Precision Nutrition / Disease Prevention / Biochemistry of Aging / Immunocompetence

Nutrigenomics for Lifelong Health

International Scientific Conference

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Abstract Book

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From the WELCOME2 Project Coordinator

Mariusz Piskuła
WELCOME2 Project Coordinator

Dear participants of the WELCOME2 International Conference "Nutrigenomics for Lifelong Health" This conference was an important milestone for the WELCOME2 project, an EU-funded ERA Chair initiative at InLife Institute of Animal Reproduction and Food Research of the Polish Academy of Sciences.

The theme of this conference reflects one of the most exciting challenges facing modern life sciences: understanding how nutrition interacts with our biology throughout the course of life. Nutrigenomics provides a powerful framework for exploring these interactions, linking dietary factors with genes, metabolic pathways, cellular processes, immune function, ageing, and disease. At the same time, rapid developments in precision nutrition, computational modelling, and digital health are creating new opportunities to translate fundamental discoveries into more individualized approaches to health promotion and disease prevention.

The scientific programme has been designed to reflect this breadth. The four sessions—Precision Nutrition and Digital Twins, Biochemistry of Ageing, Nutrigenomics and Disease Prevention, and Immunocompetence and Ageing—bring together complementary perspectives on the mechanisms that influence health across the lifespan. Together, they illustrate how advances in molecular and computational sciences can contribute to a better understanding of ageing, resilience, and individual responses to nutrition.

This Book of Abstracts represents the diversity and vitality of the scientific community gathered in Olsztyn. The contributions presented here show the wide range of approaches currently being applied to questions of nutrition and lifelong health, from molecular mechanisms and metabolic profiling to computational tools, disease prevention, and immune function. Importantly, they also demonstrate that progress in this field depends on collaboration across disciplines and across generations of researchers.

As Project Coordinator of WELCOME2, I am particularly pleased to see this conference bringing together established experts, emerging investigators, PhD students, and researchers at different stages of their careers. Scientific progress is strengthened when ideas, methods, and perspectives are shared openly, and I hope that the discussions initiated during these three days will lead to new collaborations, innovative research, and lasting scientific partnerships.

I would like to express my sincere gratitude to all invited speakers, presenters, participants, members of the scientific and organizing committees, and everyone whose efforts have contributed to making this conference possible. I also gratefully acknowledge the support provided through the WELCOME2 project, which has made this international scientific gathering possible.

I hope that "Nutrigenomics for Lifelong Health" was not only a forum for presenting excellent research, but also a place where new ideas emerge, collaborations begin, and a shared vision for healthier ageing takes shape.

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The ageing epidermis as a dynamic system: insights from mathematical modelling

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Introduction: The epidermis is the outermost layer of the skin, and its correct functioning is key in in protecting us from dehydration and environmental aggressors. Epidermal homeostasis is achieved through a complex network of regulatory interactions between the physicochemical skin barrier function, innate and adaptive immune responses, the resident microbiota and epidermal proteases. Age is a key factor in shaping epidermal function. The epidermis of both the infant and the geriatric population have a decreased skin barrier recovery time, higher pH, increased epidermal proliferation and decreased differentiation of terminal differentiation markers, such as filaggrin.Elderly skin also has higher cortisol levels, which increase epidermal proliferation and further decrease keratinocyte differentiation. These differences in epidermal composition and function make the infants and the elderly more susceptible to environmental aggressors, increasing the risk of developing dermatological conditions, such as atopic dermatitis and psoriasis. It is yet to be clarified how the age-related risk factors contribute to disease onset and progression, and how to implement effective treatment strategies.

Aim: To mathematically predict how of age-related changes in epidermal composition shape the vulnerability to develop dermatological conditions, and to design effective strategies for their prevention.
Materials: Our in-silico approach involves the computational and mathematical analysis of published experimental and clinical data. We use MATLAB software for the numerical analysis of the mathematical model.
Methods: We formalized the regulatory network controlling epidermal function into a mechanistic mathematical model and simulated the effect of age-related risk factors and preventive strategies on epidermal function.

Results: We disentangled how age-related factors shape the response of the epidermis to environmental triggers: A healthy adult epidermis is dynamically simulated as transient deviation from a homeostasis setpoint. While this phenotype is robust to parametric variations, the recovery time is proportional to age-related risk factors.
Age-related risk factors that surpass a critical severity threshold lead to intermittent epidermal dysfunction, which can eventually result in persistent "inflammaging". Co-occurring age-related risk factors have synergic effects, dramatically incasing the risk for dermatological conditions.
We used the model to systematically simulate the effect of different preventive strategies, such as emollients, pH buffers and topical lipid mixtures, on infant and geriatric epidermis, and identified specific regimes that optimally prevent the onset of inflammaging.

Summary/Conclusion: Our mathematical model mechanistically links age-related risk factors to the risk of developing dermatological conditions and offers a computational framework to design effective preventive strategies that halt their progression.

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Connecting the Dots: Pathways and Networks in Nutrition Research

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Nutrition research is undergoing a fundamental paradigm shift from general dietary guidelines to highly customized precision nutrition. Traditional "one-size-fits-all" dietary recommendations often fail because they ignore the profound inter-individual variability in metabolic, genetic, and gut microbiome-driven responses to food. Modern multi-omics, wearables, and artificial intelligence (AI) offer unprecedented opportunities to capture this complexity, but translating high-dimensional biological data into clinical utility requires a robust network-based perspective.

A 20-year scientific journey will be presented tracing the evolution of nutritional systems biology "from node to network". Beginning with influence of single proteins and how they interact. Thereafter transitioning to pathway-level biology using pathway analysis and WikiPathways, founded in 2008 to collaboratively crowd-source, curate, and annotate metabolic and gene regulatory pathways. Using these mechanistic pathway frameworks, it is demonstrated how transcriptomics and metabolomics can uncover subtle biological processes, highlighted by immunometabolic studies on vitamin D in human monocyte models. However, as precision nutrition increasingly adopts machine learning, a critical bottleneck has emerged: data quality, model reproducibility, and ecosystem fragmentation. AI models are only as robust as the datasets on which they are trained. To move beyond isolated cohorts, this talk underscores the urgent need for FAIR (Findable, Accessible, Interoperable, Reusable) data standards. Through initiatives in the ELIXIR Food & Nutrition Community and the FNS-Cloud project it is illustrate how ontologies and federated cloud infrastructures make food, wearable, and omics data truly interoperable.

Ultimately, the future of nutrition lies in "computational nutrition" a hybrid field where data-driven machine learning meets mechanistically-grounded biological networks.

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In Life

Micronutrients as modulators of stress response and aging processes

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Copper (Cu) and selenium (Se) are micronutrients required for a broad spectrum of enzymatic activities, including the activity of enzymes as crucial as cytochrome c oxidase (Cu) or enzymes involved in the regulation of thyroid hormone activities (Se), as well as a battery of enzymes involved in stress defense (Cu and Se). Selenium-binding protein 1 (SELENBP1) mechanistically links these two micronutrients, and we asked whether the activity or level of SELENBP1 in human cells and in a model organism, Caenorhabditis elegans, are associated with changes in stress response and cellular aging processes.

SELENBP1, originally identified through the eponymous binding of Se at supraphysiological doses, is a Cu-dependent enzyme: the capability of recombinant human SELENBP1 to act as methanethiol oxidase (MTO) – catalyzing the conversion of the volatile and toxic sulfur compound methanethiol – strictly depends on the presence of Cu. It appears, however, that Se modulates the Cu-dependent activity; the roles of Cu and Se are supported by studies in mice and the nematode C. elegans: the level of Cu achieved through its dietary availability defines MTO activity; dietary Cu deficiency lowers hepatic MTO activity in mice and lowers overall activity in C. elegans.
In primary human umbilical vein endothelial cells (HUVEC), SELENBP1 levels and activity were markedly decreased during both replicative and stress-induced senescence. siRNA-mediated depletion of SELENBP1 increased the expression of senescence markers. In addition, both knockdown and overexpression of SELENBP1 modulated the expression of proteins involved in H_2S metabolism as well as oxidative and ER stress responses.

In C. elegans, expression of the ortholog of SELENBP1, SEMO-1, and its activity declined with age – similar to the finding in HUVECs. Different from primary human cells, SEMO-1 acts as a pro-aging factor under standard laboratory conditions: SEMO-1 deficiency conferred increased resistance to paraquat-induced oxidative stress and extended organismal lifespan. In the presence of its toxic substrate, however, SEMO-1 protected C. elegans, rather than acting as a pro-aging factor. Together, these findings demonstrate that the longevity and stress-resistance phenotype of SEMO-1 deficiency is strictly context-dependent and lost upon methanethiol exposure. The role of SEMO-1 in regulating aging and oxidative stress resistance is therefore critically influenced by environmental methanethiol availability.

In summary, SELENBP1 and SEMO-1 are Cu-dependent enzymes which are modulated also by Se supply. They are linked to cellular senescence and nematode aging. The exact mechanistic interplay between micronutrients Cu and Se and the proteins in a senescence/aging context requires further evaluation.

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In Life

The Impact of Nutrition on Cognitive Function across the life course; interactions with stress

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Nutrition has the potential to impact cognition across the life course from prenatal exposure to diet or malnutrition to the prevention of cognitive decline in older age. The role of diet in preventing cognitive decline and maintaining cognitive function as we age is important in the light of the ageing population and the greater old age dependency which trends such as an increase in the prevalence of dementia prevalence suggest. Epidemiological studies suggest that habitual diet and specific dietary patterns may be related to cognitive decline. Dietary interventions and interventions to increase intake of specific nutrients which may positively affect cognitive function e.g. increasing fibre and polyphenols and represent modifiable behaviour to prevent cognitive decline will be examined. Experimental evidence of the effect of these nutrients also suggests some potential mechanisms of action for effects of these compounds on the brain.

