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Preface

Over the last decades, the **Austrian Food Chemistry Days** (formerly *Österreichische Lebensmittelchemie Tage*) have developed into a unique biennial conference, primarily providing food scientists conducting research at Austrian institutions with a platform to present and discuss their work. After a break caused by the COVID19 pandemic, this long-standing tradition was successfully resumed in 2024 and will now be continued.

It is my great pleasure and honour to be the chair of the **Austrian Food Chemistry Days 2026** and to welcome colleagues and friends from the scientific community to the new campus of Graz University of Technology.

The conference covers a wide spectrum of research areas, reflecting the diversity and excellence of food chemistry research in Austria: (i) mycotoxins in foods; (ii) contaminants and allergens; (ii) food packaging, (iii) food flavour; (iv) current analytical approaches, and (v) current trends in food science. The scientific programme features eight keynote lectures, 22 short communications and 31 poster presentations.

A long-standing tradition of the conference is the Peter B. Czedik-Eysenberg Award Ceremony, held in memory of Peter B. Czedik-Eysenberg, a pioneering Austrian food chemist who was deeply committed to fostering cooperation among European food scientists. The Peter B. Czedik-Eysenberg Award is conferred biennially by the Österreichische Chemische Gesellschaft GÖCH. The awardees are selected by the GÖCH Working Group on Food Chemistry, Cosmetics and Food Contact Materials. The award recognises outstanding scientific publications by young researchers in the respective field. We are particularly pleased that two young scientists are being honoured this year and that they will present their work during the conference.

The organisation of this conference could only be achieved with the support and the help of many people. I would like to acknowledge Gabriella Köszegi, Petra Singer and Walter Schneider from GÖCH for handling registrations, submissions and financial issues. I also thank the members of the scientific committee for assessing abstracts, discussing the set-up of the scientific programme and chairing sessions. My appreciation further extends to my colleagues of the Local Organising Committee, to PhDs and staff members of the Institute of Analytical Chemistry and Food Chemistry for their support in organising and running the conference. We are grateful to all our sponsors for the financial support enabling us to keep the registration fees on an affordable level, particularly for master- and PhD students. Finally, I would like to thank Julia Gallob for her assistance, particularly in preparing this Book of Abstracts, and the colleagues from the Verlag der TU Graz for their professional support in its publication.

I wish all participants a successful and inspiring conference!

Barbara Siegmund
Conference Chair

Sessions of the Conference

The scientific sessions of the conferences were organised in five thematic areas followed by the poster session. Oral contributions were assigned to these sessions accordingly. Due to the wide range of topics that were covered by the poster presentations, no further classification by research areas was undertaken for the posters. In the following survey, keynote lectures are marked with *. In the book, the abstracts follow the order of presentations at the conference.

Mycotoxins in Foods

Doris Marko*	Emerging Mycotoxins in Food
Vanessa Partsch	Immunosuppressive modulation of NF-κB signaling by Alternaria mycotoxins in human THP-1 monocytes
Francesco Crudo	Hidden threats in the food chain: immunosuppressive and antiestrogenic properties of the Alternaria mycotoxins alterperylenol and altertoxin I
Michael Sulyok*	Determination of natural contaminants in vegan meat replacement products by LC-MS/MS

Contaminants and Allergens

Noah Ratzer	Mutagenic properties and topoisomerase-poisoning potential of selected aflatoxin B1 precursors
Florian Call	Impact of in vitro digestion on the bioaccessibility, genotoxicity and mutagenicity of mycotoxins in a complex Alternaria extract
Katrin Gradl	Confident analysis of ultra-trace pesticides residues in baby food using triple quadrupole GC-MS
Michael Wiederstein	Soybean – still an outstanding plant food with allergenic potential?

Food Packaging

Andrea Hochegger*	Food Packaging Material – Risk Assessment of Recycled Polyolefins
Lara Skef	Printing Regimes and Their Influence on Potential Migrants in Food Contact Material
Dilara Konuk Takma	Natural deep eutectic solvents as plasticizing agent for pectin and gelatine based biocomposite packaging films
Karin Gromann*	Microplastics in the Food Chain: More than just a Physical Contaminant

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Margit Cichna-Markl & Stefanie Dobrovolny*	Honey authentication by DNA analysis – a new frontier in food fraud detection

Jonathan Falchetto-Bruckner	Wild garlic and its toxic look-alikes – Analytical approaches for detecting contaminations in commercial products
Bassam Lajin	Coupling liquid chromatography with element-selective detection: analytical advances and emerging dimensions in food metabolomics
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Lena Dubois	Hydrogen-based SPME-GC×GC-TOFMS analysis for wine differentiation
Tina Rajkovic	Biomonitoring of mycotoxin exposure and exposomic characterization of plasma and urine samples from preterm infants
Andreas Matijevic	Optical Chemical Sensors for Ammonia at the Food-Water Interface

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[O 01] Risk assessment of mycotoxins

Doris Marko

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Since the discovery of aflatoxins in the 1960s, more than 300 fungal metabolites have been characterized as so-called „mycotoxins“. The respective structures are as diverse as the modes of action, comprising cytotoxic, genotoxic, immunomodulatory as well as endocrine disruptive compounds. In 1985, the FAO estimated that about 25% of the global food crop are contaminated with mycotoxins. Since then, global climate change has impacted the occurrence spectrum of respective fungi and, at the same time, improvement in analytics has enabled milestones in sensitivity. Nowadays, estimations speculate up to a contamination rate of 90%, at least in trace amounts. In addition to the few regulated mycotoxins such as aflatoxins or ochratoxin A, now numerous additional secondary metabolites can be detected. For most of these potentially „emerging“ mycotoxins data on occurrence and/or toxicity are not sufficient yet for comprehensive risk assessment. Moreover, recent studies demonstrate that mycotoxins are rarely found as single toxins but often occur in mixtures, thus further challenging risk characterisation. Thus, more than six decades after aflatoxin discovery, mycotoxins in the food chain is more than ever a highly relevant topic with respect to consumer´s safety.

In May 2022, the European Union launched the „PARC“ initiative, a « Partnership for the Assessment of Risks from Chemicals ». The 7-year partnership under Horizon Europe has a total funding volume of €400 million Euro, 50% funded by the European Union and 50% by Member States. PARC involves about 200 institutions working in the areas of the chemical safety from 28 countries and three EU authorities, including the European Chemical Agency (ECHA), the European Food Safety Authority (EFSA) and the European Environment Agency (EEA). The partnership is coordinated by ANSES, the French Agency for Food Safety, Environmental Protection and Occupational Health. PARC aims to develop next-generation chemical risk assessment to protect human health and the environment.

In the field of emerging contaminants, PARC aims to close critical data gaps for comprehensive risk assessment. One line of activity is focused on hazard characterization of the emerging mycotoxins enniatins (ENNs), beauvericin (BEA) and *Alternaria* toxins, non regulated contaminants with an increasing data base on occurrence in food and feed. Structurally, ENNs and BEA belong to the class of cyclic hexadepsipeptides, comprising three α-D-hydroxyisovaleric acid residues alternately connected to three L-configured N-methylated amino acid residues. Their lipophilic structure enables them to incorporate into membranes, where they form transmembrane cation-selective channels. This mechanism is considered the primary mode of action underlying the observed toxicological effects. A special challenge is represented by *Alternaria* mycotoxins with more than 70 compounds out of different chemical classes reported so far, which might be formed by these fungi. However, only a limited number of secondary metabolites formed by *Alternaria* fungi are commercially available und thereby accessible as reference material and test compounds for hazard characterization. Toxicity guided-fractionation revealed secondary metabolites formed by *Alternaria* fungi with genotoxic, immunotoxic and/or endocrine disruptive activity. Depending on the respective *Alternaria* strain and the growth conditions, complex toxin mixtures with different activity profile can be observed, underlining the difficulties for hazard characterisation and risk assessment.

[O 02] Immunosuppressive modulation of NF-κB signaling by Alternaria mycotoxins in human THP-1 monocytes

Vanessa Partsch[1,2], Francesco Crudo[1], Giorgia Del Favero[1,3], Doris Marko[1]

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[3]Core Facility Multimodal Imaging, University of Vienna, Vienna, Austria

Alternaria mycotoxins include over 70 diverse compounds, some of which exhibit immunomodulatory properties. Among the most prevalent are alternariol (AOH), alterperylenol (ALTP) and altersetin (AST), which have been shown to suppress LPS-induced inflammation and target the NF-κB signaling pathway in THP-1 monocytes and macrophages [1,2,3]. However, the specific molecular mechanisms remain unclear. This study aimed to elucidate intracellular events underlying the immunoinhibitory properties of selected Alternaria mycotoxins on THP1 monocytes in an inflamed environment.
For this purpose, the NF-κB reporter gene assay was conducted in THP1-Lucia™ monocytes after co-exposure of the cells to LPS and the mycotoxins of interest. Given the complex nature of the NF-κB signaling pathway, changes in different constituents of the cascade were examined. Immunofluorescence microscopy and Western blot analyses were employed to assess changes in key signaling proteins. The results of the confocal microscopy and Western Blot experiments revealed that AOH, ALTP and AST alter the expression levels of central proteins involved in the NF-κB cascade. Specifically, the inhibitory protein IκB and its phosphorylated form emerged as primary targets of the toxins and exposure resulted in a concentration-dependent up-and downregulation, respectively. Additionally, AST and ALTP lead to a reduced protein content of the IκB kinase (IKK) enzyme complex and the NF-κB p65 subunit. Analysis of nuclear fractions by Western blot demonstrated altered nuclear translocation of NF-κB p65 and phospho-p65: exposure to AOH and AST resulted in decreased nuclear protein levels, whereas ALTP led to increased nuclear p65 content.
In conclusion, these findings support that the *Alternaria* mycotoxins under investigation interfere with the NF-κB pathway by modulating the expression of regulatory proteins within this signaling cascade and affecting the nuclear translocation of the transcription factor itself. These findings offer novel insights into the molecular mechanisms underlying the immunotoxicity of *Alternaria* mycotoxins.

This project was carried out under the framework of the European Partnership for the Assessment of Risks from Chemicals (PARC), with funding provided by the European Union's Horizon Europe research and innovation program.

