total polyphenols and total flavonoids with statistically significant results with respect to different extraction parameters. Interestingly, coupling ultrasonication with conventional solvent extraction protocol seems to be complementing the extraction efficiency to acquire higher phenolic compounds at lower ethanol concentrations. Similarly, the distribution of phenolic acids and flavonoids in the obtained extracts characterized by LC-ESI-QTOF-MS/MS was preferentially influenced by the coupled extraction parameters. Likewise, a strong correlation between antioxidant capacity and phytochemical densities was found. Conclusively, the optimized ultrasonic-assisted extraction parameters are recommended for maximizing the yields of phenolic compounds in red beetroot with potent antioxidant potential.

The Impact of dietary macronutrient distribution on the gut microbiota and colonic tumor development

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Abstract

Background: Colorectal cancer (CRC) is the third most common cancer worldwide and is strongly associated with Western-style diets rich in red meat and saturated fat. Diet is a major modifiable risk factor for CRC and shapes the gut microbiome, but the interactions between dietary composition, microbial communities, and CRC risk remain incompletely understood.

Methods: Using the Geometric Framework for Nutrition, we developed twelve diets differing in protein and fat content and source, including red meat, soy protein, saturated fat, and unsaturated fat. Female C57BL/6 and BALB/c mice were fed these diets to assess microbiome responses. A selected subset of diets was subsequently tested in the azoxymethane/dextran sulfate sodium (AOM/DSS) model of CRC to determine effects on tumour development, colitis, survival, and gut microbial composition.

Results: Red meat diets produced distinct microbial profiles characterised by reduced diversity and enrichment of taxa associated with inflammatory bowel disease, metabolic dysfunction, and CRC. In contrast, soy-based diets maintained more favourable microbial communities. Responses differed between mouse strains, with stronger effects of red meat in BALB/c mice and greater influence of macronutrient composition in C57BL/6 mice. In the CRC model, high-protein diets, regardless of protein source, had the greatest impact on tumour burden, colitis severity, and survival, indicating that elevated protein intake during inflammation may promote CRC progression through microbiome-mediated mechanisms.

Conclusions: Dietary composition and nutrient source significantly influence gut microbial communities and CRC outcomes. These findings identify diet-microbiome interactions as potential targets for CRC prevention and intervention.

A Pre-colonial Blueberry? Antioxidant Testing of Muntries (*Kunzea pomifera*)

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Abstract

Native Australian foods are being sought after like never before, with research increasingly positioning native ingredients in the spotlight for their nutritional and bioactive properties. However, these foods and the knowledges surrounding them existed long before their interest by Western science. All research therefore has a responsibility to ethically engage with native foods and acknowledge the cultural, historical and ecological contexts from which they originate.

Indigenous-led research generally supports more holistic approaches to foods and health, including authentic engagement with communities and consideration of pre-colonial and traditional uses alongside quantitative scientific outcomes. Conversely, Eurocentric research often solely focuses on individual compounds or antioxidant activity and risks continuing to reduce native foods to their measurable bioactive properties and separating them from broader First Nations Knowledge systems.

This poster presents the antioxidant component of a broader Aboriginal-led investigation of Muntries (*Kunzea pomifera*). Western scientific methodologies are utilised as analytical tools to quantitatively investigate total phenolic content and antioxidant activity, with blueberries included as a commonly consumed berry comparator. Rather than using antioxidant measurements to establish the value of Muntries, this research aims to contribute additional Western scientific knowledge about the berry while recognising that these measurements represent only one way of understanding the food. The research is guided by Aboriginal-led priorities, community leadership and accessibility for food applications, with potential contributions to health and wellbeing serving as key motivations.

Panax ginseng Attenuates Cigarette Smoke-Induced Oxidative Stress, Inflammation and Senescence in Human Airway Basal Epithelial Cells

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Abstract

Background: Cigarette smoke is a major risk factor for chronic airway diseases and promotes oxidative stress, inflammation, airway remodelling, and cellular senescence in airway epithelial cells. Panax ginseng possesses antioxidant and anti-inflammatory properties; however, its effects on cigarette smoke-induced epithelial injury remain unclear. This study investigated whether Panax ginseng root extract attenuates CSE-induced cellular dysfunction in BCI-NS1.1 airway basal epithelial cells

Methods: BCI-NS1.1 human airway basal epithelial cells were treated with 5% cigarette smoke extract (CSE) in the presence or absence of 100 µg/mL Panax ginseng root extract (commercial product provided by Hivita Monotherapy Pty Ltd). Oxidative stress, gene expression, protein expression, and cellular senescence were assessed using DCF fluorescence, qPCR, protein array, and SA-β-gal staining

Findings: Exposure to 5% CSE increased ROS production, altered the expression of NQO1, HIF1A, MMP3, ALOX5, MAPK3, RIPK3, and SIRT1, elevated MPO, IL-4, IL-5, IL-15, IL-22, MMP-9, and osteopontin protein levels, and increased cellular senescence. Treatment with 100 µg/mL Panax ginseng significantly attenuated these CSE-induced changes, reducing ROS production and senescence while modulating oxidative stress-, inflammatory-, and remodelling-associated markers.

Conclusion: Panax ginseng mitigated CSE-induced oxidative stress, inflammation, airway remodelling, and cellular senescence in airway basal epithelial cells, supporting its potential as a therapeutic strategy for smoke-related airway injury.

Mescaline in Cacti: Analytical Challenges, Quantitative Variation, and Implications for Sustainable Bioactive Resource Development

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Abstract

Australia faces a growing mental health burden marked by rising prevalence of depression,

anxiety, and unmet treatment needs, which has prompted increasing interest in natural psychedelic-assisted therapies. Mescaline is one of the best-known naturally occurring psychoactive alkaloids, yet surprisingly little quantitative information exists regarding its concentration, distribution, and variability within mescaline-producing cacti. Much of the published literature is based on small sample numbers, inconsistent sampling methodologies, or analytical approaches that predate modern instrumentation. Consequently, significant uncertainty remains regarding mescaline content across species, cultivars, and growing conditions.

This presentation examines mescaline as a naturally occurring plant bioactive through the lens of analytical chemistry and bioactive resource development. Drawing on a review of the published literature alongside recent LC–MS analysis of cultivated cactus collections, we evaluate mescaline concentrations in *Trichocereus* and *Lophophora* species and explore patterns of variation both within and between taxa. Particular attention is given to methodological considerations, tissue-specific alkaloid distribution, and the interpretation of historical analytical data.

Beyond analytical considerations, findings have implications for conservation and sustainability. Comparisons between rapidly growing cultivated *Trichocereus* species and slow-growing, threatened *Lophophora williamsii* populations suggest substantial differences in bioactive production efficiency, raising important questions regarding sustainable sourcing and conservation-focused cultivation strategies.

By integrating contemporary analytical techniques with ethnobotanical and horticultural knowledge, this work contributes to a more robust understanding of mescaline-containing cacti as bioactive organisms and highlights opportunities for improving the evidence base surrounding plant-derived alkaloids.

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Presenters are listed in alphabetical order by surname.

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