Obesity can impact cognitive function with long term increased likelihood of cognitive decline. This may be related to impaired glucose tolerance where data shows impact on cognitive performance before people are even aware of their impaired glucose handling and which precedes the impact seen in type 2 diabetes. Improvement in glucose tolerance can reverse cognitive impact.

Diet may also positively impact cognitive development. The cost of living crisis has increased exposure to food insecurity which on impacts psychological well-being and is a major source of stress for children and young people. Currently more than 4.8m children live in food insecure households in the UK. Adults with one or two children are 1.7 times more likely to have very low food security compared to those without children. Levels of food insecurity and obesity are not evenly distributed across the population. Evidence from animal studies demonstrates effects of food insecurity on telomere length and implies that exposure to this type of stressor could have long lasting impact on children and young people growing up under conditions of austerity. It is critical therefore to examine how to give children nutritional input to support cognitive development and how to protect people against cognitive decline in older age.

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Bidirectional Interplay Between Immunocompetence and Premature Aging

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Aging and declining immunocompetence are mutually reinforcing processes. Loss of immune surveillance facilitates the persistence of damaged cells and the selection of malignant clones, while chronic DNA damage, inflammation, and tumor-derived signals further accelerate immune dysfunction. Fanconi anemia (FA) provides a unique human model in which to study this interaction because defective genome maintenance, premature tissue dysfunction, and an exceptionally high risk of early-onset epithelial cancer converge within the same individuals.

Rather than viewing cancer risk as a direct and static consequence of the inherited FA mutation, this talk will consider tumorigenesis as an evolving interaction between genetically unstable epithelial cells and an aging immune microenvironment. In the oral mucosa, premalignant clones emerge in a setting of chronic cellular stress and impaired tissue resilience. During progression, persistent antigenic and inflammatory stimulation may promote functional T-cell exhaustion and senescence, while alterations in natural killer cells and myeloid populations may further compromise immune editing and tumor control. Conversely, ineffective clearance of damaged or senescent cells can perpetuate inflammation, accelerate tissue aging, and create conditions that favor malignant selection.

Drawing on longitudinal oral cancer screening cohorts, immunophenotyping, brush cytology, genomic markers, and spatial and cytology-based single-cell analyses, the lecture will explore how systemic immunoaging relates to local changes in immune surveillance during premalignant and malignant progression.

The central concept is bidirectional: premature aging reduces immune resilience, while declining immunocompetence accelerates tissue dysfunction and tumor evolution. Identifying stage-specific immune alterations may therefore provide new biomarkers and opportunities for precision prevention in FA and other cancer-predisposition syndromes.

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In Life

Multi-Omics Dissection of Vitamin D_3 Responses Reveals Context-Dependent Immune Regulation in Multiple Sclerosis

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Vitamin D deficiency is a major environmental risk factor for multiple sclerosis (MS) and has been linked to impaired immune regulation and accelerated immunological aging. However, the in vivo molecular mechanisms underlying individual responses to vitamin D_3 supplementation remain poorly defined, limiting its implementation in precision nutrition strategies. Here, we applied longitudinal multi-omics profiling combining RNA-seq and ATAC-seq in peripheral blood mononuclear cells (PBMCs) from MS patients undergoing distinct vitamin D_3 supplementation regimens, alongside healthy individuals receiving monthly bolus dosing. This design enabled within-individual resolution of transcriptional and epigenetic responses over three months under real-world intervention conditions. Despite supplementation, MS patients maintained distinct transcriptomic and chromatin accessibility landscapes compared to healthy controls, indicating persistent disease-associated immune states. Rather than inducing global transcriptomic reprogramming, vitamin D_3 elicited selective, context-dependent modulation of immune regulatory networks. In MS patients receiving daily high-dose supplementation, responsive genes were enriched in innate immune and inflammatory pathways, including Toll-like receptor signaling and cytokine regulation. Integration with chromatin accessibility data revealed widespread disease-associated regulatory differences and only partial concordance between epigenomic and transcriptional responses, underscoring complex multilayered regulation. Strikingly, intersection of vitamin D-responsive genes with vitamin D receptor (VDR) binding datasets identified a focused set of candidate target genes with high relevance to MS pathophysiology, providing a mechanistic link between supplementation and immune modulation. Importantly, substantial inter-individual variability was observed at both transcriptional and epigenetic levels, highlighting personalized response patterns that are not captured by clinical parameters alone. These findings redefine vitamin D_3 supplementation as a context-dependent immune modulator rather than a uniform anti-inflammatory intervention and emphasize the importance of multi-omics approaches to resolve individual response trajectories. By integrating transcriptional and epigenetic information, this study provides a framework for developing predictive biomarkers and digital twin models of immune regulation in MS. Overall, our results support the implementation of nutrigenomics-driven precision nutrition strategies aimed at restoring immune homeostasis, improving disease management, and promoting healthy aging in chronic inflammatory conditions.

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In Life

The Brain Derived Neurotrophic Factor Gene and Dietary Decisions

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The brain derived neurotrophic factor (BDNF) rs6265 G>A (Val66Met) single nucleotide polymorphism (SNP) modifies reward processing and subsequently dopaminergic-related behaviours. Psychological drivers of food choice include food adventurousness (FA), or neophilia, a high willingness to try novel foods, and loss aversion (LA), where the fear of loss exceeds any potential gain. Individual with LA may select familiar foods or opt to retain items in preloaded food choice scenarios. While rs6265 variation may modify these behaviours, the topic remains under-researched. Therefore, we aimed to assess the influence of rs6265 variation on FA and LA, considering food choices and body mass index (BMI).

In study 1, there was an interaction effect between LA_H and LA_L groups and rs6265 ($p<0.05$; Figure 1). Those that were LA_L with the ValVal genotype added fewer healthy items (34 ± 24%) than Met carriers (56 ± 30%; $p<0.05$), and LA_H Met carriers added more unhealthy items (47 ± 26%) than the ValVal genotype group (34 ± 22%; $p<0.05$). There was no interaction effect between LA_H and LA_L groups and rs6265 with removed or kept healthy and unhealthy toppings ($p>0.05$) However, in the removed setting, those that were LA_H with the ValVal genotype removed more healthy items (38 ± 25%) than Met carriers (20 ± 30%; $p<0.05$).

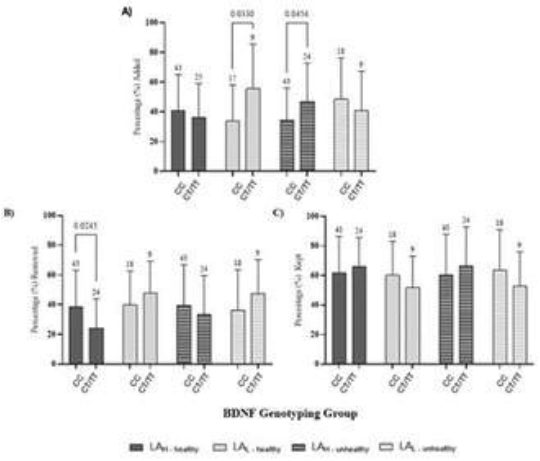

Figure 1. Total (A) added, (B) removed and (C) kept healthy and unhealthy toppings by LA and BDNF rs6252.
Exact p-values shown in figure.

In study 2, the MetMet genotype was associated with a higher FA and BMI. Additionally, FA was associated with liking of alcohol, vegetables and fruit, and BMI was associated with liking meat and foods high in saturated fat. No association was found between rs6265 and food liking.

Together, these results indicate that rs6265 variation may influence food choice through dopaminergic-related dietary behaviour. Specifically, high LA combined with genetic predispositions to reduced dopamine activity may promote greater food retention irrespective of perceived healthiness, and rs6265 variation may influence FA with potential BMI outcomes. Future longitudinal approaches are necessary to clarify the mechanisms linking BDNF variation to eating behaviour and metabolic outcomes.

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In Life

Adjustments in meal timing and macronutrient composition improve postprandial metabolic and inflammatory markers in night-shift workers

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Background: Night work disrupts circadian rhythms and alters glucose homeostasis, increasing long term metabolic risk. Although nutritional interventions show beneficial short-term effects under controlled conditions, evidence from real life settings in night-shift workers remains limited.
Objectives: To evaluate whether a personalized nutrition intervention improves metabolic and inflammatory responses in night shift workers.

Methods: In a non-blinded controlled intervention study, healthy male night shift workers aged 18 to 60 years participated in a three-month personalized nutrition intervention following a one-month run in period. Personalization was based on demographic characteristics combined with postprandial metabolic responses to a standardized mixed meal tolerance test. Advice focused on advancing the timing of energy intake, reducing caloric intake during night shifts, and adjusting macronutrient composition to reflect diurnal fluctuations in insulin sensitivity, with relatively higher carbohydrate earlier in the day and higher fat intake later in the day. Controls continued habitual dietary behavior. Food intake was assessed using a digital food diary, and diet quality was quantified using the Dutch Healthy Eating Index. Postprandial metabolic and inflammatory markers were measured before and after intervention.

Results: In the intervention group (n=22), the timing of total energy intake during night shifts advanced by 180 minutes at intervention start and by 120 minutes at intervention end relative to baseline, driven mainly by earlier intake of carbohydrates and fat. Total energy intake and diet quality remained unchanged, and no dietary changes were observed in controls. Postprandial total and HDL cholesterol levels improved following the intervention, while glucose, insulin and triglyceride responses did not change. Postprandial concentrations of several inflammatory markers, including IL 10, E selectin, ICAM 1 and TNF α were reduced after intervention.

Conclusion: A three-month personalized nutrition intervention targeting meal timing and macronutrient distribution is feasible in night shift workers and associated with improved postprandial lipid and inflammatory responses. Adjusting meal timing may represent an effective strategy to mitigate metabolic disruption in real life night work settings.