1) Crudo, F.; Partsch, V.; Braga, D.; Blažević, R.; Rollinger, J.M.; Varga, E.; Marko, D., Discovery of the Alternaria mycotoxins alterperylenol and altertoxin I as novel immunosuppressive and antiestrogenic compounds in vitro, 2025: 99 (1) 407-421. doi: 10.1007/s00204-024-03877-1
2) Kollarova, J.; Cenk, E.; Schmutz, C.; Marko, D, The mycotoxin alternariol suppresses lipopolysaccharide-induced inflammation in THP-1 derived macrophages targeting the NF-κB signalling pathway, 2018: 92 (11) 3347–3358. doi: 10.1007/s00204-018-2299-4
3) Partsch, V; Crudo, F.; Piller, D.; Varga, E.; Del Favero, G.; Marko, D, Resolving complexity: Identification of altersetin and toxin mixtures responsible for the immunomodulatory, antiestrogenic and genotoxic potential of a complex Alternaria mycotoxin extract, 2025: 198. doi: 10.1016/j.fct.2025.115315

[O 03] Hidden threats in the food chain: immunosuppressive and antiestrogenic properties of the *Alternaria* mycotoxins alterperylenol and altertoxin I

Francesco Crudo[1], Vanessa Partsch[1,2], Dennis Braga[1], Ruzica Blažević[3], Judith M. Rollinger[3], Elisabeth Varga[1,4], Doris Marko[1]

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Mycotoxins produced by *Alternaria* species are increasingly recognized as a potential threat to food safety and public health, having been linked to diverse adverse biological outcomes. However, owing to the limited availability of robust occurrence and toxicity data, these emerging contaminants remain unregulated. Consequently, their capacity to interfere with immune function and estrogen signaling is still poorly understood. The objective of this work was to determine which individual mycotoxins are responsible for the immunosuppressive and antiestrogenic effects observed for a complex extract of *Alternaria* metabolites (CE) obtained from an *Alternaria alternata* strain cultivated on rice. A toxicity-guided fractionation approach was applied, integrating supercritical fluid chromatography for extract separation with targeted LC–MS/MS quantification and in vitro bioassays. Based on the chemical profiles of the resulting fractions, alternariol (AOH), tenuazonic acid (TeA), altertoxin I (ATX-I), and alterperylenol (ALTP) were initially identified as putative contributors to the biological activity of the CE. Their role in modulating immune responses was subsequently examined using an NF-κB reporter gene assay in THP1-Lucia™ monocytes. These experiments indicated that AOH played only a minor role in the immunomodulatory effects of the extract. In contrast, ATX-I and ALTP markedly suppressed LPS-induced NF-κB activation at concentrations of 1 µM or higher. The antiestrogenic potential of the selected mycotoxins was assessed in Ishikawa cells using the alkaline phosphatase assay, demonstrating that ALTP (≥ 0.4 µM) and ATX-I (≥ 2 µM) significantly inhibited estrogen-dependent enzyme expression. In light of the possible negative consequences of immune and endocrine disruption, further studies are required to elucidate the mechanisms underlying these effects and to enable a more comprehensive assessment of the health risks associated with *Alternaria* mycotoxins.

[O 04] Determination of natural contaminants in vegan meat replacement products by LC-MS/MS

Michael Sulyok, Rudolf Krska

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Plant-based foods are expanding rapidly across global markets and consumer segments, driven by perceived health and sustainability benefits. With this shift, the chemical safety profile of these products—shaped by diverse botanical inputs and innovative processing—has become a critical topic for food chemistry. Several natural contaminants, including mycotoxins and tropane alkaloids, can be present in common raw materials such as soybeans, peas, and other legumes [1, 2], and recent dietary studies suggest higher exposure to specific mycotoxins (e.g., ochratoxin A) among vegans compared with omnivores [3]. Despite this, regulatory limits often do not cover these raw materials or many plant-based alternatives, and occurrence data remain limited, typically focusing on a narrow range of analytes and product types (e.g., soy-based burgers), with sparse information on seitan, pea-derived products, and fungal protein.

This study addresses these gaps by applying an extended multi-analyte screening method based on liquid chromatography coupled to tandem mass spectrometry (LC–MS/MS) to a broad set of finished vegan foodstuffs spanning different matrices and ingredient sources. Beyond regulated mycotoxins, the method encompasses Alternaria toxins, tropane alkaloids, emerging mycotoxins (e.g., beauvericin, enniatins), and other secondary metabolites with notable prevalence. We will present occurrence profiles for the most frequently detected compounds—such as cytochalasins observed in raw soybeans—and discuss trends across product categories and raw material origin.

By generating robust occurrence data across contemporary plant-based foods, this work provides a chemistry-centered evidence base to inform risk prioritization, guide quality assurance and sourcing strategies, and support future regulatory and processing interventions in the evolving plant-based sector.

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[O 05] Honey authentication by DNA analysis – a new frontier in food fraud detection

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Honey is a popular food product, appreciated for its natural sweetness and complex flavour profile. Moreover, honey consumption has been associated with nutritional and health benefits. However, honey is among the most frequently adulterated food products in Europe. Geographic authentication of honey is a major analytical challenge. Traditional approaches for geographic honey authentication include chemical profiling and pollen analysis (melissopalynology). While these methods are well established, they are often labor-intensive, technically demanding, and insufficiently robust.
Since honey contains traces of DNA from various sources, including plants, bees, and other insects, DNA analysis offers strong potential for honey authentication. Among DNA based methods, DNA barcoding and DNA metabarcoding play an increasing role.
After addressing the challenges of detecting traces of DNA in honey and introducing the principles of DNA barcoding and DNA metabarcoding, DNA metabarcoding assays for plant taxa and insects and DNA barcoding approaches allowing differentiation of honeybee subspecies will be presented. The lecture will highlight the strengths and limitations of DNA barcoding and metabarcoding for honey authentication.

Keywords: honey, authentication, DNA barcoding, DNA metabarcoding, plants, honeybee subspecies

[O 06] Wild garlic and its toxic look-alikes – Analytical approaches for detecting contaminations in commercial products

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AGES, Group for Contaminant and Special Analysis

Wild garlic (*Allium ursinum*) is a popular seasonal ingredient, often used in pestos, cheeses, and other specialty foods. However, its morphological similarity to toxic plants such as lily of the valley (*Convallaria majalis*) and autumn crocus (*Colchicum autumnale*) poses a significant food safety risk. Accidental contamination or substitution can lead to severe poisoning incidents.

For these reasons a targeted analytical approach to detect relevant toxins was developed. The liquid chromatography triple quadrupole mass spectrometry (LC-QqQ-MS) method allows for the quantification of Convallatoxin and Colchicin down to 10 µg/kg. These substances indicate a contamination of a product by lily of the valley and autumn crocus, respectively. Covered matrices include pestos and cheeses. The method will be presented in detail and validation data will be discussed. Additionally, first results of real samples will be shown.

To gain a deeper understanding beyond targeted analysis an additional untargeted approach was pursued. For this purpose authentic lily of the valley leaves were collected and analysed for the presence of other toxin related analytes for which no analytical standard is commercially available. Utilizing high resolution MS (hrMS) a molecular profile of the sample was recorded. The findings will be presented in this contribution.

The mutual benefits from bringing together an untargeted and a targeted approach will be discussed. Transformation of qualitative data gathered from hrMS experiments into useful information for quantitative routine analysis by QqQ-MS will be demonstrated. Hence, the well-known risk of confusing poisonous plants with edible plants will be put into a modern analytical setting.

[O 07] Coupling liquid chromatography with element-selective detection: analytical advances and emerging dimensions in food metabolomics

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The inductively coupled plasm mass spectrometry (ICPMS) is an element-selective detector. ICPMS response is a product of the element mass rather than a general physical or chemical property and therefore enables the detection of a wide range of elements with high selectivity at low limits of detection. The relatively recent advent of tandem mass spectrometry to ICPMS (ICPMS/MS) further enhanced selectivity and applicability to include key elements in food science such as the non-metals, particularly sulfur and the halogens. However, coupling ICPMS with liquid chromatography has been hampered by fundamental limitations in the technique. Herein, we present novel analytical approaches that enable overcoming these limitations including new chromatographic elution approaches that address the long-standing limitation of the compatibility between ICPMS and reversed-phase liquid chromatography. Furthermore, we highlight the associated emerging potential of the technique in food science by showing a series of applications involving multi-elemental speciation analysis in common foods and beverages such as asparagus, mushrooms, and wine for characterization of their elemental metabolomes as well as for assessing inter-regional variation in nutrient profiles, and discovering novel biomarkers of food intake. These applications underscore the possibilities offered by the element-selective liquid chromatographic detection, providing complementary information to current techniques in food metabolomics.

[O 08] Shimadzu's ABC of Food Analysis

Jan Peter Mayser

Shimadzu Europa GmbH

Shimadzu provides end-to-end solutions for the complete food analysis lifecycle, from raw material screening to finished product verification. "Shimadzu's ABC of Food Analysis" demonstrates how a single technology portfolio can address diverse challenges in food safety, quality, and authenticity through robust, instrument-agnostic analytical pipelines.

We present an integrated approach spanning molecular classes, sample matrices, and regulatory requirements.

Cereulide was analyzed in fried rice, with recovery tested at 10 ng/g—below levels reported in food poisoning cases—using the implicated food as reference. The optimized method achieved 80–120% recovery with simple pretreatment. Unlike the time-consuming HEp-2 cell vacuolation test, this approach enables rapid analysis from pretreatment to measurement.

A rapid SPE enrichment combined with MALDI-TOF (MALDI 8030) enables sensitive profiling of honey polyphenols and detection of Manuka-specific markers (e.g., leptosperin, 4-hydroxyphenyllactic, and 3-phenyllactic acids), facilitating fast authenticity screening with minimal sample preparation.

Volatile profiling via HS-GC-MS, coupled with the Smart Aroma Database and multivariate statistics (PCA, hierarchical clustering), allows rapid, high-sensitivity aroma fingerprinting, exemplified by discrimination of apple varieties based on ~20 identified volatiles.

Elemental safety monitoring using ICP-MS (ICPMS 2040/2050) with microwave digestion and online internal standards delivers low detection limits and reliable quantitation across diverse baby food matrices; automated rinse strategies minimize carryover and support long-term stability for high-throughput regulatory testing.

These examples illustrate a coherent strategy: select the analytical mode best suited to the analyte class and decision objective, then apply validated sample preparation and software tools to deliver fit-for-purpose results. The integrated workflows provide high sensitivity, specificity, and robustness in real-world matrices, supporting compliance, quality control, and fraud detection across the food value chain. Attendees will gain actionable workflows and decision rules for designing comprehensive food analysis programs spanning the entire "A to Z" of food testing.

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Anita Emmerstorfer-Augustin, the lab teacher who won this award, will be present at our booth during some breaks, a perfect chance to ask her anything about her lab course.

We look forward to meeting you at our booth.

[O 09] First Certified Reference Material for the Emetic Toxin Cereulide in Food

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Cereulide is a cyclic lipophilic dodecapepsipeptide from *Bacillus cereus* ubiquitous in soil and food. It is a causative agent in food poisoning outbreaks; ingestions of minute amounts typically lead to emesis and nausea. However, in rare but documented cases, cereulide ingestion has led to death caused by liver failure or encephalopathy. Starch-rich foods such as rice and pasta dishes are often affected. Certified reference materials (CRMs) are important tools for laboratories to implement and safeguard reliable measurements. The presentation summarizes the steps to develop and produce a CRM for cereulide in cooked rice. In a feasibility study preceding the CRM production, it could be shown that cooked rice that was converted into rice powder by means of cryogenic milling, spiking with cereulide, freeze-drying and a final mixing step behaved similarly to a mimicked real sample (cooked rice, spiked with cereulide, homogenised). The CRM batch was prepared in the same way, with a target cereulide concentration of 10 mg/kg. A homogeneity study revealed suitable between-unit homogeneity. Transport and storage stability studies showed that the CRM shall be dispatched to the customer with cooling elements and that the CRM shall be kept at -20 °C for long-term storage, respectively. Ten laboratories all employing a method based on extraction of cereulide with an organic solvent and subsequent analysis using LC-MS/MS participated in the characterisation exercise. After technical and statistical scrutiny, a certified value and its corresponding expanded uncertainty was assigned. The CRM is to be used for method performance verification and quality control. It will help laboratories to implement and safeguard reliable cereulide measurements in food and will thus contribute to effective consumer protection.

Keywords: certified reference material (CRM), cereulide, *Bacillus cereus,* rice, food

[O 10] Risk Assessment of Recycled Polyolefins for Food Contact Applications

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The new European Packaging and Packaging Waste Regulation sets a minimum content of recycled material in all plastic-based packaging, including contact-sensitive applications. By 2030, at least 30% of PET packaging and single-use beverage bottles must consist of post-consumer recycled material (PCR), while non-PET plastics must contain a minimum of 10% PCR; these targets will increase further by 2040. [1] Achieving these goals represents a major challenge, particularly for recycled polyolefins such as polyethylene and polypropylene, as PCR materials of sufficient quality and availability remain scarce.

To accelerate innovation, Commission Regulation (EU) 2022/1616 introduces the concept of "novel technologies", allowing recycled materials to enter the market prior to final safety evaluation by the European Food Safety Authority (EFSA). This conditional authorization places high demands on scientific evidence, including detailed contaminant profiling, identification of contamination sources, evaluation of decontamination efficiencies, assessment of residual substances—especially genotoxic compounds and endocrine disruptors—and batch-to-batch screening of relevant parameters.

From a safety perspective, recycled plastics must comply with Regulation (EC) No 1935/2004 and Commission Regulation (EU) No 10/2011, which require food contact materials to be sufficiently inert to prevent harmful substance transfer to food, unacceptable changes in food composition or changes in its organoleptic properties. [2,3] Despite considerable efforts, no recycling process currently delivers polyolefinic PCR materials that consistently meet these stringent requirements and the existing knowledge gaps are huge: Limited data are available on typical contaminants, their concentration ranges, recycling-induced degradation products, and odour-active substances. Importantly, no single analytical technique can capture the chemical, toxicological, and sensory dimensions required for a holistic safety assessment.

This work demonstrates how an interdisciplinary strategy—combining advanced instrumental analytics, bioassays, and sensory evaluation—can overcome these limitations, providing a fundamental data set for future developments: Using this integrated approach, several critical contributors to PCR material risk profiles were identified using Ames MPF tests, including pigment degradation to primary aromatic amines, nitrocellulose degradation, and adhesive degradation. These findings highlight key leverage points within recycling and converting processes that would remain undetected by isolated analytical workflows.

At the same time, our results emphasize the next critical step: translating qualitative hazard identification into quantitative metrics. Current efforts focus on identifying relevant marker compounds, establishing concentration–effect relationships and defining robust methods suitable for routine batch-to-batch screening. Such markers are essential to enable efficient process control, regulatory compliance, and ultimately the safe large-scale deployment of recycled polyolefin materials in food contact applications.

This work was carried out as part of the Collective Research project "Aurelia", led by the ecoplus "Plastics-Cluster". The authors acknowledge the financial support of the project with the no. FO999913380 & FO999930785 from the Austrian Research Promotion Agency (FFG).

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[O 11] Printing Regimes and Their Influence on Potential Migrants in Food Contact Material

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Food packaging materials are printed using a variety of printing regimes, including flexographic, gravure, offset, digital, and UV-curable technologies. Each regime imposes specific requirements on ink formulation, curing/ drying mechanisms, and substrate interaction, resulting in fundamentally different chemical systems. These differences strongly influence the type and profile of substances that may migrate from printed packaging into food [1].

This can be further illustrated by several migration cases. Mineral oil saturated and aromatic hydrocarbons (MOSH/MOAH), associated primarily with offset printing inks and recycled paper substrates, have been detected in a wide range of packaged foods [2]. Similarly, in 2005 the migration of the photoinitiator isopropyl thioxanthone (ITX) from UV-cured inks into packaged cereal products led to a food crisis and product withdrawals. These cases highlighted uncertainties in consumer exposure and toxicological evaluation of migrating ink constituents. Together, they demonstrate that chemically distinct printing technologies can give rise to different migration pathways and health-relevant contaminants.

From a regulatory perspective, the assessment of printing ink migrants remains challenging due to lack of a harmonised European-specific regulation. The general requirements are placed in Regulations (EC) No. 1935/2004 and (EC) No. 2023/2006, supplemented by national provisions such as the Swiss Ordinance on materials and articles in contact with food and the German Printing Ink Ordinance becoming applicable in 2026 [3].

As paper-based materials represent the primary substrate of interest in this work, the migration occurs via gas-phase migration of volatile and semi-volatile compounds released from printed surfaces. In this context, gas chromatography (GC) represents a powerful and versatile analytical platform for addressing the challenges arising from the chemical complexity of printing inks and their migrants. Accordingly,testing different sample preparation, separation and detection methods in combination with GC are essential for advancing the assessment of migration behaviour across different printing technologies.

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[O 12] Natural deep eutectic solvents as plasticizing agent for pectin and gelatine based biocomposite packaging films

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An increasing attention has been directed toward improving the efficiency of plasticizers and minimizing the amount of plasticizers in biodegredable packaging films. Natural-based plasticizers such as glycerol, sorbitol, xylitol, fatty acid sucrose esters, and soybean oil are used depending on the type of film however, their high hydrophilicity and tendency to migrate often result in increased water sensitivity and compromised barrier properties. Natural deep eutectic solvents (NADESs) are novel agents that have been explored for their capacity to facilitate effective plasticization in biodegradable films. The study investigates effect of NADESs type and concentration on properties of pectin and gelatine based biocomposite films in terms of water vapor permeability (WVP), mechanical properties, color, opacity and thermal properties. NADESs based on choline chloride (ChCl) and organic acids including citric acid (CA), malic acid (MA), tartaric acid (TA), and oxalic acid (OA) were used as plasticizers at 10, 20 and 30 % w/w dry basis and their performance in the film was compared with glycerol plasticized films. ChCl–CA films exhibited the lowest WVP (0.105 g.mm/m2.h.kPa) at 20%, which were lower than those of the glycerol-plasticized film. Increasing the ChCl–CA and ChCl–MA contents to 30% led to higher WVP values while ChCl–TA films displayed stable WVP values (0.213-0.244 g.mm/m^2.h.kPa). Tensile strength (TS) decreased with increasing DES content for all DES-based films. At 10% dry basis, ChCl–MA films showed the highest TS (17.74 MPa), followed by ChCl–CA (15.30 MPa), while ChCl–TA exhibited lower values. The peak value (42.18%) for elongation at break was observed films plasticized with ChCl–CA at 30%. ChCl–CA and ChCl–MA films exhibited low opacity values. In contrast, ChCl–TA films showed markedly higher opacity values (2.75-3.04) compared to glycerol-plasticized film. No significant differences in color parameters were observed between the glycerol-plasticized film and the films plasticized with ChCl–CA and ChCl–MA, but ChCl–TA decreased L*, a*, and b* values of film. The melting point decreased from 63.5 to 58.7 °C with increasing ChCl–CA concentration while increase in melting point from 63.17 to 78.42 °C was observed with increasing ChCl–MA concentration. Films plasticized with ChCl–TA had melting point ranging between 60.81 and 61.79 °C. Overall, the use of NADESs contributed functionality of biodegradable food packaging films by enhancing barrier properties, mechanical properties and thermal properties. Ongoing research focus on the interactions of selected NADESs with additional antioxidant/antimicrobial compounds for the development of active food packaging applications.

Keywords: biodegradable film, green plasticizers, deep eutectic solvents, food packaging, functionality

[O 13] Microplastics in the Food Chain: More than Just a Physical Contaminant

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Microplastics are ubiquitous anthropogenic contaminants that are increasingly perceived not only as physical particulate matter but also as chemically complex systems. Beyond the polymer matrix, additives, degradation products, and adsorbed environmental chemicals are receiving growing attention, as they may enter the human body via the food chain and, due to their persistence, mobility, and biological activity, pose an increasing toxicological risk to human health.

Recent studies identify tire wear particles, synthetic textile fibers, and the secondary fragmentation of polymer-based materials as dominant sources of microplastics in the environment. In the food context, microplastics are introduced both through environmental contamination and through food contact materials such as packaging, coatings, and processing operations. Analytically, microplastics represent heterogeneous particles composed of polymer backbones, residual monomers, plasticizers, stabilizers, and surface-bound contaminants. Advances in chemical characterization using μ-FTIR and Raman microscopy as well as pyrolysis-GC/MS now enable the detection of microplastics in food, drinking water, and increasingly also in human samples. Oral intake represents a relevant exposure pathway alongside inhalation, with particular interest in small particles and nanoplastics. Experimental studies indicate oxidative stress responses and inflammatory signaling pathways associated with chemical composition and additive release; however, causal conclusions cannot yet be drawn.

The pronounced chemical and physical heterogeneity of microplastics constitutes a major challenge for analytical approaches and risk assessment, necessitating the standardization of methodological frameworks.

[O 14] Mutagenic properties and topoisomerase-poisoning potential of selected aflatoxin B_1 precursors

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Mycotoxins are naturally occurring food contaminants with severe adverse effects on human health. Among mycotoxins, aflatoxins are of particular concern, with aflatoxin B_1 (AFB_1) being their most significant representative. AFB_1 is the most potent naturally occurring human carcinogen, primarily targeting the liver. Hence, its presence in food is strictly regulated in the European Union. However, the biosynthesis of AFB_1 involves various enzymatic reactions that produce a variety of intermediates, collectively referred to as aflatoxin B_1 precursors. In contrast to AFB_1, maximum levels for these AFB_1 precursors in food have not been established to date, due to the lack of toxicological and occurrence data.

The present study aimed to address this knowledge gap, by investigating the mutagenic properties, and the topoisomerase poisoning potential, of selected AFB_1 precursors (averantin (AVN), averufin (AVF), versicolorin A (VerA), *O*-methyl-sterigmatocystin (OMST), sterigmatocystin (STC)). Mutagenicity was assessed using the Ames test with *Salmonella typhimurium* strains TA98 and TA100, enabling the detection of frameshift mutations and base-pair substitutions. In addition, the hypoxanthine-guanine phosphoribosyltransferase (HPRT) mutagenicity test was carried out for AVN, which showed ambiguous results in the Ames test. This assay employs the mammalian V79 cell line, derived from Chinese hamster fibroblasts. Both assays were executed in the presence and absence of S9 fraction to elucidate the role of metabolism on the mutagenic properties of the test compounds. To further investigate topoisomerase poisoning, the *in vivo* complex of enzyme (ICE) assay was implemented using precursors containing an anthraquinone moiety.

Results of the Ames test demonstrated that VerA, OMST and STC induced both frameshift mutations and base-pair substitutions in a concentration-dependent manner upon metabolic activation. In the absence of S9 mix, only AVN exhibited mutagenic effects, AVF showed no mutagenicity under any tested condition. The HPRT test indicated that AVN did not induce mutations of the HPRT gene, regardless of metabolic activation. Results of the ICE assay displayed the ability of AVF and VerA to poison both topoisomerase IIα and IIβ at the highest concentration tested (25 µM).

In conclusion, the results of this study provide first insights into specific toxic effects of several AFB_1 precursors. All precursors except for AVF exhibited mutagenic properties, while VerA and AVF acted as topoisomerase poisons targeting topoisomerase II. These findings underscore the need for further research on these poorly described compounds, while also serving as an important foundation for a future, comprehensive toxicological evaluation.

This work was conducted as part of the project “Are aflatoxin precursors of concern for human health?” funded by the Austrian Science Fund FWF (Grant-DOI: 10.55776/I6720) and the French National Research Agency ANR (ANR-23-CE34-0017).