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In Life

Investigation of the impact of melatonin receptor 1B (MTNR1B) genotype on continuous glucose monitor derived metrics

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Background: The risk allele (G) MTNR1B rs10830963 has been associated with increased fasting glucose, impaired glucose tolerance, and type 2 diabetes (T2D). Our research has demonstrated that fasting glucose and post-prandial glucose response to a high-carbohydrate breakfast were significantly greater in participants with a GG genotype than those with a CC or CG genotype. Continuous glucose monitors (CGMs) are increasingly used in individuals with euglycemia and several CGM-derived metrics have been associated with health in people without diabetes.
Objective: Firstly, to determine associations between CGM-derived metrics (time in range (TIR), glycaemic variability, mean glucose concentration) and participant characteristics (age, BMI, fasting glucose, chronotype score). Secondly, to compare CGM-derived metrics between participants with a GG, GC and CC MTNR1B rs10830963 genotype.

Methods: Post-prandial glucose levels were recorded for two weeks using a CGM. TIR was calculated using two different cut-offs: 3.9–7.8 mmol/L American Dietetic Association target range (TIR_{ADA}) and 3.9–5.6 mmol/L published by Berry et al. (2023) associated with need for diabetes screening (TIR_{Berry}). The associations between CGM-derived metrics and participant characteristics were assessed using correlation analysis. CGM-derived metrics were compared between genotype groups for MTNR1B using a one-way ANOVA.

Results: Data was available for 53 participants. Age was significantly correlated with glucose variability (r_s=0.305, p=0.026). Mean glucose was significantly associated with fasting glucose (r=0.758, p<0.001). TIR_{Berry} was significantly correlated with mean glucose levels (r=-0.947, p<0.001) and fasting glucose (r=-0.793, p<0.001). GG participants had a significantly higher mean glucose concentration over the two-week collection period than CG (p=0.004) or CC participants (p=0.009). GG participants had a significantly lower TIR using the more stringent cut-offs (TIR_{Berry}) compared to CG (p=0.01) or CC (p=0.005) participants.

Conclusion: The study findings demonstrate, in a relatively young and healthy population, MTNR1B genotype significantly affects CGM-metrics associated with need for T2D screening.

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In Life

Obesity-related leptin dysregulation and developmental programming of mouse preimplantation embryos

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The worldwide prevalence of obesity continues to increase due to excessive caloric intake and reduced physical activity. Besides its well-established association with metabolic and cardiovascular disorders, obesity negatively affects female fertility by impairing ovarian function, oocyte quality and developmental competence. Chronic hyperleptinemia, a hallmark of obesity, contributes to ovarian dysfunction and leptin resistance, disrupting physiological processes essential for successful reproduction.

According to the Developmental Origins of Health and Disease concept, environmental conditions during early development can permanently influence health outcomes later in life. Maternal obesity and associated metabolic disturbances may alter the molecular and metabolic landscape of the oocyte, thereby affecting embryo development and long-term offspring health. Since the oocyte provides the molecular machinery required to support early embryogenesis, alterations in the maternal metabolic environment may compromise the oocyte legacy and developmental potential of the embryo.

We hypothesised that obesity-related hyperleptinemia and altered leptin signalling impair oocyte quality, leading to delayed embryo development and altered embryonic energy demands. To investigate this hypothesis, we employed two complementary mouse models: diet-induced obesity (DIO) in C57BL/6J females and genetically hyperleptinemic db/+ females. Following superovulation and in vitro fertilisation, embryo development was monitored until the blastocyst stage. Blastocysts were subsequently analysed for ATP content as an indicator of energy demands.

Embryos derived from both DIO and db/+ females exhibited delayed developmental kinetics compared with controls. In the DIO model, blastocyst formation occurred approximately 94h and 130h post-fertilisation, whereas embryos from db/+ females reached the blastocyst stage at 85h and 95h post-fertilisation. While most groups showed comparable ATP levels, late blastocysts derived from hyperleptinemic db/+ females displayed significantly lower ATP content than age-matched controls (7.89 vs.10.37 Units/µl; $p<0.05$), indicating reduced metabolic competence.

These findings demonstrate that maternal metabolic status influences preimplantation embryo development and metabolism, potentially through obesity-associated leptin dysregulation. The study provides evidence that developmental programming begins at the earliest stages of life and highlights the importance of maternal metabolic health for reproductive success and offspring well-being. Given the central role of mTOR signalling in nutrient sensing, protein synthesis and cell fate specification during preimplantation development, further studies are needed to determine whether obesity-associated alterations in leptin signalling affect embryonic mTOR activity and contribute to the developmental programming of offspring health.

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Metabolomic Signatures of a Energy-Restricted Ketogenic Diet: Alterations in Plasma and Urine Amino Acids in Young Wistar Rats with Diet-Induced Obesity

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Energy-restricted ketogenic diets (KD) are increasingly explored as metabolic interventions capable of modulating amino acid homeostasis, yet their effects under conditions of diet-induced obesity remain insufficiently characterized. Therefore, this study investigated how a caloric-restricted KD alters plasma and urinary free amino acid profiles in young Wistar rats with diet-induced obesity.

The experiment complied with EU Directive 2010/63/EU, ARRIVE guidelines, and was approved by the Local Institutional Animal Care and Use Committee (No. 34/2019). Thirty-four male Wistar rats were assigned to three groups: a standard-diet control (S), and two groups initially fed a high-fat diet for 8 weeks to induce obesity. Subsequently, obese rats received either an energy-restricted standard diet (RSD) or an energy-restricted KD (RKD) for 4 weeks. The RKD group was fed TD.96355 (91.6% kcal from fat; 8.4% from protein; 0% from carbohydrates). Free amino acids in plasma and urine were quantified at baseline (T0), after obesity induction (T1), and after dietary intervention (T2) using GC-MS following propyl chloroformate derivatization.

In total, 23 and 24 free amino acids were quantified in urine and plasma, respectively. The applied intervention modified the plasma and urinary amino acid profile. At T0, no significant differences in amino acid concentrations were observed among the experimental groups. Obesity induction (T1) led to among others marked alterations in urinary amino acid excretion, with significant changes in α-aminobutyric acid (ABA), aspartate (ASP), β-aminoisobutyric acid (BAIB), methionine (MET), leucine (LEU), tryptophan (TRP), and γ-aminobutyric acid (GABA). After the 4-week dietary intervention (T2), urinary profiles again diverged, showing significant differences in ABA, ASP, BAIB, TRP, LEU, and asparagine (ASN), indicating a diet-dependent metabolic response.

In summary, energy-restricted KD feeding modulated amino acid metabolism patterns in obese rats, suggesting shifts in nitrogen metabolism, amino acid catabolism, and tissue-specific utilization. These findings highlight amino acid signatures as sensitive biomarkers of metabolic adaptation to ketogenic dietary restriction in the context of obesity.

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In Life

Vitamin D_3 Induces Divergent Epigenetic State Transitions in Human Immune Cells: Implications for Precision Nutrigenomics

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Vitamin D_3 is a key regulator of immune function and has been implicated in promoting immune resilience and healthy aging through epigenetic mechanisms. However, the extent to which individuals exhibit distinct epigenomic responses to supplementation in vivo remains poorly understood, limiting the translation of vitamin D interventions into precision nutrition strategies. Here, we investigated inter-individual variability in chromatin accessibility dynamics using ATAC-seq in peripheral blood mononuclear cells (PBMCs) from participants of the VitDPAS cohort following high-dose vitamin D_3 supplementation (1,000 IU/kg body weight monthly for three months). Samples were collected at baseline (day 0) and 24 hours after supplementation (day 1), enabling high-resolution mapping of early epigenetic responses. Chromatin accessibility profiles were integrated with ChromHMM-derived epigenetic state annotations to characterize functional regulatory changes. Unsupervised clustering of ATAC-seq signal changes revealed three distinct response phenotypes: Positive (increased chromatin accessibility), Negative (decreased accessibility), and Moderate (minimal change). These groups exhibited fundamentally different epigenetic remodeling trajectories. In the Positive group, chromatin accessibility shifted toward enhancer regions, accompanied by a relative reduction in active transcription start site (TSS) annotations, suggesting a redistribution of regulatory activity toward distal control elements. In contrast, the Negative group displayed the opposite pattern, with reduced enhancer representation and stable or increased TSS-associated accessibility. These differences were statistically robust following FDR correction and were most pronounced for enhancer and active TSS states. These findings demonstrate that vitamin D_3 supplementation induces rapid, individual-specific epigenetic state transitions rather than uniform regulatory responses. The observed divergence in enhancer versus promoter dynamics suggests that vitamin D-mediated immune regulation operates through personalized rewiring of gene regulatory networks. Importantly, this study provides in vivo evidence that inter-individual variability in nutritional epigenomics is a defining feature of immune modulation. By capturing early chromatin accessibility changes, PBMC-based ATAC-seq emerges as a powerful and minimally invasive tool to stratify individuals according to molecular responsiveness. Together, these results establish a mechanistic basis for integrating epigenomic biomarkers into precision nutrition frameworks and digital twin models, enabling targeted vitamin D interventions aimed at optimizing immune function and promoting healthy aging.