[O 15] Impact of *in vitro* digestion on the bioaccessibility, genotoxicity and mutagenicity of mycotoxins in a complex *Alternaria* extract

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Fungal contamination of food is a global concern. Species of the genus *Alternaria* produce a wide range of structurally diverse mycotoxins, some of which may pose a significant health risk to consumers. *Alternaria* mycotoxins have been reported to exert a wide variety of toxicological effects, with the most significant being genotoxic, mutagenic, immunomodulatory, and (anti)estrogenic effects [1]. Although ingestion is the primary route of exposure to these mycotoxins, there is currently a lack of information about the impact of digestive processes on the chemical stability of these mycotoxins and, consequently, on the possible changes in their toxicological properties.

The present study aimed to address this gap by evaluating the genotoxicity and mutagenicity of *Alternaria* mycotoxins following an *in vitro* digestion process. Specifically, tomato puree samples were spiked with a well-characterized *Alternaria* mycotoxin extract and subjected to *in vitro* digestion using the INFOGEST 2.0 protocol [2]. To evaluate changes in genotoxicity, samples were analyzed in Caco-2 cells using the alkaline single-cell gel electrophoresis (COMET assay). The assay was performed both in the presence and absence of formamidopyrimidine glycosylase (FPG) enzyme to assess not only the induction of DNA strand breaks but also the presence of FPG-sensitive sites, indicative of oxidative DNA damage. The Ames test was implemented to assess whether the digestive processes may influence the mutagenicity of the complex extract. Additionally, to investigate the fate of the mycotoxins during the digestion process, LC-MS/MS analyses were performed.

The results of the study demonstrated that the complex *Alternaria* extract retained most of its genotoxic activity even after *in vitro* digestion. The DNA strand breaking potential of the extract was not affected by the digestive process. However, in the presence of the FPG enzyme, a significant reduction in tail intensity was observed, when comparing the digested to the undigested extract, indicating a decreased contribution of oxidative DNA damage and/or DNA adduct formation after *in vitro* digestion.

Results from the Ames test indicated that although *in vitro* digestion slightly attenuated the mutagenic potential of the extract, its mutagenic activity remained significantly higher than the solvent control.

LC-MS/MS measurements showed that *in vitro* digestion did not uniformly reduce the bioaccessibility of mycotoxins. While overall concentrations of most mycotoxins decreased throughout digestion, selected *Alternaria* mycotoxins, including altertoxin-I, alterperylenol, alternariol, and tenuazonic acid, reached pre-digestion levels after the intestinal phase, whereas others, such as the epoxide-bearing perylene quinones altertoxin-II and stemphyltoxin-III, were degraded during the process and were no longer detectable.

In conclusion, the results of this study suggest that the digestive processes play a key role in shaping the bioaccessibility and toxic effects of *Alternaria* mycotoxins. These findings serve as a crucial foundation for the comprehensive toxicological evaluation of *Alternaria* mycotoxins, contributing to a deeper understanding of their potential health risks and guiding future research in this field.

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[O 16] Confident analysis of ultra-trace pesticides residues in baby food using triple quadrupole GC-MS

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Ensuring the highest level of food safety in infant nutrition requires analytical methods capable of detecting pesticide residues at ultra-trace concentrations with excellent sensitivity, selectivity, and robustness. This study demonstrates the performance of a the Thermo Scientific™ TSQ™ 9610 triple quadrupole mass spectrometer coupled with the TRACE™ 1610 GC and a programmable temperature vaporizing (PTV) injector, for the determination of more than 200 pesticides in complex baby food matrices. Using QuEChERS extraction and timed-selected reaction monitoring (t-SRM), the method provides confident identification and quantification in compliance with SANTE/12682/2019 guidelines.

All target analytes showed linear responses over a concentration range of 1–500 µg/kg with coefficients of determination $R^2 > 0.99$. Instrument detection limits averaged 0.073 µg/kg, with individual IDLs ranging from 6 to 650 fg on-column. Recoveries for pre-spiked samples at 3 µg/kg ranged from 70–119% with ≤10% precision. Long-term robustness testing across 500 consecutive injections of diverse baby food extracts demonstrated remarkable signal stability, confirming the durability of the NeverVent™ AEI ion source, the PTV injector, and the inert flow path.

In addition, automation can further enhance the workflow efficiency. Employing µSPE as an automated clean-up step improves extract purity compared to manual dSPE, while enabling fully unattended operation overnight or during weekends.

These results confirm that the TSQ 9610 GC-MS/MS system meets the stringent analytical requirements for ultra-trace pesticide residue monitoring in baby food, while also supporting high sample throughput and minimal downtime, making it a powerful solution for routine and high-productivity residue testing laboratories.

[O 17] Soybean – still an outstanding plant food with allergenic potential?

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Soybean (Glycine max) is one of the most used vegetarian protein sources and common ingredient in industrially produced foods, with global cultivation and consumption further increasing. Besides its numerous nutritional and health advantages, soybean contains several allergenic proteins known to induce (severe) allergic reactions in soy-sensitized individuals. In 2022, the FAO/WHO reclassified soybean as a Group B food allergen based on criteria such as prevalence, severity of allergic reactions, and eliciting dose levels, suggesting its impact is predominantly regional. However, the rising global consumption of soy-based food products, potentially accompanied by an increase in soy allergy prevalence and severity, necessitated detailed monitoring of these trends. A critical aspect of food allergy management is allergen avoidance based on accurate food allergen detection methods, such as antibody-based immunoassays or mass spectrometry. To enhance food labeling and assist soy-sensitized individuals in making informed purchasing decisions, food allergen detection may focus on targeting specific clinically relevant allergens rather than confirming the presence of the entire food source, aligning with the diagnostic trend of personalized component resolved analysis.

Soy-allergen specific monoclonal antibodies and soybean polyclonal antibodies were produced, respectively. Antibodies were thoroughly characterized for their specificity, cross-reactivity, and assay performance using immunological methods such as Western Blot and different ELISA formats. These antibodies were used for assay development and applied to analyze raw materials and food samples. Immunization and cell fusion successfully yielded six soy-allergen specific monoclonal antibodies: one targeting Gly m 4, two targeting Gly m 5, and three targeting Gly m 6, in addition to two separate batches of polyclonal antibodies. Characterization confirmed the distinct functionalities of monoclonal and polyclonal antibodies. Monoclonal antibodies demonstrated high specificity by detecting an individual target epitope on an individual soy allergen, making them suitable for detecting and quantifying individual allergens in food samples. Conversely, polyclonal antibodies detected multiple epitopes, including proteins not derived from soybean, making them a tool for rapid pre-screening of raw materials in food industry.

Although soybeans have been removed from the list of major food allergies, it remains a significant and widely utilized allergenic food source requiring ongoing monitoring. Antibody-based immunoassays represent a robust, state-of-the-art method for detecting food allergens in raw materials and food products. Adopting component resolved allergen analysis enhances food labeling and allergen avoidance, thereby supporting soy-sensitized individuals in managing their food allergy.

This work was supported by the Government of Lower Austria under grant agreement K3-T-74/001-2019.

[O 18] More than one century of Maillard Reaction – is there anything left to explore?

Thomas Henle

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The Maillard reaction, first described by Louis-Camille Maillard in 1912, has been a cornerstone of food chemistry research for over a century. This nonenzymatic browning process, also known as glycation, is vital for understanding the flavor, color, and aroma of processed foods, as well as the formation of compounds that influence food safety and quality. Despite extensive research, significant gaps remain in our understanding of the reaction's mechanisms and its broader implications for food science, human biology, and biotechnology.

Case studies, such as those involving brewery processes and peanut roasting, have provided valuable insights into the formation of glycation products during food processing and storage. These studies have also enabled a quantitative assessment of the daily intake of such compounds through the diet.

Beyond the food matrix, glycation products play a role in biological systems. For example, the human intestinal microbiota demonstrates the ability to degrade Amadori products - key intermediates in the Maillard reaction - through deglycation processes, utilizing them as a source of lysine. Similarly, brewer's yeasts exhibit varied capacities to detoxify dicarbonyl intermediates, likely as a result of selective domestication.

The Maillard reaction extends its influence beyond food chemistry, with implications for protein functionality and biological processes. Post-translational modifications induced by glycation can alter the functional properties of proteins, presenting challenges for both food processing and human health. Despite the progress made in understanding these modifications, many questions remain unanswered, particularly regarding their impact on human physiology and evolutionary biology.

Even after more than 100 years of study, the Maillard reaction continues to captivate researchers across disciplines. Its complexity, coupled with its importance to food quality, safety, and human health, ensures that this field remains vibrant and filled with opportunities for further exploration. The Maillard reaction is far from fully understood, and its interdisciplinary challenges will continue to inspire research for years to come.

[O 19] Integrated analytical, sensory, and receptor-based strategies to identify bitter-tasting and bitter-masking food constituents

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Bitterness is a key sensory attribute often driving food acceptance, particularly in plant-based foods, protein hydrolysates, and functional ingredients. While bitterness originates from chemically diverse low-molecular-weight compounds, effective mitigation strategies require both reliable identification of bitter tastants and a mechanistic understanding of bitterness modulation. This presentation outlines integrated analytical, sensory, and receptor-based strategies to identify bitter-tasting food constituents and compounds capable of masking bitterness.

Using a combination of targeted and untargeted chemical analyses, human sensory evaluation, and in vitro bitter taste receptor assays, bitter-active compounds were systematically characterized and linked to specific taste receptor responses. Sensory-guided fractionation enabled the prioritization of bitterness-relevant fractions, while receptor-based assays provided mechanistic insight into bitter taste perception at the molecular level. In parallel, food constituents exhibiting bitterness-masking effects were identified and evaluated for their ability to attenuate receptor activation or modulate perceived bitterness without altering overall flavor intensity.

The presented work demonstrates how multidisciplinary approaches can be employed to disentangle complex bitterness profiles in foods and to identify natural bitterness-masking compounds, e.g. 4'-Demethyl-3,9-dihydroeucomin from the Resin of Daemonorops draco[1]. These findings provide a foundation for the rational design of improved food formulations with enhanced sensory acceptance, supporting product development in the areas of plant-based foods, functional nutrition, and sustainable ingredient innovation.

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[O 20] GCxGC-TOF-SCD- A new tool for the identification of odor active sulfur compounds

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Volatile sulfur compounds represent a large group of compounds that can make an important contribution to the aroma of a product in a wide variety of foods. With extremely low odor thresholds, they are among the most potent flavorings, which can still be relevant in the nanogram per kilogram range, sometimes even below. They can influence the odor of a product positively or negatively, with concentration playing a decisive role. They can be formed either enzymatically (Allium species) or thermally (Maillard reaction with sulfur-containing amino acids as precursors).
These conditions play an important role in the selection of analytical methods for detecting these compounds. Although sulfur-selective detectors are available (e.g., flame photometric detector, chemiluminescence), identification is a challenge, especially in very complex samples such as roasted coffee.
This presentation introduces a combination of instruments that greatly facilitates the identification and determination of sulfur-containing organic compounds. This is a comprehensive two-dimensional gas chromatographic system with a flow-modulated splitter and dual simultaneous detection. For identification purpose a fast scanning time-of-flight mass spectrometer is used and for the sulfur species a chemiluminescence detector is used as a secondary detector.
The usefulness of this novel device configuration is demonstrated using selected examples from different foods and packaging materials.

1) Shankaranarayana ML, Raghavan B, Abraham KO, Natarajan CP, Brodnitz HH. Volatile sulfur compounds in food flavors. C R C Critical Reviews in Food Technology. 1974; https://doi.org/10.1080/10408397409527163
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3) Boswell H, Borton DJ, Merrick M, Mohler RE. Evaluation of a prototype reverse fill/flush flow modulation-splitter system for the highly detailed separation required in industrial settings. Journal of Chromatography Open. 2024; https://doi.org/10.1016/j.jcoa.2024.100115

[O 21] Predictive flavor tuning of matured cheese by targeted formation of kokumi peptides

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The kokumi perception providing a complex and long-lasting mouthfulness in matured cheese has previously been linked by molecular sensory studies to the class of γ-glutamyl dipeptides. To further study the biosynthesis of these peptides and predict the formation of the consumer preferred sensory profile of ripened cheese, we developed and validated a high-throughput LC–MS/MS workflow that comprehensively quantifies all three glutamyl dipeptide subgroups (α-Glu–X, X–Glu, γ-Glu–X; 56 analytes) using simplified extraction and optimized chromatographic separation. Validation demonstrated robust performance (repeatability, detection limits, recovery), and application to 122 commercial cheeses (2 weeks–15 years maturation time; diverse origins, molds, and styles) revealed pronounced, maturation-dependent increases across all classes, with mold-ripened cheeses showing the strongest increase. For targeted flavor engineering leading to the accelerated formation of the desired peptides, γ-glutamyl transferase activity in raw milk was preserved via microfiltration, while substrate availability was enhanced by incorporating glutamine into the curd of semi-hard cheese. Longitudinal peptide profiling showed that after 3 months of maturation, γ-glutamyl dipeptide levels were equivalent to those observed after ~8 months of natural ripening, without compromising texture or melting behavior. Together, the analytical and dairy technology tools, as well as the predictive models, enable the targeted development of novel products with partial or complete replacement of dairy proteins, yielding sustainable cheese alternatives with high consumer preference.

1) Fröhlich, S.M., Jünger, M., Mittermeier-Kleßinger, V.K., Dawid, C., Hofmann, T.F., Somoza, V., Dunkel, A. Towards prediction of maturation-dependent kokumi taste in cheese by comprehensive high throughput quantitation of glutamyl dipeptides. Food Chem. 2025, 463, 141130.
2) Braitmaier, S.H., Fröhlich, S.M., Somoza, V., Dunkel, A., Hinrichs, J. Flavor tuning of semi-hard cheese by targeted formation of γ-glutamyl dipeptides. Int. Dairy J. 2025, 166, 106240.

[O 22] Hydrogen-based SPME-GC×GC-TOFMS analysis for wine differentiation

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The chemical analysis of the aromas associated with wine provides useful information for understanding the quality of a product. Different production steps such as skin maceration, barrel and stainless-steel fermentation, use of selected or indigenous yeasts, malolactic fermentation have a major impact on the aroma development and, understanding these factors is of major interest to wine producers. The qualitative characterization of the volatile fraction of wine can be attained by gas chromatography-mass spectrometry (GC-MS). To obtain optimal separation, the volatile components in the wine sample were first extracted with solid phase microextraction (SPME) and then separated by two-dimensional gas chromatography (GC×GC), which couples two columns with complementary stationary phases to increase the peak capacity. This technique allows to separate more individual analytes in complex wine samples. The use of time-of-flight mass spectrometry (TOFMS) facilitates full mass range spectra to be collected at fast acquisition rates, producing high quality data which allows automated deconvolution to be applied efficiently.

GC×GC-TOFMS data was generated using both He and H2, and results were compared in terms of chromatographic separation and spectral quality. A large set of wine samples subjected to different treatments was analyzed to evaluate the method's quality and robustness. Statistical analysis tools played a crucial role in determining relevant compounds which were impacted by the different treatments and production steps showing altered concentrations.

[O 23] Biomonitoring of mycotoxin exposure and exposomic characterization of plasma and urine samples from preterm infants

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Mycotoxins are naturally occurring food contaminants produced by various molds and play a relevant role in food and consumer safety worldwide. Extremely premature infants are highly vulnerable to the toxic effects of xenobiotics due to their naive immune system and lower detoxification capacity. Thus, monitoring the levels of mycotoxins in biofluids during early-life is important to provide exposure data and assess potential health risks. This study aimed to assess mycotoxin and other xenobiotic exposures in 26 extremely premature infants delivered in Vienna by applying ultra-sensitive targeted LC-MS/MS and non-targeted high-resolution mass spectrometry (HR-MS) assays. A total of 100 biological samples comprising plasma (n=48) and urine (n=52) collected at two time-points, 7- and 28-days post-partum, were quantitatively analyzed for mycotoxin exposure. For a more comprehensive exposome-scale analysis, a non-targeted workflow was applied to a subset of 20 plasma samples. The targeted results indicated comparatively low mycotoxin exposures with the regulated mycotoxin ochratoxin A (OTA) quantified in all plasma samples (median: 139 ng/L), and in 27% (14/52) of urine samples (median: 40 ng/L). Alternariol monomethyl ether (AME) was quantified in 31% (16/52) of urine samples (median: 25 ng/L). During non-targeted analysis, 21 compounds were identified at the highest confidence level with reference standards. This includes key environmental exposure compounds found in many food contact materials, often leading to dietary intake, including PFOA and PFOS, diethyl phthalate, bisphenol A and 2-phenylphenol. Albeit a small cohort, this study showed that extremely premature infants are exposed to a mixture of dietary, endogenous and chemical exposures. However, many of the analyzed mycotoxins, including carcinogenic aflatoxins, were not detected, indicating very low overall mycotoxin exposure. Future research is necessary to link exposure patterns to potential acute or long-term health outcomes with the general aim of improving public health and personal prevention measures.

This study was approved by the ethical committee of the Medical University of Vienna with the approval number 1061/2021 and received funding from the Exposome/EIRENE Austria Research Infrastructure and the Austrian Science Fund project P33188-B.

[O 24] Optical Chemical Sensors for Ammonia at the Food-Water Interface

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Ammonia is a key chemical parameter in aquaculture and other food-related systems, where elevated concentrations can negatively affect organism health, product quality, and environmental sustainability. In fish farming, ammonia originates from protein metabolism and feed degradation and exists in a pH- and temperature dependent equilibrium between the non-toxic ammonium and toxic free ammonia, making continuous chemical monitoring essential.[1] Toxic effects on fish and the environment have been reported at concentrations as low as 25 µg/L.[2]

This contribution presents the development of an optical chemical sensor for the sensitive and selective detection of ammonia in aqueous environments relevant to food production. The sensor enables real-time, non-invasive monitoring of ammonia concentrations, supporting improved chemical process control in aquaculture systems and reducing stress-related losses in fish stocks. Beyond fish farms, the sensing approach is applicable to other ammonia-relevant areas within and outside the food chain, including wastewater treatment, biotechnological processes and nitrogen management in circular food systems. By providing chemically precise and fast ammonia monitoring in the ppb-range, the presented technology contributes to improved food quality, safer production conditions, and more sustainable management of ammonia in food-related environments.

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[O 25] The microbiome of vegetables and fruits and its potential health implications

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Fresh fruits and vegetables harbour diverse, complex, and abundant microbial communities. These microorganisms are not incidental contaminants but native members of the plant microbiome, and thus become an important part of the human diet, especially when fruits and vegetables are consumed raw or minimally processed. Recent metagenomic studies revealed genetic similarities between microbes found on edible plants and those present in the human gut, supporting the concept of a “microbial continuum” along the food-gut axis.

The microbiome associated with edible plants impacts many areas of food science and human health. In agriculture, these microbes contribute to nutrient cycling, hormone production, and disease resistance. After harvest, they influence food preservation by producing bioactive compounds such as organic acids and bacteriocins. During fermentation, specific microbial taxa shape the flavour profile, texture, and nutritional composition of foods. Fermented foods are typically lower in microbial diversity compared to raw produce, but are enriched with taxa known for their gastrointestinal resilience and their probiotic functions. Also, beyond fermentation, microbes isolated from fruits and vegetables have demonstrated functional health benefits. These include the production of essential vitamins like B12 and K2, the synthesis of short-chain fatty acids, antagonism to opportunistic human pathogens, the degradation of isothiocyanates from cruciferous vegetables, and the breakdown of plant fibres. In the gut, these microbes are linked to reduced inflammation, improved metabolic health, and enhanced nutrient absorption.

However, the plant microbiome also presents food safety considerations. While most plant-associated microbes are harmless or beneficial, fruits and vegetables can occasionally carry opportunistic or pathogenic species such as *Salmonella*, *Listeria monocytogenes*, and *Escherichia coli*. Additionally, antimicrobial resistance genes ARGs have been identified in plant-associated microbes, e.g., in connection with sale and postharvest conditions. Therefore, maintaining food safety monitoring is essential, alongside a balanced view of the largely beneficial role of these microbial communities.

Ultimately, the edible plant microbiome connects environmental microbiomes and human health. As our understanding evolves, the plant microbiome emerges as a potential tool for dietary innovation, probiotic development, and strategies to improve both personal and One health.

[O 26] Assessment of nutrient bioavailability and functional food properties in microalgae-fortified mixed rye bread

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Microalgae are rich in both macro- and micronutrients a well as bioactive compounds such as polyunsaturated fatty acids (PUFA) and pigments. In conjunction with the potential for environmentally sustainable production, their use in food formulations such as fortified bread is of high interest. However, impact of microalgae fortification on dough and bread quality as well as nutritional properties largely depends on the employed strains and culture conditions.

In this work, the incorporation of microalgae biomass into traditional mixed rye bread to enhance nutritional value and functional properties was addressed. Two strains of autotrophic *Chlorella vulgaris* and one heterotrophic strain of *Parachlorella kessleri* were grown under optimized conditions and incorporated at 1 and 3% (w/w) into the dough formulations after lyophilization. Texture analysis and multispectral imaging were used to evaluate impact on processing parameters, while volatile compounds in crumb and crust were analyzed by Headspace-SPME-GC-MS analysis. PUFA and lutein content of the biomass and the baked bread were analyzed by means of GC-MS and HPLC-DAD, respectively. Intestinal cellular uptake assays using differentiated Caco-2 cells were performed as proxy to gauge bioavailability of lutein and PUFA.

While processing parameters were scarcely affected by microalgae addition, distinct volatile profiles were found for each bread variant, which were mainly related to xanthophyll and lipid degradation products. Despite a lower initial lutein content, stability during the baking process was higher in breads incorporating the heterotrophic strain than in the autotrophic strains. Relative intestinal cellular uptake of PUFA was more efficient in all microalgae strains than the control condition using linseed oil, while bioavailability of lutein was comparable among the conditions.

Overall, this work provides an elaborate framework for the selection of microalgae strains to improve the nutritional value of traditional mixed rye bread. However, impact of sensory characteristics on consumer acceptance needs to be further evaluated.

[O 27] Physico-Chemical Characterization in Modern Food Analysis

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Global Market Development Manager – Anton Paar GmbH

Modern food systems are increasingly complex multi-phase matrices whose quality, stability, and safety depend on subtle structural and physicochemical parameters. Traditional compositional analysis alone is often insufficient to explain changes in texture, stability, oxidation behavior, and processing performance. Therefore, complementary physico-chemical techniques are required to provide deeper mechanistic understanding.