NUTRIGENOMICS ERA CHAIR | WELCOME2

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In Life

Lifestyle-behavior factors affect obesity and T2DM genetic predisposition risk

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Obesity and type 2 diabetes mellitus (T2DM) arise from complex interactions between genetic susceptibility and modifiable lifestyle and behavioral factors. Across several sequential and complementary studies conducted in Israeli adult cohorts, several obesity-related genetic variants and their environmental interactions were identified as significant determinants of metabolic risk. FTO rs9939609 was associated with significant elevated obesity risk. inactive rs9939609 risk-allele carriers had higher obesity risk compared to their active counterparts (OR=2.54 and OR=3.7, with 3.1 and 3.5 BMI increment for heterozygotes and homozygotes, respectively; n=1720, p<0.001). Sugar-sweetened-beverages (SSB) consumption (≥1 serving/day) significantly raised obesity risk, and wine consumption (1–3 drinks/weekly) significantly lowered obesity risk for risk-allele carriers (OR=1.54, p=0.028 and OR=0.61, p<0.001, respectively). SH2B1 rs7498665 polymorphism was significantly associated with obesity, where carriers of the risk genotype showed increased odds across genetic models (OR 1.24-2; n=3,070). Physical activity (PA) and moderate wine consumption (1-3 drinks/week) reduced obesity risk (OR=0.35 and 0.71, respectively), whereas high stress levels, ≥median eating-habits-score and fasting glucose (≥90 mg/dL) increased risk up to OR=5.82 in homozygotes. TMEM18 rs939583 and TMEM18 rs1879523 were associated with increased obesity risk (O=1.35 and OR=1.66; n=3089, p<0.01), while PA and moderate wine consumption attenuated this genetic susceptibility (OR = 0.82 and OR=0.74, p<0.001). The MC4R rs17782313 variant was associated with increased obesity susceptibility (recessive OR=1.38; n=5785, p<0.005), particularly in females (OR=1.41; p=0.01). MC4R rs17782313 significantly interacted with several eating behaviors to enhance the risk of obesity. Extending these findings, FTO rs9939609 polymorphism interacted with behavioral factors affecting T2DM risk, where longer daily eating windows (OR=1.029), later last-meal timing (OR=1.066), prolonged sleeping windows (OR=1.137) and poorer sleeping quality (OR=1.185) were associated with increased T2DM susceptibility (n=12,254). BDNF rs925946 carriers had higher risk for gestational-diabetes-mellitus (recessive model, OR=2.05, p=0.03). Finally, a polygenic obesity risk score (GRSBMI, n=5,824) demonstrated that each unit increase in GRSBMI was associated with a 3.06 kg/m² increase in BMI (p≤0.0001), with unhealthy eating-habits-score and SSB intake amplifying genetic predisposition. Altogether, these findings demonstrate that obesity risk results from additive genetic effects that are substantially modified by lifestyle and behavioral exposures, highlighting the potential of community precision-nutrition approaches for prevention and management.

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Personal-MetaboHealth: a plasma metabolomics-based marker of global health valuable for prevention of disease

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There is an urgent need for biomarkers of ageing that capture the pathophysiological state of an individual as a function of time and predict the risk of loss of function, (multi)morbidity, and mortality. To generate biomarkers of ageing, the main focus in the field has been on CpG methylation and, more recently, proteomics data. Because of the affordable and scalable potential, we focused on (NMR-based) metabolomics data using much larger datasets than those available for any of the other omics-based measurements used to identify biomarkers of ageing. To compare which endpoints are best for training markers of ageing we generated two metabolomics biomarkers; MetaboAge, trained on chronological age (N>25K), and Personal-MetaboHealth, trained on mortality (N>44K). By comparing both, we have subsequently shown that especially Personal-MetaboHealth predicts multiple ageing-related conditions related to overall health, such as cancer survival, respiratory deficiencies, endpoints in hospitalized COVID patients, hip fractures, cognitive decline and frailty.

We found that Personal-MetaboHealth represents many aspects of inflammation and cholesterol transport and is 60% of its variation is explained by environmental factors and 40% by heritable ones. Predictions of prospective mortality and frailty are largely independent of smoking, alcohol consumption and income. We showed in the GOTO and VOILA study that older people with poor health can improve their Personal-MetaboHealth by lifestyle interventions involving lower caloric intake and increase in physical activity. We are currently exploring the use of Personal-MetaboHealth as a personalized health check for the general population of people aged 50 years and older in the Netherlands. We aim to identify target groups that will be offered support by changing their lifestyle and subsequently delay the onset of age-related disease.

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In Life

Dynamic System Identification from Longitudinal Vitamin D Perturbations Reveals Regulatory Control Architecture of Interindividual Responsiveness

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Introduction: Vitamin D signaling modulates immune and metabolic gene expression through the vitamin D receptor (VDR), yet the mechanisms underlying interindividual variability in responsiveness remain poorly understood. Large randomised trials have yielded inconsistent outcomes, in part because they assume uniform molecular responses across participants.
Aim: To characterise longitudinal transcriptional dynamics following repeated vitamin D_3 supplementation, define a personal vitamin D response index, and reconstruct the regulatory network architecture driving differential responsiveness.

Materials and Methods: Forty-one healthy adults received weight-adjusted vitamin D_3 boluses (1,000 IU/kg) on days 0, 28, and 56 (VitDPAS; NCT06104111). PBMCs were collected before and 24 h after each bolus. RNA-seq data were analysed with edgeR, and participants classified as high, mid, or low responders by integrating transcriptional fold-changes with serum 25(OH)D_3 pharmacokinetics via k-means clustering. A vitamin D-responsive gene regulatory network was reconstructed from persistently regulated transcription factors using DoRothEA, condensed by kernel reduction, and modelled with Hill-type ordinary differential equations (ODEs).

Results: Individual boluses induced modest acute changes (23 consistently regulated genes), while sustained supplementation drove progressive amplification: 698, 2,137, and 2,619 differentially expressed genes at weeks 4, 8, and 12. Participants clustered into 19 high, 16 mid, and 6 low responders. Kernel reduction yielded a compact module of 11 transcription factors (117 interactions), with TP53, MYC, JUN, FOS, and HIF1A as dominant hubs. ODE modelling faithfully reproduced expression trajectories across all cycles and phenotypes, showing that interindividual variability arises from quantitative rewiring within a conserved TP53-MYC-AP1-HIF1A regulatory axis.

Summary/Conclusions: Intervention-driven dynamic system identification links vitamin D exposure to transcriptional regulatory control in vivo. Vitamin D responsiveness is a stable yet plastic systems property, providing a mechanistic basis for precision nutrition and personalised supplementation.

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In Life

Impact of Food Processing on the Intestinal Bioactivity of Pigmented Wheat: A Nutrigenomic Perspective

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Diet–gene interactions at the intestinal level play a central role in the regulation of inflammation and oxidative stress, key processes involved in chronic diseases and aging. Whole grains, particularly pigmented wheat varieties, are rich in bioactive phytochemicals such as anthocyanins and phenolic compounds; however, their biological effects are often limited by low bioaccessibility. Food bioprocessing may represent a key strategy to enhance the release of these compounds and modulate their downstream effects.

In this study, pigmented wheat was subjected to different bioprocessing strategies, including germination (0–72 h), solid-state fermentation with Aspergillus awamori and Rhizopus oligosporus (0–72 h), and enzymatic treatments with Ultraflo XL and Viscozyme (0–16 h). The optimal conditions for each treatment, identified based on the antioxidant capacity, were selected for flour production and subsequent porridge preparation. Porridges were characterized for rheological properties and subjected to in vitro digestion to assess rapidly digestible starch (RDS) and slowly digestible starch (SDS), and phenolic bioaccessibility. Polyphenol profiles (HPLC-DAD) were characterized in flours, porridges, and digested samples. The bioaccessible fraction was applied to Caco-2 cells cultured on transwell inserts to investigate intestinal responses. Epithelial barrier integrity was evaluated by TEER, while the expression of genes involved in inflammatory and antioxidant pathways was assessed by RT-PCR. The basolateral compartment was analyzed by HPLC-DAD to assess the transport and potential absorption of phenolic compounds.

Processing significantly enhanced antioxidant capacity, the highest values were observed after 72 h of fermentation (7.30 ± 0.27 mg TE/g), followed by germination (5.14 ± 0.56 mg TE/g), and Viscozyme treatment (5.42 ± 0.54 mg TE/g after 16 h), corresponding to an increased antioxidant potential of up to ~3–4-fold increases compared to untreated samples. Preliminary results indicate that processing modulates starch digestibility and porridge rheology, enhances polyphenol bioaccessibility, and induces beneficial intestinal responses, including improved epithelial barrier integrity and modulation of genes related to oxidative stress and inflammation.

These findings highlight food processing as a key modulator of the nutrigenomic response to pigmented wheat, with potential implications for chronic disease prevention and healthy aging.

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In Life

Vitamin D Shapes Immune Cell Epigenetic Memory under Inflammatory Challenge: Implications for Precision Nutrition in Healthy Aging

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Aging is characterized by progressive dysregulation of immune function, often linked to chronic low-grade inflammation and impaired adaptive responses. Nutritional factors, such as vitamin D, play a critical role in modulating immune homeostasis; however, their mechanistic contribution to immune cell programming in the context of inflammatory challenges remains insufficiently understood.

In this study, we investigated how the active form of vitamin D_3 ($1,25(OH)_2D_3$) interacts with bacterial-derived lipopolysaccharide (LPS) to reshape the epigenomic and transcriptomic profile of human monocytes, a key cell type in innate immunity and age-related inflammation. Using ATAC-seq and RNA-seq in THP-1 cells, we demonstrate that co-stimulation with vitamin D and LPS induces a highly distinct and synergistic regulatory program that cannot be explained by additive effects of either stimulus alone.

Epigenomic profiling revealed that up to 81% of chromatin accessibility changes were unique to the combined treatment, indicating a profound reprogramming of immune regulatory regions. Motif enrichment analysis identified JUN/FOS (AP-1) transcription factors as central mediators of this response, suggesting a convergence of inflammatory and nuclear receptor signaling pathways. At the transcriptomic level, hundreds of genes displayed synergistic regulation, including a large subset not previously recognized as vitamin D targets. Functionally, these genes are predominantly associated with monocyte differentiation and T cell interaction rather than classical inflammatory pathways.

These findings support a model in which inflammatory stimuli sensitize immune cells to nutritional signals, enabling vitamin D to reprogram immune responses through epigenetic mechanisms. In the context of aging, such adaptive plasticity may contribute to maintaining immune resilience while preventing maladaptive chronic inflammation.

Our results provide a mechanistic basis supporting the integration of micronutrient status into precision nutrition strategies and highlight the potential of integrating multi-omics data as a foundation for future development of digital twin models of immune aging. This approach may help enable personalized nutrition strategies aimed at promoting healthy aging and mitigating age-associated inflammatory diseases.