This presentation outlines an integrated analytical approach for modern food analysis, combining thermal analysis, rheological profiling, particle size characterization, density measurement, and accelerated oxidation testing. Differential scanning calorimetry enables identification of phase transitions such as lipid melting, protein denaturation, and crystallization phenomena that directly affect texture and shelf stability. Rheometry provides quantitative insight into viscoelastic properties and structure development under thermo-mechanical stress. Particle size distribution and zeta potential measurements allow evaluation of colloidal stability, sedimentation behavior, and emulsion integrity. Accelerated oxidation analysis supports rapid assessment of lipid stability and matrix protection effects.

Selected application examples from lipid systems, protein-based matrices, emulsions, and powdered foods demonstrate how these complementary physico-chemical parameters contribute to food quality evaluation, process understanding, and stability prediction. By correlating thermal transitions, mechanical behavior, microstructure, and oxidation kinetics, this multimodal framework strengthens analytical capabilities in food chemistry and supports both research and regulatory quality control environments.

[O 28] 10 YEARS EU NOVEL FOOD REGULATION – A REASON TO CELEBRATE?

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10 years ago, the revised EU Novel Food Regulation [1] (the "Regulation") entered into force. Back then, the European Commission promised that the new Regulation would improve conditions so that food businesses can easily bring new and innovative foods to the EU market, while maintaining a high level of food safety for European consumers. The EU Novel Food Regulation's anniversary is a good opportunity to assess whether the Regulation has met these promises.

The key elements of the Regulation include definitions including, most importantly, one for Novel Foods, procedures for the determination of novel food status, for authorising the placing on the market within the EU of a novel food, for notifications of traditional foods from third countries, for authorisation procedures in case of data protection or based on protected proprietary scientific evidence or scientific data, as well as for the authorisation in case of a parallel application for the authorisation of a health claim.

To help food businesses determine whether a food product is novel and requires authorisation in the EU, the European Commission created the EU Novel Food Status Catalogue. This catalogue is a non-binding, non-exhaustive and advisory guide, which is maintained by the European Commission. It serves as an indicator of whether a food is novel under the Regulation, based on input from EU Member States. It is a living document that is regularly updated based on new information. One of its main limitations is that it is not exhaustive, and individual Member States may still have specific national legislation

restricting the marketing of certain foods.

Experience over the last 10 years shows that the process for authorizing novel foods in the EU usually takes too long, with a minimum of two to three years. The data requirements for new authorisations are very high, particularly for SMEs, and are hardly affordable due to the significant time and cost involved, as well as the uncertain outcome. The European Food Safety Authority's strict risk assessment process exacerbates these issues, ultimately having a negative impact on the innovation and competitiveness of European industry.

The ever-growing number of authorisations and changes to their scope and specifications within the scope of the Regulation complicates the regulatory assessment of products. It would be helpful to reintroduce the concept of substantial equivalence, which was included in the old Novel Food Regulation [3] but not carried over into the new Regulation.

1) Regulation (EU) 2015/2283 of the European Parliament and of the Council of 25 November 2015 on novel foods, amending Regulation (EU) No 1169/2011 of the European Parliament and of the Council and repealing Regulation (EC) No 258/97 of the European Parliament and of the Council and Commission Regulation (EC) No 1852/2001, *Official Journal of the European Union* L 327 of 11 December 2015
2) https://ec.europa.eu/food/food-feed-portal/screen/novel-food-catalogue/search
3) Regulation (EC) No 258/97 of the European Parliament and of the Council of 27 January 1997 concerning novel foods and novel food ingredients, *Official Journal of the European Union* L 043 of 14 February 1997

[O 29] Dried Milk Spots: A new approach for assessing food contaminants in mothers and their infants

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Peter B. Czedik-Eysenberg Lecture 2026

Human health is affected by a variety of exposures from conception onward. For monitoring early-life exposure, human breast milk represents a particularly suitable matrix, as it is the primary source of nutrition for newborns. Previous studies have demonstrated the presence of numerous food- and environment-related contaminants in breast milk, likely originating from diet, air, or lifestyle-related products. As an alternative to the analysis of liquid breast milk, dried milk spots (DMS) offer a promising approach for monitoring chemical residues relevant for infant food safety. DMS require only small sample volumes and offer advantages for collection, transport, storage, and analyte stability. In addi-tion, emerging microsampling techniques such as volumetric absorptive microsampling (VAMS) ad-dress limitations regarding quantitative analysis. This contribution presents the optimization of a sam-ple preparation protocol for the analysis of 216 xenobiotics using an LC-MS/MS workflow to evaluate the suitability of dried breast milk spots. Furthermore, compound stability was assessed, and Mitra VAMS were compared with the introduced DMS approach.

DMS were prepared by adding spiked human breast milk onto Whatman 903 Protein Saver cards, with additional DMS generated from NIST standard reference material (SRM 1954) for benchmarking. Whole spots were extracted and two extraction solvents were evaluated, showing comparable performance. Approximately 50% of analytes exhibited matrix effects within predefined limits (60-140%), while nearly 80% met extraction recovery criteria (42-134%). In a proof-of-principle experiment, contaminant levels were compared between pooled human breast milk samples from Austria and SRM 1954 from the United States. In total, 30 analytes were detected in SRM 1954, of which 22 were also present in the Austrian samples, including food safety-relevant contaminants such as phthalates, bisphenols, per- and polyfluoroalkyl substances (PFOA and PFOS), parabens, and pharmaceuticals (acetaminophen and fluconazole), but also bioactive substances like isoflavones (daidzein and genistein). The stability assessment demonstrated that most analytes remained stable under common storage conditions, particularly at -20 °C. In addition, the performance of DMS was compared with that of Mitra VAMS. Both sampling approaches showed comparable results with respect to the number of detected analytes, signal suppression/enhancement, and recovery rates. Differences between the two methods were primarily attributed to variations in background contamination.

This study shows that DMS are a promising option for assessing food contaminants and other environmental/industrial toxicants, with acceptable recovery, matrix effects, and stability. In addition, Mitra tips offer a simpler quantitative approach regarding at-home sampling and large-scale studies.

[O 30] Comprehensive Analysis of Oxidative Stability and Nutritional Values of Germinated Linseed and Sunflower Seed Oil

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Peter B. Czedik-Eysenberg Lecture 2026

Cold-pressed vegetable oils are highly valued for their nutritional quality but are often limited by their susceptibility to oxidative degradation. In this study, seed germination was investigated as a natural pre-processing strategy to improve the compositional and oxidative stability of oils derived from linseeds and sunflower seeds. Oils obtained from germinated seeds were compared with conventional cold-pressed oils using a comprehensive analytical approach including LC-MS, GC-MS, HPLC, NMR and oxidative stability assays. Germination markedly enhanced the antioxidant composition of the oils, leading to strong increases in polyphenols, tocopherols, chlorophylls and carotenoids. In particular, polyphenol concentrations increased up to 37-fold in linseed oil and 12-fold, accompanied by the identification of numerous previously undetected phenolic compounds. These compositional changes were associated with improved oxidative stability, including reduced peroxide values and significantly prolonged oxidative induction times in Rancimat analysis. Shelf-life predictions indicated a four-fold increase for linseed oil from germinated seeds. The results demonstrated that controlled germination represents a sustainable approach to enhance the nutritional quality and stability of PUFA-rich oils without the need for additives.

[O 31] Getting Published in 2026 and Beyond: How to adapt to a rapidly changing publication landscape

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The speaker outlines Wiley's global publishing activities and introduces the Wiley Transformational Agreement with Austria (KEMÖ). This Transformational Agreement enables researchers at Austrian institutions to publish Open Access in more than 1,940 Wiley journals, provided the corresponding author is affiliated with an institution that is member of KEMÖ. The agreement simplifies workflows, covers Open Access fees, and increases the visibility of research.

The presentation underscores the impact of Open Access, showing that openly accessible articles achieve substantially more views, citations, and attention. It then summarizes the role of editors, who manage peer review, journal development, production, and community engagement. Success relies on sound judgment, integrity, and clear communication.

Editorial decisions focus on scope fit, scientific coherence, data quality, and writing. The publication process—from screening to acceptance—is designed to identify strong manuscripts efficiently, with journal transfers offered as a supportive alternative. Plagiarism is assessed contextually, distinguishing between minor text overlap and misconduct. Authors may appeal decisions if they provide strong, objective scientific arguments.

To improve writing, the speaker recommends the KISS principle, emphasizing clarity and brevity. Titles should be precise and accessible; abstracts must convey the core message quickly. Given modern reading habits dominated by scanning and short attention spans, manuscripts require clear structure and visual accessibility.

The section on AI highlights its benefits and limitations. It reinforces COPE's guidance that AI cannot be listed as an author and that any use must be transparently disclosed following the LOCAD framework. The talk concludes by stressing that successful publishing depends on reader-oriented writing, responsible use of tools, and constructive collaboration between authors and editors.

[O 32] Next-Generation Frying Oils: From Optimized Plant Oils to Novel Insect Lipids

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Deep-frying accelerates lipid oxidation, hydrolysis, and polymerization, leading to compromised oil quality. While refined oils often lack protective minor constituents, cold-pressed oils contain higher antioxidant levels but are not heat-stable. This presentation outlines two strategies to enhance frying oil stability and functionality.

The first strategy focuses on improving the heat stability of cold-pressed high-oleic (HO) plant oils through green extraction technologies. Optimized HO sunflower oil (OHOSO) was produced using press-cake-based enrichment to selectively increase antioxidant levels. Green extraction increased polyphenols in OHOSO by 50% and enhanced antioxidant capacity, resulting in the highest oxidative stability in the Rancimat test. During a three-day frying trial at 150°C, OHOSO formed 33% fewer polar compounds and reduced hydrolytic and polymeric degradation products compared to refined sunflower oil, indicating improved performance under thermal stress.

The second strategy explores insect oils as a novel animal-based lipid source with potential sustainability advantages over conventional animal fats. A comparative analysis of the lipid profile and frying stability of cold-pressed and refined oil from black soldier larvae (*Hermetia illucens*) and refined sunflower oil was performed. The insect oils exhibited a 2.5-3.0-fold higher total phospholipid content than sunflower oil, with a more than 100 -fold and 44-fold enrichment in phosphatidylserine (PS) and phosphatidylglycerol (PG), respectively. During deep-frying, PG and PS in sunflower oil were significantly degraded by 94.6% and 90.4%, respectively, while phospholipids in cold-pressed insect oil demonstrated enhanced heat stability.

In conclusion, the utilization of optimized HO sunflower and insect oils represent two promising alternatives towards more heat-stable, sustainable, and bioactive frying oils.

[P 01] Neo-formed Contaminants in Coffee and Coffee Substitutes

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Coffee is one of the most widely consumed beverages worldwide and owes its popularity not only to its stimulating effects, but also to the complex aroma profile that develops during roasting. During recent years, coffee-substitutes such as 'lupin coffee' as a sustainable alternative to coffee have gained increasing popularity. In addition to the formation of the desired coffee flavor, the thermal reactions responsible for creating characteristic coffee flavor may also lead to the formation of neo-formed contaminants (NFCs) with potential health implications, such as acrylamide and furan derivatives including furaneol, 5-hydroxymehtylfurfural (HMF), and alkylated furans. These thermal-process contaminants primarily arise from the Maillard reaction, but – as for furan derivatives – also from the degradation of ascorbic acid, carbohydrates, and amino acids, as well as from lipid oxidation, particularly from polyunsaturated fatty acids (PUFAs) as precursors. Although several NFCs are considered potentially carcinogenic to humans, regulatory guidance remains limited, with benchmark levels defined only for acrylamide, whereas no thresholds have yet been established for furan derivatives.

Achieving an optimal balance between sensory quality and the reduction of thermally induced contaminants therefore represents a central challenge during processing of coffee and coffee substitutes. This contribution provides an overview of current knowledge on NFC formation in coffee and substitutes, with emphasis on key formation pathways, analytical approaches, and challenges in process optimization. Understanding these mechanisms is crucial for developing processing strategies that minimize contaminant levels while maintaining sensory quality, and thus forms the basis for future experimental investigations in this field.

Keywords: coffee; coffee-substitutes; neo-formed contaminants; acrylamide; furan derivatives

[P 02] Enhancing Nutritional Quality and Oxidative Stability of Black Cumin Seed Oil through Green Extraction and Roasting

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Black cumin oil contains many bioactive substances that promote health, particularly terpenes like thymoquinone (TQ). This study investigates an oil-assisted green extraction process, where the press cake is valorized, to enhance the oxidative stability of cumin oil from Egyptian (E) and Austrian (AT) origins. Chlorophyll and Carotenoid content was measured by UV-Vis spectroscopy and increased significantly by 45.56 ± 22.66 % and 15.72 ± 4.75 %, respectively, in optimized AT oil. α-Tocopherol content measured with HPLC-UV was also significantly raised by 46.75 ± 9.67 % in optimized AT oil. The ABTS assay indicated that optimization led to a significant increase in antioxidant capacity in both AT and E oils. Peroxide value decreased significantly from 9.56 ± 0.36 meq O_2/kg fat to 3.98 ± 0.13 meq O_2/kg fat in AT oil and from 10.66 ± 0.71 meq O_2/kg fat to 2.04 ± 0.22 meq O_2/kg fat in E oil after green extraction. Optimization increased acid value in both oils, possibly due to lipase activity. This effect was abolished by roasting the seeds before pressing and green extraction, decreasing the acid value before optimization by 63.63 ± 1.24 % and 79.06 ± 0.28 % in AT and E oils respectively. Similarly, the peroxide value decreased significantly in conventional oil from roasted seeds by 56.71 ± 1.65 % (AT) and 69.13 ± 2.10 % (E). Despite optimization in an open system, the GC-MS determined TQ content remained unaffected. These results demonstrate oil-assisted green extraction can positively affect antioxidant content and oxidative stability in black cumin seed oil while retaining a high TQ concentration, potentially enhancing shelf-life and nutraceutical value. Utilizing oil from roasted seeds effectively prevents the increase in acid values and decreases peroxide values during optimization.

Keywords: Green extraction, Oxidative stability, Antioxidant capacity, Acid value, Shelf-life, Valorization

[P 03] Do Coffee Substitutes Smell Like Coffee? Molecular and Sensory Insights

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Coffee belongs to the most popular hot drinks worldwide. However, climate change shows significant impact on coffee cultivation leading to a steady coffee price increase. This – together with an increasing awareness for sustainable foods – leads to an increased market share of coffee substitutes produced from domestic raw materials. In this study, we investigated the flavour properties of common commercially available coffee substitutes with respect to their volatile compounds and flavour properties.

Coffee substitutes produced from lupin seed, figs, chicoree and dandelion were investigated with instrumental as well as sensory methods. The volatilome of the ground products was analysed by HS-SPME GC-MS. Analysis of the sensory properties of French press infusions was performed by trained panellists and the use of Check-All-That-Apply (CATA). Multivariate statistical data treatment was applied to correlate the data and to compare the products with respect to their volatiles and the sensory properties.

The results of this study revealed significant differences between the investigated coffee substitutes in their sensory properties, but also in the composition of the volatiles. High similarities were found for dandelion and chicoree 'coffee' – both of them were dominated by ashy, dusty and also fermented, vegetable-like aroma, while flavour reminding of dried fruits and honey play an important role in fig 'coffee'. Lupin 'coffee' shows highest similarities to coffee, which is also reflected by a high number of alkylated pyrazines being responsible for the roasted, coffee-like notes of this product.

These results show that new and innovative products such as lupin 'coffee' are interesting alternatives to coffee, while the traditionally used coffee substitutes neither remind of coffee flavour nor show similarities to coffee in the composition of the volatilome.

[P 04] Quantification of minerals and metals in honey from Upper Austria and Styria using ICP-OES and ICP-MS

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In this study, the content of minerals, metals and non-metals in nine honey samples from Upper Austria and Styria was determined using ICP-OES (Al, Ca, K, Mg, Mn, P, S, Zn) and ICP-MS (B, Ba, Co, Cr, Cu, Fe, Li, Mo, Ni, Pb, Sr, Ti). Undesirable substances such as toxic metals and metalloids can also be present in honey, which is why the analysis is relevant for food safety and environmental protection.

A uniform type of honey (blossom honey) was used to ensure better comparability between the samples. Two samples deviate slightly from this criterion (1 x blend of blossom and honeydew honey, 1 x lime blossom honey). A significant part of the work involved optimizing the sample digestion procedure. During the development of the method, the influence of the acid in microwave-assisted digestion (HNO_3 vs. HNO_3 + HCl) and the amount of sample (0.3 g vs. 0.5 g) were investigated. In addition, sample preparation by mere pre-reaction, that is reacting the sample with nitric acid but without microwave-assisted digestion, was evaluated. The residual carbon content after digestion was employed as criterion for sample mineralization effectivity. Moreover, spike recovery tests were carried out to evaluate the accuracy.

Honey is a valuable source of minerals, with potassium being the most important element in terms of quantity (g/kg range). In the analysed samples, potassium accounts for approximately 81 % to 93 % of the total minerals. After potassium, the elements calcium, magnesium, phosphorus and sulphur have the next highest contents (mg/kg range). Trace elements essential for humans such as Co, Ni, Cu and Zn were detected in the µg/kg range, Fe and Mn were present in the single-digit mg/kg range. The total mineral content range is between 0.09 % and 0.29 %. The highest mineral content was found in a blend of blossom and honeydew honey.

Differences between the two federal states were statistically tested using a t-test ($\alpha = 0.10$). Regional differences were found for the elements potassium, magnesium and sulphur. However, due to the small number of samples, this can only be considered a trend.

The analysis of toxic metals and metalloids did not reveal any significant contamination in the samples.

[P 05] Application of PCR-based high-resolution melting analysis for apple DNA detection in commercial juices and smoothies

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Apple is frequently incorporated into mixed fruit juices and smoothies because of its mild, neutral flavor, natural sweetness, and low production costs associated with its easy cultivation and processing. The use of relatively inexpensive apple juice as a major component in mixed fruit beverages without explicit labeling, a practice known as applejuicification, [1] is frequently observed in commercial products.

To investigate this issue, a selective PCR-based high-resolution melting (HRM) method was applied for the detection of apple DNA in commercial juice and smoothie products. As a first step, several DNA extraction approaches were systematically evaluated and optimized for processed apple juice matrices. Among the tested commercial kits, the DNeasy mericon Food Kit demonstrated higher DNA extraction efficiency than the NucleoSpin Plant II kit. In addition, centrifugation parameters, including sample amount, duration, and speed, as well as the concentration of polyvinylpyrrolidone (PVP), were optimized to reduce inhibitory effects caused by polyphenolic compounds.

PCR and HRM analysis was performed using the primer pair Hi02f12, which produced amplicons with a characteristic melting profile specific to apple DNA and independent of apple cultivar. [2][3] The investigated sample set comprised twelve commercial apple juices, five blended juices containing apple, eight smoothies, and three model smoothie matrices representing red, yellow, and green formulations based on different fruit combinations.

Apple DNA was successfully detected in the majority of cloudy samples, with a detection limit of approximately 1.4% apple content in model smoothies. Furthermore, the effect of thermal processing was assessed by subjecting model smoothies to heat treatment at 85 °C for 5, 10, and 15 minutes. Although increased heating time led to enhanced DNA degradation and reduced detection sensitivity, apple DNA remained detectable even after thermal treatment, indicating the applicability of the method to processed smoothie products.

In contrast, DNA extraction proved challenging for clear juices and certain smoothies derived from clear juice bases, where DNA concentrations were extremely low. In these cases, freeze-drying did not significantly improve detectability. Despite these limitations, PCR-based HRM analysis exhibited high sensitivity and selectivity for apple DNA detection in most processed beverage matrices.

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[P 06] Discrimination of North Macedonian grape cultivars (Vitis vinifera L.) targeting simple sequence repeats (SSRs) using high-resolution melting (HRM) analysis

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Viticulture and wine production have a long-standing tradition in the Republic of North Macedonia and represent an important pillar of the country´s agricultural sector. To ensure grapevine authenticity, which is essential for fraud prevention, traceability, and consumer protection, reliable methods for accurate cultivar identification are required. Capillary electrophoresis based on simple sequence repeat (SSR) analysis is commonly used for this purpose; however, it is time-consuming and costly [1].

This study investigated the suitability of nine SSR markers recommended by the Organisation Internationale de la Vigne et du Vin (OIV) for differentiating eleven grape cultivars commonly grown in North Macedonia using PCR followed by high-resolution melting (HRM) analysis [2]. Genomic DNA was extracted from grape leaf samples of the cultivars Vranac, Prokupec, Stanušina, Plovdina, Temjanika, Smederevka, Rkatsiteli, Cardinal, Muscat Hamburg, Afus Ali, and Muscat Italia, and analyzed by PCR followed by HRM analysis. Among the markers evaluated, assays targeting VrZAG62 and VrZAG79 exhibited the highest discriminatory power, enabling the differentiation of 50 and 53 out of 55 cultivar pairs, respectively. In addition, preliminary experiments hinted at an enhanced discriminatory power by using multiplex assays for PCR-HRM. The high complexity of the resulting melt curves was influenced by both the number of repeats and the base composition. PCR-HRM thus represents a cost-effective and rapid screening tool for grapevine cultivar differentiation.