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In Life

Vitamin D selectively reprograms the monocyte inflammatory landscape through context-dependent chromatin-transcriptional coupling

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Vitamin D (1,25D) is a critical immunomodulator of the innate immune response, yet the specific epigenetic and transcriptional mechanics through which it shapes primary human monocyte (HPM) activation remain incompletely understood. In this study, we performed paired RNA-seq and ATAC-seq analysis of classical HPMs stimulated with 1,25D, lipopolysaccharide (LPS), and tumor necrosis factor (TNF). While inflammatory ligands dominated global transcriptional and epigenetic variance, 1,25D functioned as a context-dependent fine-tuner that selectively reprogrammed distinct biological modules. Transcriptionally, 1,25D enhanced antimicrobial and interferon-associated programs (e.g., HLA-DRB5, OAS1) while attenuating inflammatory metabolic pathways including glycolysis (ENO1, ALDOA) and lipid signaling (APOE, CD36). Integration of chromatin accessibility and gene expression revealed that 1,25D specifically targets the chromatin-transcriptional link to modulate activation. Notably, while LPS stimulation was almost exclusively characterized by concordant activation-associated coupling (867 upregulated vs. 2 downregulated genes), co-treatment with 1,25D shifted this trajectory toward a repressive landscape, inducing the concordant repression of key signaling and stress-response nodes such as MAP3K10, DUSP6, and GADD45B. These targeted modulations were embedded within a stable regulatory framework of conserved integrated hubs, including IL1RN, BRD7, DUSP4, and SLC7A7, which remained robustly coupled across all activated states. Comparative analysis further demonstrated that these regulatory programs are largely system-specific, with primary monocytes exhibiting a unique 1,25D-responsive epigenetic architecture that is only partially recapitulated by cell line models. Together, our findings provide a multi-layered map of the epigenetic-transcriptional nodes through which vitamin D selectively reprograms the monocyte response to inflammation, favoring resolution and metabolic adaptation over sustained activation.

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In Life

Lipids Rewire the Immunoreactivity and Functional Profile of Microbial Proteins in Lactic Acid Bacteria

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Microbial proteins (MPs) from lactic acid bacteria (LAB) represent a substantial antigenic load in fermented foods. Their expression is strongly shaped by environmental factors, including lipid composition of the growth matrix. Individuals with impaired tolerance mechanisms, such as dysregulation of the MyD88–RORγt axis, may respond to MPs with IgE-mediated hypersensitivity. This study examined how triglycerides (TG) and phospholipids (PL) modulate LAB proteome, immunoreactivity, epithelial responses and systemic immunity.

To determine how milk-matrix lipids program the expression, immunoreactivity and immunomodulatory potential of LAB proteins across in vitro, in vivo and ex vivo models.

Three LAB strains (L. delbrueckii 151, L. casei LcY, L. rhamnosus GG) were cultured in MRS, MRS+TG or MRS+PL. Proteomic profiling (LC-MS/MS), lipid metabolism, SCFA production and immunoreactivity (IgE/IgG1) were assessed. Biological effects were tested in Caco-2 and HIEC-6 cells, BALB/cJRj mice (immunoglobulins, cytokines, tissue expression) and ex vivo splenocytes. Microbiota composition was analyzed by 16S rRNA sequencing.

Lipid composition significantly altered bacterial proliferation (strain×matrix interaction 44.5% variance) and proteome structure (PCA 80–90%). BM and CM induced distinct profiles of stress proteins, moonlighting enzymes (GroEL, GAPDH, LDH, enolase) and lipid metabolism proteins. Single-cell protein production differed between strains (GG > LcY > 151), and BM increased FFA release and oxidative stress markers.

Matrix-dependent shifts in IgE/IgG1 reactivity of MPs were observed. In strain 151, BM increased IgE-reactive proteins, whereas in LcY and GG, CM/BM reduced IgE and IgG1 signals. Recombinant immunoreactive proteins induced pro-inflammatory cytokines in epithelial cells, while lipid-conditioned isolates modulated inflammasome (IL-6, IL-8, IL-25, TSLP and CCL20). Barrier-related genes (zonulin, occludin, mucin) were regulated in a strain×matrix×maturity-dependent manner.
In vivo, IRP immunization increased IgE and IgG1, whereas feeding lipid-conditioned isolates (IMCP) reduced IgE, enhanced IgA and shifted cytokines toward IL-10 and IFNγ in mice model. Ex vivo splenocytes confirmed reduced Th2-type cytokines after IMCP exposure. Microbiota analysis showed diet-dependent restructuring of genera (Shannon 3.1–3.9; Bray–Curtis clustering).

Lipids profoundly program the proteome, immunoreactivity and biological activity of LAB proteins. Matrix-specific lipid profiles can enhance or attenuate IgE-reactive proteins, modulate epithelial responses and reshape systemic immunity. The findings complement current research exploring diet-driven modulation of immune and barrier functions relevant to aging and immunocompetence.
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The effect of naringenin on the activity of the genes associated with Toll-like receptor pathway in MCF-7 breast cancer cells

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Breast cancer is the most common cancer in women worldwide. Chronic inflammation may contribute to cancer development, while immune responses may have important role in control and management of cancerous cells. Toll-like receptors (TLRs) participate significantly in inflammatory processes and modulate the tumour microenvironment, which may either hinder or enhance cancer growth. Dietary compounds, including flavonoids like naringenin, are able to influence inflammatory processes.
The aim of the study was to determine the effects of naringenin on the expression of the genes associated with TLR pathway in MCF-7 breast cancer cells.

The MCF-7 cells were incubated for 48h with naringenin to determine the effect of the flavonoid on gene expression (10 μM). The expression of 84 genes associated with TLR pathway was evaluated using RT^2 Profiler PCR Array Human Toll-like Receptor Signalling Pathway (PAHS-018ZF, Qiagen). A minimum 2-fold change in gene expression was used as a threshold for marked alteration.

Naringenin induced global transcriptional modulation of the TLR pathway, resulting in a trend toward increased expression for 76 genes and decreased expression for 7 genes. The mRNA expression of interferon alpha 1 (IFNA1) was not detected under the experimental conditions. Based on the 2-fold change cutoff, seven key genes were markedly up-regulated by naringenin: endosomal receptors (Toll-like receptor 7, TLR7, FC=2.1; Toll-like receptor 8, TLR8, FC=3.3), the transcription factor AP-1 subunit (FBJ murine osteosarcoma viral oncogene homolog, FOS, FC=2.1) and effector cytokines or chemokines, namely tumour necrosis factor (TNF, FC=2.1), chemokine (C-C motif) ligand 2 (CCL2, fold change FC=2.1), interleukin 8 (CXCL8, FC=3.1) and granulocyte colony-stimulating factor 3 (CSF3, FC=2.0).

In conclusion, naringenin at subtoxic concentrations exhibits a strong potential for transcriptional regulation of the TLR pathway in MCF-7 cells through a coordinated, global cascade effect. The complex nature of these transcriptional changes suggests that naringenin may actively modulate the inflammatory expression profile of breast cancer cells, which warrants further validation at the protein level and in co-culture models with immune cells.

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In Life

Linking Functional Food Design to Nutrigenomics: Opuntia ficus-indica-Enriched Goat Yogurt Modulates Bioaccessibility, Metabolic Activity and Gut Microbiota

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The combination of fermented dairy matrices with Opuntia ficus-indica represents a promising strategy to enhance the delivery of bioactive compounds that remain stable after gastrointestinal digestion and interact with gut microbiota. This study aimed to evaluate the bioaccessibility, antioxidant and antidiabetic activities, and microbiota-modulating potential of goat yogurt enriched with O. ficus-indica, within a nutrigenomic framework.

The yogurt formulation was subjected to the standardized INFOGEST in vitro gastrointestinal digestion protocol. Antioxidant capacity and antidiabetic activity were assessed before and after digestion. The bioaccessible fraction obtained at the end of digestion was further characterized in terms of fatty acid and amino acid profiles. Subsequently, this fraction was used as a substrate in in vitro fecal fermentation using human fecal inoculum. Microbial DNA was extracted, and gut microbiota composition was analyzed using sequencing-based approaches.

Simulated gastrointestinal digestion modulated the bioactive profile of the yogurt and enhanced the availability of selected nutrients in the bioaccessible fraction. Antioxidant and antidiabetic activities were preserved or increased after digestion, suggesting the release and/or stabilization of functional compounds during digestion. The final digest contained relevant amino acids and fatty acids contributing to the nutritional quality of the product. During fecal fermentation, the bioaccessible fraction induced shifts in microbial community structure, increasing the abundance of bacterial groups associated with carbohydrate fermentation and gut health, while reducing taxa commonly linked to dysbiosis.

Goat yogurt enriched with O. ficus-indica demonstrated bioaccessible antioxidant and antidiabetic activities after INFOGEST digestion and showed the capacity to beneficially modulate gut microbiota. These findings highlight its potential as a functional food within a nutrigenomics context, supporting precision nutrition strategies and lifelong metabolic health.

Keywords: Cactus; Goat milk; Bioactivities; Fecal fermentation; Gut microbiota; functional foods.

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In Life

Bacteriophages on the Fork: A State-of-the-Art Review from Concept to Personalised Nutrition

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Introduction: Bacterio(phages) are viruses that infect and lyse only bacteria and archaea. They are ubiquitous in nature, highly bacterial host-specific (which limits their impact on gut microbiota dysbiosis), and harmless to eucaryotic cells. Due to these properties, they are increasingly recognised as potential therapeutic agents in gut microbiota disorders. Phage-enriched foods, as a novel food segment, could form the basis of personalised nutrition, offering a novel strategy for non-invasive, repeated administration to support intestinal homeostasis. While bacteriophages are gaining momentum in food science, legislation remains one of the key barriers to their widespread implementation.

Aim: To analyse the research on strictly lytic (virulent) bacteriophages in gut dysbiosis, assessing their therapeutic efficacy, safety, and the potential of phage-enriched foods for personalised nutrition.
Materials and Methods: A systematic review of peer-reviewed literature from the last 10 years (as conducted from PubMed, Web of Science, and Scopus databases.

Results: (1) In immunocompetent hosts with an intact gut barrier, lytic phages efficiently eliminate pathogens or reduce bacterial overload in small intestinal bacterial overgrowth (SIBO) without disrupting the commensal microbiome. (2) In "leaky gut" associated with inflammatory bowel disease (IBD), phage-induced lysis correlates with elevated inflammatory markers (TNF-α, IL-6). (3) Successful implementation of phage-enriched foods requires rigorous validation of encapsulation strategies for gastrointestinal survival, target specificity, and consumer safety.

Summary and Conclusions: Future priorities include the development of encapsulation technologies, safety validation, and clinical trials to enable phage-enriched foods as evidence-based components of personalised nutrition. Despite growing scientific interest, regulatory frameworks for bacteriophage application in food systems still lag behind technological advances.

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In Life

Dosing Matters: Longitudinal Immune Cell Dynamics Reveal Regimen-Specific Effects of Vitamin D_3 Supplementation

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Vitamin D_3 is a key modulator of immune function and has been implicated in maintaining immune homeostasis and resilience during aging. However, how different supplementation strategies shape immune cell composition over time in vivo remains poorly defined, limiting the optimization of vitamin D interventions in precision nutrition. Here, we performed high-resolution longitudinal immune profiling in 28 healthy individuals from the VitDPAS cohort undergoing two distinct vitamin D_3 supplementation regimens: daily dosing and monthly bolus administration. Peripheral blood mononuclear cells (PBMCs) were collected at nine time points, enabling detailed temporal analysis of immune cell dynamics across supplementation phases. Multiparameter flow cytometry (FACS) was applied using a standardized antibody panel (CD45, CD3, CD4, CD8, CD14, CD16, CD19, CD56) to quantify major immune cell populations, including T cells, B cells, natural killer (NK) cells, and monocytes. This approach allowed robust and reproducible assessment of immune composition over time and between supplementation strategies. Longitudinal analysis revealed that vitamin D_3 supplementation induces dynamic, time-dependent remodeling of peripheral immune cell populations rather than static shifts. Notably, distinct temporal patterns emerged between supplementation regimens, indicating that dosing strategy is a critical determinant of immune modulation. Daily supplementation was associated with more stable and gradual immune cell adjustments, whereas bolus dosing induced more pronounced fluctuations in immune cell distributions over time. These findings demonstrate that vitamin D_3 does not exert uniform immunological effects but instead drives regimen-specific immune dynamics. Such temporal variability highlights the importance of considering dosing strategies when evaluating vitamin D interventions and underscores the limitations of single time-point assessments. By providing longitudinal, high-resolution insights into immune cell remodeling, this study establishes a framework for linking supplementation regimens to immune system behavior. These results support the development of precision nutrition strategies that tailor vitamin D dosing to individual immune profiles, with the goal of enhancing immune homeostasis and promoting healthy aging.

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In Life

Astaxanthin and kokum modulate hepatic fatty acid composition and lipid peroxidation in mice with diet-induced NAFLD

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Introduction: Alterations in hepatic fatty acid composition and increased lipid peroxidation are important features associated with hepatic steatosis. An increased proportion of saturated fatty acids (SFA) may contribute to a more lipotoxic hepatic lipid environment, whereas oxidative degradation of lipids results in the formation of reactive products such as malondialdehyde (MDA). Nutraceuticals with antioxidant properties may therefore represent a promising approach to modulating these alterations.

Aim: The study aimed to assess whether astaxanthin and kokum supplementation could attenuate steatosis-associated changes in hepatic fatty acid composition and lipid peroxidation in mice.
Materials and Methods: The study included 120 male Swiss Webster mice. Hepatic steatosis was induced by feeding a methionine- and choline-deficient (MCD) diet. Following steatosis induction, mice received astaxanthin, kokum, or their combination for 90 days. The hepatic fatty acid profile was determined by gas chromatography-mass spectrometry, with fatty acids classified as saturated (SFA), monounsaturated (MUFA), or polyunsaturated (PUFA). Lipid peroxidation was assessed based on hepatic malondialdehyde (MDA) concentration. Statistical analysis was performed using one-way ANOVA followed by Tukey's post hoc test.

Results: Mice with diet-induced steatosis showed a significant shift toward a more saturated hepatic fatty acid composition, with the proportion of SFA increasing from 37.1% in the control group to 45.8% in steatotic mice. This change was accompanied by elevated MDA concentration, which reached 49.67 µmol/L compared with 34.89 µmol/L in controls. Supplementation was associated with a shift toward a higher proportion of unsaturated fatty acids and reduced lipid peroxidation. The combined supplementation in steatotic mice resulted in the lowest SFA proportion among all experimental groups (29.7%) and the highest total unsaturated fatty acid content. This group also exhibited the lowest MDA concentration among steatotic groups (25.45 µmol/L), representing an approximately 49% reduction compared with untreated steatotic mice.

Conclusion: Diet-induced hepatic steatosis was associated with a more saturated fatty acid profile and increased lipid peroxidation. Astaxanthin and kokum supplementation was associated with a shift toward greater hepatic fatty acid unsaturation and lower MDA levels, with the most pronounced changes observed following combined supplementation. These findings suggest that modulation of hepatic fatty acid composition and lipid peroxidation may contribute to the beneficial effects of these nutraceuticals in diet-induced steatosis.

NUTRIGENOMICS ERA CHAIR | WELCOME2

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In Life

Changes in reduced glutathione (GSH) levels in mice with induced diabetes after administration of different doses of ginger

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Diabetes mellitus is a rapidly growing global health problem characterized by chronic hyperglycemia caused by impaired insulin secretion, insulin resistance, or both. Poor glycemic control leads to complications such as retinopathy, nephropathy, cardiovascular diseases and cell degradation. Hyperglycemia promotes oxidative stress by increasing reactive oxygen species (ROS) production and weakening antioxidant defenses, contributing to β-cell damage, insulin resistance, cataracts, impaired healing, liver steatosis, and inflammation. It can also lead to atherosclerosis. Reduced glutathione (GSH) is a key cellular antioxidant protecting against oxidative damage. Ginger (Zingiber officinale) contains bioactive compounds with antioxidant and hepatoprotective properties and may support diabetes therapy.

The study aimed to determine the effect of different ginger doses on reduced glutathione levels in mice with induced diabetes.

The study was conducted on 84 male Swiss Webster mice with streptozotocin-induced diabetes. Animals were housed under standard conditions, with welfare status and food and water intake monitored throughout the experiment. Mice were randomized into six groups, including non-diabetic and diabetic animals receiving standard feed or feed supplemented with 0.6% or 1.8% ginger powder for three months. After supplementation, blood, liver, eyes, and tendons were collected for analysis.
Diabetes reduced GSH levels in the blood, eye, and tendons, but did not affect the liver. The effect of ginger was tissue-dependent: in the liver and eyes, ginger increased GSH in a dose-dependent manner, restoring levels reduced by diabetes in the eye, and even exceeding them at higher doses. Ginger did not restore GSH in the blood. The most noticeable effect was observed in the eyes of the diabetic group with ginger supplementation.

These findings confirm that diabetes is associated with reduced antioxidant capacity in selected tissues. Ginger supplementation showed a tissue-specific antioxidant effect, particularly in the eyes, where it restored or increased GSH levels in diabetic mice. The results suggest that ginger may support antioxidant protection in diabetes, especially in the eyes.

NUTRIGENOMICS ERA CHAIR | WELCOME2

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In Life

A longitudinal multi-omics study of vitamin D-induced epigenetic memory in human PBMCs

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Vitamin D is a key immunomodulatory micronutrient regulating the transcriptional programming of immune cells, including peripheral blood mononuclear cells (PBMCs). Although the molecular effects of vitamin D signaling have been extensively studied, the epigenetic mechanisms underlying long-term memory following vitamin D exposure remain poorly understood.

The primary aim of this study is to determine whether different vitamin D_3 supplementation regimens, such as a monthly bolus administration versus daily supplementation, induce epigenome- and transcriptome-wide changes in human PBMCs. We investigate inter-individual variation in these responses over time.

PBMCs are collected from peripheral blood of 45 participants across five defined time points (months 0, 3, 12, 15, 24) during a two-year longitudinal study. Complete longitudinal datasets were obtained from 29 participants, while the remaining 16 contributed to partial time-course datasets. During the first winter season, participants received monthly bolus vitamin D_3 supplementation (1000 IU/kg for three months) followed during the second winter by daily supplementation (40 IU/kg for three months).

Isolated PBMCs are cultured in vitro for 24 hours in the presence of either 10 nM 1,25-dihydroxyvitamin D_3 (1,25D) or ethanol as vehicle control. Samples from each experimental condition are subjected to RNA-sequencing (RNA-Seq) and Assay for Transposase-Accessible Chromatin using sequencing (ATAC-Seq), followed by downstream bioinformatic analyses. The controlled in vitro stimulation approach enables the identification of both immediate and persistent vitamin D-induced changes in gene expression and chromatin organization, including alterations in regulatory elements associated with epigenetic memory.

We hypothesize that wintertime vitamin D_3 supplementation induces long-term epigenetic reprogramming in immune cells and that the magnitude and nature of these responses depend on the supplementation regimen. Furthermore, this study is expected to advance our understanding of vitamin D-mediated epigenetic memory mechanisms in the context of trained immunity.

NUTRIGENOMICS ERA CHAIR | WELCOME2

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In Life

Sensory Living Lab for Developing Innovative Berry-Based Food Products with High Consumer Acceptance

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Polish berry fruits, including blackcurrant, chokeberry, and haskap berry (Lonicera caerulea L.), are valuable raw materials for the development of innovative functional foods due to their high content of phenolic compounds and anthocyanins. These fruits exhibit strong antioxidant activity and documented health-promoting properties. Despite their nutritional value, their market potential remains underutilized because consumer awareness is limited and food producers often face technological and market-related barriers when introducing novel berry-based products.

The international HORTIFOODTRENDS project addresses these challenges by combining advanced food processing technologies with consumer-oriented product development. Its goal is to create innovative berry-based foods that preserve the nutritional and functional properties of raw materials while offering sensory characteristics attractive to consumers. Particular attention is given to haskap berry, whose dominant anthocyanin, cyanidin-3-glucoside, contributes to both its high antioxidant potential and its stable, appealing dark color, making it a promising ingredient for novel food products.

A central element of the project is the implementation of a Living Lab approach that brings together researchers, food technologists, producers, processors, entrepreneurs, and consumers in a collaborative innovation environment. This model supports co-creation of products based on real consumer needs and market expectations. The newly established HortiFood Processing Centre in Skierniewice integrates pilot-scale processing facilities with a sensory and consumer research laboratory, providing infrastructure for interdisciplinary cooperation and rapid product prototyping.

The Living Lab methodology incorporates a two-stage consumer involvement process. The first stage focuses on understanding consumer attitudes and expectations regarding berry fruits and berry-based foods. The second stage involves the evaluation of developed prototypes, including sensory acceptance, purchase intention, and feedback relevant to commercialization.

The project contributes to the objectives of the European Union's "Farm to Fork" strategy by supporting sustainable food systems, innovation in the agri-food sector, and healthier food choices. By integrating food technology, sensory science, consumer research, and market knowledge, the project increases the likelihood of successful commercialization of nutritionally valuable berry products. Ultimately, it aims to increase the utilization of Polish berry fruits and deliver attractive, health-promoting products with high consumer acceptance across European markets.

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Can sirtuin activators affect lipid metabolism and senescence in women?

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Introduction: Sirtuins play an important role in the regulation of cellular homeostasis, in particular glucose and lipid metabolism, inflammation, oxidative stress, and senescence. Numerous food compounds have been suggested to modulate sirtuin activities, including resveratrol, berberine, quercetin, curcumin, and fisetin. The effects of a single activator on human metabolism have already been tested, but to date no studies have evaluated combined supplements containing several sirtuin activators.

Aim: The aim of the study was to analyze the effects of six months supplementation with sirtuin activators on biomarkers of lipid and glucose metabolism as well as markers of ageing and senescence, in women with increased body weight.

Materials and methods: Females aged 40-65 years, BMI ≥ 25kg/m^2 were recruited in Poznan, Poland between October 2025 and January 2026. Eligible participants were randomly allocated to one of two groups supplemented with sirtuin activators (SIRT) or placebo (PLA) for six months (Clinical Trials: NCT07245979). Capsules containing the daily doses of the sirtuin activators included 500 mg resveratrol, 467 mg leucine, 100 mg Epigallocatechin gallate, 100 mg quercetin, 100 mg curcuminoids, and 10.7 mg niacin. Moreover, the sirtuin activators were provided in an innovative micropellet formulation containing a leucine-complexed trans-resveratrol system, enriched with the other compounds. This formulation has threefold higher resveratrol availability compared with the pure compound. A Bod Pod (Cosmed, Italy) was used to analyze body mass and composition. The plasma concentrations of total cholesterol, HDL cholesterol, LDL cholesterol, glucose, and activities of ALT, AST, and GGTP were determined using an automated analyzer Konelab 20i. DNA was isolated from whole blood and average telomere lengths were assessed using comparative $^{\Delta\Delta}$Cq method with the reference genomic DNA sample as a reference for calculating the telomere length of samples.

Results: Altogether 88 women were randomized, 44 to the SIRT group and 44 to the PLA group. The mean age was 50.3±6.1 and 50.9±6.1 years and the mean body mass index was 29.9±4.7 and 31.0±4.3 kg/m^2 in the SIRT and PLA group, respectively. Ten women have already dropped out: 4 from the SIRT group and 6 from the PLA group. The study will be fully completed in July 2026 and will enable a comprehensive assessment of the effect of several sirtuin activators on lipid and glucose metabolism and markers of ageing and senescence.

Summary/conclusions: Well-designed studies are needed to test efficacy of dietary supplements currently available on the market and to assess their potential role for human health.

NUTRIGENOMICS ERA CHAIR | WELCOME2

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In Life

Phytochemical characterization and antidiabetic potential of fermented radish and fenugreek microgreen-based functional beverages

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The present study aimed to develop fermented functional beverages based on radish and fenugreek microgreens and to evaluate their potential for type 2 diabetes management. Four formulations were prepared, including a control beverage, fenugreek microgreens beverage, and radish microgreens beverages with and without roots. Fermentation was carried out for 15 days using a consortium of lactic acid bacteria. The fermented beverages were characterized through physicochemical, phytochemical, antioxidant, antimicrobial, and α-amylase inhibitory assays. The obtained results demonstrated that fermentation enhanced the bioactive potential of the beverages, leading to improved antioxidant, antimicrobial, and α-amylase inhibitory activities. Notably, the fermented radish beverage with roots showed high α-amylase inhibitory activity (70.7%), closely comparable to the fenugreek-based beverage (71.4%), whereas the radish beverage without roots exhibited much lower inhibition (25.5%). Overall, microgreen-enriched fermented beverages exhibited promising functional properties that may contribute to reducing oxidative stress and modulating glycemic response associated with type 2 diabetes. Among the investigated formulations, the radish microgreens beverage including roots showed the highest overall bioactive potential, suggesting that root incorporation may enhance the functional properties of fermented beverages intended for type 2 diabetes management. These findings highlight the potential of fermented microgreen-based beverages as innovative functional foods with promising antidiabetic properties.
Keywords: functional beverages, microgreens, bioactive compounds, antidiabetic potential, antioxidant activities.

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The influence of diet on gut microbiota composition and metabolic health

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The gut microbiota is a complex ecosystem of microorganisms that plays a crucial role in human metabolic health, immune regulation, and overall homeostasis. Dietary patterns are among the most important modifiable factors influencing its composition and diversity.

The aim of this study was to review current scientific evidence on the relationship between dietary intake and gut microbiota modulation, as well as its impact on metabolic health outcomes.

A narrative literature review was conducted based on recent peer-reviewed studies focusing on dietary patterns such as the Mediterranean diet, high-fiber diets, and Western dietary patterns. Scientific databases were used to identify relevant publications addressing the interaction between nutrition and gut microbiome composition.

The reviewed literature suggests that diets rich in fiber, plant-based foods, and polyphenols promote greater microbial diversity and the abundance of beneficial bacteria, which may contribute to improved metabolic health. In contrast, Western dietary patterns characterized by high intake of processed foods, saturated fats, and added sugars are associated with reduced microbial diversity and increased risk of metabolic disorders such as obesity and insulin resistance.

These findings highlight the importance of dietary interventions in maintaining a healthy gut microbiota and supporting metabolic health. Further research is needed to better understand individual responses to dietary changes and their long-term effects on the microbiome.

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In Life

Molecular effects of enriched Matcha Tea: insight from an in-vitro intestinal model

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Introduction: Leaky gut syndrome and gut dysbiosis are increasingly recognized as major health concerns worldwide, due to their association with the development of inflammatory and metabolic disorders. Thus, growing interest has been addressed to the development of functional foods enriched in bioactive compounds and probiotics aimed at improving intestinal health. Matcha is a finely ground powder obtained from Camellia sinensis leaves and it is consumed as a whole-leaf suspension, naturally rich in bioactive compounds. Lachancea thermotolerans is a newly discovered non-Saccharomyces yeast with probiotic effects.

This study aims at evaluating the biological effects of digested matcha tea, digested matcha fortified with Lachancea thermotolerans, and digested probiotic yeast alone, using an in vitro model of intestinal epithelium.

Methods: Samples were subjected to in vitro digestion. The viability of the probiotic was assessed before and after the digestion. The resulting digests were analysed for antioxidant activity, and their polyphenol composition was characterized by HPLC-DAD. Subsequently, a Caco-2 in-vitro intestinal epithelial model was pre-treated with the digests and exposed to inflammatory conditions. The experiment was performed in triplicates. Epithelial barrier integrity was assed and gene expression analysis was also performed.

Results: The probiotic yeast remained viable after in vitro digestion. Polyphenol content was higher in the matcha–probiotic mixture than matcha alone. Both matcha and the matcha–probiotic combination exerted a protective effect against inflammation-induced disruption of epithelial barrier integrity.
The matcha–probiotic combination, as well as the digested probiotic alone, reversed the inflammation-induced modulation of claudin gene expression. A similar trend was observed for the expression level of NF-κB gene.

Conclusions: The addition of the probiotic yeast to matcha tea improves its properties, potentially enhancing its health benefits.

NUTRIGENOMICS ERA CHAIR | WELCOME2

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In Life

Dietary patterns and insomnia occurrence in peri- and postmenopausal women: a preliminary cross-sectional study

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Introduction: The most commonly observed sleep disorder in women is insomnia. Available studies suggest that consuming foods containing tryptophan and phytochemicals may be associated with improved sleep through the diet's effect on serotonin and melatonin activity. However, the results of studies on dietary patterns (DPs) and the prevalence of insomnia in women are limited and inconclusive.

Aim: This study aimed to assess the association between dietary patterns, including the Mediterranean diet as expressed in the Polish-adapted Mediterranean Diet® (Polish-aMED®) score[1] and the occurrence of insomnia in peri- and postmenopausal women.

Methods: This preliminary cross-sectional study involved 210 women aged 50-72 (56.9±5.6) years from north-eastern Poland. Insomnia was diagnosed in 98 women using the Women's Health Initiative Insomnia Rating Scale (WHIIRS)[2]. The food frequency consumption data were collected using a food frequency questionnaire (62-item FFQ-6®)[3]. Data on the frequency of consumption of 62 food items were expressed as times per day and summed to 22 food groups. These data were included in the Principal Component Analysis (PCA), and DPs were identified. The Polish-aMED® score involving 8 items: vegetables, fruit, whole grain, fish, legumes, nuts/seeds, the ratio of vegetable oils to animal fat, and red and processed meat was calculated (range: 0-8 points).

Results: Three PCA-derived DPs were identified: 'Meat-fats-eggs-dairy', characterised by relatively frequent consumption of meat and meat products, animal and vegetable fats, eggs, milk and natural dairy drinks, and cheese; 'Sweets and refined cereals', characterised by frequent consumption of sugar, honey, sweets, refined cereal products, and sweetened dairy drinks; and 'Fish and legumes'. A significantly higher percentage of women with insomnia (vs. no insomnia) showed greater adherence to the 'Meat-fats-eggs-dairy' pattern (42 vs. 26%, p=0.0157), while a higher adherence to the ´Fish and legumes´ pattern (46 vs. 20%, p=0.0002) and the Polish-aMED® score (44 vs. 28%, p=0.0438) was noted in women without insomnia.

Conclusions: These results suggest that dietary patterns based on fish and legumes, as well as the Mediterranean diet in Polish adaptation, may be inversely associated with the occurrence of insomnia in women. On the other hand, to prevent insomnia, it is recommended to reduce the consumption of animal foods, including meat and fats.

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[1]https://pubmed.ncbi.nlm.nih.gov/29641468/
[2]https://pubmed.ncbi.nlm.nih.gov/15673630/
[3]https://pubmed.ncbi.nlm.nih.gov/31514354/

Dose-dependent effects of erythritol and xylitol on platelet function and HMGCR/COX-1 activity

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Introduction: Global sucrose consumption surpasses 180 million tons annually, and its excessive intake is closely linked to metabolic disorders such as obesity and diabetes, with growing concerns also raised about artificial sweeteners [1]. As a result, natural polyols like xylitol and erythritol have become popular sugar substitutes. However, recent evidence suggests that increased plasma levels of these compounds may be associated with a higher risk of major adverse cardiovascular events, possibly through increased platelet reactivity [2,3].
Aim: This study examines how erythritol and xylitol affect platelet aggregation , focusing on key signaling pathways mediated by the P2Y12 and PAR1 receptors. Simultaneously, the study evaluates the inhibitory effects of these polyols on human 3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMGCR) and cyclooxygenase-1 (COX-1). These enzymes were targeted because their inhibition reduces cholesterol synthesis and decreases thromboxane-driven platelet activation, thus lowering platelet thrombogenicity.
Materials and methods: An integrated approach combining in vitro platelet aggregation tests performed in platelet-rich plasma from healthy donors with in silico molecular docking of polyols to targeted platelet receptors was used to assess polyol-mediated platelet function and enzyme modulation.
Results: The findings showed a clear concentration-dependent increase in platelet aggregation in the presence of both xylitol and erythritol upon P2Y12 and PAR1 stimulation, alongside observable inhibition of HMGCR and COX-1 activity. Notably, in silico analyses revealed that these polyols do not block the access of endogenous ligands to the receptor binding sites, indicating that their pro-aggregatory effects are not due to competitive antagonism at the receptor level. It's worth noting that a single 30 g dose of these polyols can raise plasma concentrations by nearly 1000 times (from micromolar to millimolar levels) [2], and their dietary intake may have significant physiological and clinical consequences.
Conclusions: These findings underscore a complex, dual role of polyols in influencing platelet function and metabolic pathways, highlighting the need for further mechanistic and translational research to fully understand their impact on human health.

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References

[1] C. Debras, E. Chazelas, B. Srour, et al., Artificial sweeteners and health outcomes: prospective cohort studies from the NutriNet-Santé cohort, PLoS Med. 2022, 19, e1003950.
[2] M. Witkowski, I. Nemet, H. Alamri, et al., The artificial sweetener erythritol and cardiovascular event risk, Nat. Med. 2023, 29, 710–718.
[3] M. Witkowski, I. Nemet, X. S. Li, et al., Xylitol is prothrombotic and associated with cardiovascular risk, Eur. Heart J. 2024, 45, 2439–2452.

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Enzymatic activity of the human gut microbiota and its role in (poly)phenol bioavailability and metabolism

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Introduction. Dietary (poly)phenols have been associated with cardiovascular health benefits; however, their bioavailability and biological effects depend largely on gut microbial biotransformations. Given the substantial inter-individual differences in microbial enzymatic activity, investigating this variability may help clarify differences in (poly)phenol metabolism.

Objectives. This study aims to quantify gut microbial enzyme activities involved in (poly)phenol catabolism and to explore their associations with host characteristics, dietary patterns, urinary metabolites, aggregate phenolic metabotypes, and gut microbial communities.

Methods. Baseline faecal samples were obtained from 77 healthy adults enrolled in a standardized oral (poly)phenol challenge test (OPCT), involving acute supplementation with multiple (poly)phenol classes. Activities of five gut microbial glycosidases (β-glucosidase, β-galactosidase, β-glucuronidase, α-glucosidase and α-galactosidase) were quantified spectrophotometrically at 405 nm using chromogenic p-nitrophenyl-conjugated substrate analogs and normalized to faecal protein content. Associations with host-related variables (BMI, age, sex), dietary patterns, urinary metabolites, phenolic metabotypes, and microbial taxa were evaluated.

Results. Gut microbial glycosidase activities showed marked inter-individual variability. Selected glycosidase activities were associated with host-related factors (age and sex), specific nutrient intakes, and dietary pattern scores. Exploratory integration with urinary phenolic metabolites and gut microbial taxa suggested potential links between microbial enzyme function. Conversely, individual glycosidase activities were not associated with the aggregate metabotype classification.

Conclusions. Host characteristics and dietary habits are key drivers shaping gut microbial enzymatic activities involved in (poly)phenol metabolism. Understanding these factors is crucial, as they directly modulate inter-individual variability in (poly)phenol bioconversion and influence host–microbiota metabolic interplay.

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In Life

Phenolic Compounds Shape Lactate-Dependent Signaling and Gene Regulation: A Nutrigenomic Perspective

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Lactate has recently emerged as a key signaling metabolite linking nutrition, metabolism, immunity, and gene regulation. Beyond its classical role as an end-product of glycolysis, lactate acts through specific G protein-coupled receptors, including GPR81 and GPR132, and influences cellular responses through metabolic reprogramming and protein lactylation. These mechanisms are increasingly recognized as important components of nutrigenomic regulation, connecting dietary factors with cellular signaling networks and transcriptional activity.

Phenolic compounds, abundant in fruits, vegetables, herbs, and plant-derived foods, are among the most extensively studied bioactive dietary constituents. Their health-promoting properties have traditionally been attributed to antioxidant and anti-inflammatory activities; however, growing evidence suggests that phenolics can directly influence cell signaling pathways and gene expression. The ability of these compounds to modulate lactate-responsive receptors may represent a previously underappreciated mechanism linking diet to metabolic and immune homeostasis.

The aim of this study was to evaluate the potential of selected dietary phenolic compounds to regulate lactate-sensitive receptors GPR81 and GPR132. Candidate compounds were initially screened using computational approaches to identify potential receptor interactions and subsequently evaluated in cellular models exposed to lactate.

The obtained results indicate that several phenolic compounds significantly influence lactate-dependent cellular responses, suggesting their ability to modulate receptor-mediated signaling. These effects could be associated with altered expression of genes involved in inflammation, cellular metabolism, and stress adaptation supporting the hypothesis that dietary phenolics can influence lactate sensing and downstream transcriptional programs, potentially affecting processes relevant to chronic inflammation, metabolic disorders, and cancer.

Our findings highlight lactate-responsive receptors as promising molecular targets of food-derived bioactive compounds and provide new evidence for the involvement of dietary phenolics in nutrigenomic regulation. Understanding how nutritional components interact with metabolite-sensing pathways may facilitate the development of personalized nutritional strategies and novel dietary interventions aimed at improving metabolic and immune health.

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Molecular effects of enriched Matcha Tea: insight from an in-vitro intestinal model

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[3] Chemistry Interdisciplinary Project (CHIP), School of Pharmacy, University of Camerino, 62032 Camerino, Italy.

Introduction: Leaky gut syndrome and gut dysbiosis are increasingly recognized as major health concerns worldwide, due to their association with the development of inflammatory and metabolic disorders. Thus, growing interest has been addressed to the development of functional foods enriched in bioactive compounds and probiotics aimed at improving intestinal health. Matcha is a finely ground powder obtained from Camellia sinensis leaves and it is consumed as a whole-leaf suspension, naturally rich in bioactive compounds. Lachancea thermotolerans is a newly discovered non-Saccharomyces yeast with probiotic effects.

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Methods: Samples were subjected to in vitro digestion. The viability of the probiotic was assessed before and after the digestion. The resulting digests were analysed for antioxidant activity, and their polyphenol composition was characterized by HPLC-DAD. Subsequently, a Caco-2 in-vitro intestinal epithelial model was pre-treated with the digests and exposed to inflammatory conditions. The experiment was performed in triplicates. Epithelial barrier integrity was assed and gene expression analysis was also performed.

Results: The probiotic yeast remained viable after in vitro digestion. Polyphenol content was higher in the matcha–probiotic mixture than matcha alone. Both matcha and the matcha–probiotic combination exerted a protective effect against inflammation-induced disruption of epithelial barrier integrity.
The matcha–probiotic combination, as well as the digested probiotic alone, reversed the inflammation-induced modulation of claudin gene expression. A similar trend was observed for the expression level of NF-κB gene.

Conclusions: The addition of the probiotic yeast to matcha tea improves its properties, potentially enhancing its health benefits.

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In Life