Keywords: Vitis vinifera, cultivar discrimination, SSRs, high-resolution melting, DNA, leaves

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[P 07] Enrichment of Catechin in Extracts from Aronia Pomace by NADES-Based Ultrasound-Assisted Green Extraction

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Catechin-rich extracts are in high demand for applications in functional foods, nutraceuticals, and cosmetic formulations due to their antioxidant and bioactive properties. However, current commercial catechin sources are mainly derived from green tea, cocoa, or grape seeds and are often limited by caffeine content, high fat matrices, intensive processing, or the use of organic solvents. Therefore, there is a clear need for a green, sustainable, and clean-label catechin-rich extract from alternative sources. Aronia pomace is a valuable by-product of aronia fruit juice production, and a promising alternative source of catechin to commercial sources. This study investigates the ultrasound-assisted extraction (UAE) of catechin from aronia (Aronia melonacarpa) pomace using different types of Natural Deep Eutectic Solvents (NADESs). Choline chloride (ChCl)-based NADESs combined with various hydrogen bond donors including citric acid, malic acid, tartaric acid, and oxalic acid, at molar ratios 1:1, were used as green solvents. Extracts were evaluated in terms of total phenolic content (TPC), antioxidant activity, phenolic profile, catechin content, and catechin enrichment ratio. UAE was performed by using ultrasonic probe-type homogenizer at an ultrasonic power of 100W for 3 min. Conventional extraction was carried out with methanol at 65°C for 30 min. ChCl:oxalic acid resulted in the highest TPC (1383.37 mg GAE/100 g dry matter) among the NADESs, approaching that of the conventional extract (1410.71 mg GAE/100 g dry matter). Although the higher viscosity of NADES can limit mass transfer, ultrasonication enhanced mass transfer. The antioxidant activity of NADES-based extracts ranged between 40.41 and 50.73 % DPPH radical scavenging inhibition and were found to be lower than methanol-based extract (77.41 %). Despite lower antioxidant activity, NADES-assisted UAE enriched extraction of catechin, a phenolic compound highly relevant for food and health applications. Major phenolic compounds in aronia pomace extracts were catechin, quercetin, and p-coumaric acid. Considerably high catechin contents (400.38 and 397.34 mg/100 g dry matter) in citric acid- and oxalic acid-based NADES indicated a markedly enhanced catechin extraction with highly polar NADESs compared to methanol extraction (306.7 mg/100 g dry matter). Catechin yield in NADES extract increased by 30% compared to conventional extraction. Citric acid–based NADES exhibited highest catechin enrichment ratio (ER=1.31) and the lowest ER as 0.94 was determined in tartaric acid-based NADES. The catechin enrichment ratios (>1) of citric acid and oxalic acid–based NADES indicate a greater enrichment of catechin extraction by ultrasound process and aronia pomace represents a novel and sustainable catechin source, providing a high catechin yield from an underutilized by-product.

Keywords: aronia pomace, ecofriendly extraction, catechin recovery, deep eutectic solvents, sustainability

[P 08] Metabolic Fate of *Alternaria* Mycotoxins and Toxicological Characterization of the Produced Metabolic Mixtures

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Alternaria fungi produce a wide range of secondary metabolites, some of which act as mycotoxins and occur ubiquitously in food, thus posing a risk to human health. The most relevant *Alternaria* toxins include the dibenzo-α-pyrones alternariol (AOH), alternariol monomethyl ether (AME), and altenuene (ALT), the perylene quinone altertoxin I (ATX-I), as well as miscellaneous structures, such as tentoxin (TEN), tenuazonic acid (TeA), and altersetin (AST). Numerous studies have shown that these compounds can exert adverse effects in mammalian cells, including cytotoxicity and immunomodulation. A crucial factor in this context is hepatic metabolism, since *Alternaria* toxins may undergo both phase I and phase II biotransformation. It remains unclear whether and to what extent hepatic metabolism alters the toxicological properties of *Alternaria* mycotoxins and which specific metabolites are responsible for potentially remaining effects. This knowledge gap limits a comprehensive toxicological evaluation and requires systematic investigation.

A former study of our research group investigated how metabolic conversion influences the immunomodulatory properties of the *Alternaria* mycotoxins mentioned above. The current project builds upon the existing toxicity results and aims to explain the observed alterations in immunomodulation with changes in the composition of the metabolic mixture. Particular focus is laid on identifying which metabolites are formed during phase I biotransformation, as well as phase II sulfation and glucuronidation processes. Using liquid chromatography coupled to tandem mass spectrometry (LC–MS/MS), parent compounds and their metabolites are quantified to characterize metabolic profiles.

For example, glucuronidation led to a pronounced decrease of the initial AOH concentration (10 µM), the parent toxin level falling below the lower limit of quantification (< LLOQ) after 2 h of incubation with rat liver S9 fractions. These analytical findings are consistent with results obtained from the NF-κB reporter gene assay on THP1-Lucia™ monocytes. In this system, the glucuronidated AOH mixture exhibited strongly diminished anti-inflammatory effects compared to the parent compound, indicating a loss of immunomodulatory activity upon metabolic conversion.

By combining the analytical detection and characterization of *Alternaria* metabolites with cell culture–based assays, this work links chemically defined metabolites to their immunomodulatory effects in cellular systems. This integrated approach provides a more comprehensive evaluation of *Alternaria* toxins and contributes to a deeper understanding of their biological relevance.

[P 09] Development and Validation of a DNA Metabarcoding Approach for Bivalve Authentication in Processed Foods

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Food fraud has become an increasing concern [1], as global food systems face pressures from various events, such as the COVID-19 pandemic and the cost-of-living crisis [2]. The seafood sector is particularly vulnerable because of its complex and opaque supply chains [3] and high commercial value [4]. Within this sector, bivalves account for a substantial share of global aquaculture production and trade and are therefore susceptible to fraudulent practices, as documented in previous studies [5].
Seafood labeling is regulated at the EU level by Regulations (EU) No. 1169/2011 and No. 1379/2013 [6,7] as well as nationally by the *Codex Alimentarius Austriacus* [8]. Correct labeling is essential for both food authenticity and consumer safety, as molluscs are recognized food allergens. Although global bivalve production is dominated by relatively few taxa, these belong to multiple taxonomic families, necessitating untargeted analytical methods with broad taxonomic coverage for official food control.
DNA-based methods are widely used for species authentication, including endpoint real-time polymerase chain reaction (PCR) techniques (qPCR), and DNA barcoding. However, most existing approaches target single bivalve families [9-11]. There is currently no validated method combining multi-family coverage and short barcodes suitable for authentication of bivalves in processed foods.
DNA metabarcoding, which integrates DNA barcoding with next-generation sequencing (NGS), enables massive parallel sequencing and untargeted species screening in mixed or processed food samples. In this study, the mitochondrial 16S rDNA marker was selected due to its high conservation and suitability for short minibarcodes (100–300 bp), allowing compatibility with established in-house metabarcoding workflows.
This study presents the first validated DNA metabarcoding method with broad taxonomic coverage for bivalves, enabling genus- and species-level identification across seven families (Ostreidae, Pectinidae, Mytilidae, Pharidae, Veneridae, Glycymerididae, and Cardiidae) in diverse food matrices. This method employs two PCR assays, a singleplex and a duplex, to amplify mitochondrial 16S rDNA fragments (160–203 bp). Validation using reference materials, model foods, DNA mixtures, and 70 commercial products demonstrated reliable detection of low-level components (0.008–0.014% w/w) and simultaneous species identification. Overall, 29% of products were found to be mislabeled, with scallops being the most frequently affected, underscoring the method's suitability for detecting species substitution and adulteration as well as supporting compliance with current EU labeling regulations.

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[P 10] Recycled Plastics and Food Safety: Insights from Analytical Characterization

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The increasing incorporation of post-consumer recycled (PCR) plastics into packaging is a key element of the European Union's circular economy strategy. According to Regulation (EU) 2025/40, a minimum recycling content of 10% is mandatory by 2030 for non-PET packaging in contact-sensitive applications such as food packaging [1].

In contrast to PET, the current availability and quality of recycled polyolefins suitable for food-contact is insufficient to meet these targets. This problem is addressed in Regulation 2022/1616, which establishes a regulatory framework for recycled plastic materials intended for food contact. Under this framework, products produced by new recycling technologies may be placed on the market prior to a final authorization by the European Food Safety Authority (EFSA), under the condition that a comprehensive safety documentation is provided. This includes contaminant characterization in input and output materials, assessment of decontamination efficiencies and initial batch-to-batch monitoring of contamination levels. Moreover, compliance of the materials with Regulations (EC) 1935/2004 and (EU) 10/2011 has to be ensured [2]. Due to the lack of harmonized analytical methods, the generation of this data remains challenging.

This work addresses these regulatory requirements by systematically characterizing PCR polyolefins, including HDPE, LDPE and PP. Solid-phase microextraction, solvent-based extraction and migration experiments are coupled with advanced chromatographic techniques, including GC-FID, GC-MS, GC-ECD, GC×GC-ToFMS, as well as LC-MS/MS. This approach enables both targeted quantification and non-targeted screening of a broad range of substance classes. In parallel, a genotoxicity screening using the Ames MPF test is performed, with particular emphasis on identifying correlations between positive genotoxic responses and specific substance classes detected in the materials.

The generated data support the development of a centralized contaminant database for post-consumer recycled plastics. This forms the basis for an automated, risk-based evaluation concept that aims to support regulatory decision-making and the safe implementation of novel recycling technologies.

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[P 11] Anti-Inflammatory, Antioxidant Activity, and Fatty Acid Profiling of Monodora Myristica Seed Oil using (ATR) FT-IR Spectroscopy

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The demonstrated health benefits associated with plant oil consumption, including their role as sources of dietary energy, essential fatty acids, and bioactive compounds with anti-inflammatory and antioxidant properties, have driven increased demand. This has spurred research into underutilized plant seed oils with historical ethnobotanical or archeological evidence of nutritional and medicinal use. In the pursuit of alternative sources of high-quality vegetable oils for nutraceutical and pharmaceutical applications, this study characterized *Monodora myristica* seed oil. Specifically, its anti-inflammatory activity was evaluated using the carrageenan-induced paw edema model in rodents, while its antioxidant potential was assessed through 2,2-diphenyl-1-picrylhydrazyl (DPPH) radical scavenging assays and total antioxidant capacity via the phosphomolybdenum (PM) method. The fatty acid profile was determined using Attenuated Total Reflectance Fourier-Transform Infrared (ATR-FT-IR) Spectroscopy. The results indicate that Monodora myristica seed oil possesses significant antioxidant and anti-inflammatory activities, demonstrating efficacy comparable to standard reference compounds (ascorbic acid, diclofenac, and dexamethasone). This suggests its potential as a natural source of these bioactive agents. ATR-FT-IR spectroscopic analysis revealed a fatty acid composition of 24.1% saturated and 75.9% unsaturated fatty acids, supporting its classification as a high-quality oil.

Keywords: Anti-inflammatory, Antioxidant, *Monodora myristica*, High-quality oil.

[P 12] Flavour Development in New Pear Cultivars in the Course of Postharvest Ripening

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Climate change poses enormous challenges for the domestic fruit cultivation. Hot and dry vegetation periods do not only shift the time windows for blooming and harvesting but also lead to altered properties of the fruits. A careful selection of varieties that can cope with these demanding conditions is of great importance for fruit farmers, particularly for perennial plants, as a change in cultivar requires several years. New varieties need to be investigated with respect to their sensory properties and their development during postharvest ripening.

In this study, we investigated the formation of volatile/aroma-active compounds and the development of the sensory properties of 11 partially new pear cultivars after harvest; furthermore, the properties were re-evaluated after one month of postharvest ripening. The volatile compounds were analysed by headspace SPME-GC-MS to gain deep insight into the formation of odour active compounds during postharvest ripening with a focus on esters derived from saturated and unsaturated C10 acids. For the sensory evaluation, the Check-All-That-Apply (CATA) method using trained panellists was selected. For deeper insight into fruit development, CATA was divided into three sections, (i) ortho-nasal odour perception, (ii) taste and retro-nasal odour perception and (iii) perception of texture. Multivariate statistical data treatment was used to correlate the data from these different methods.

This comprehensive evaluation allows for a critical consideration of new pear cultivars for the cultivation in our region.

[P 13] Differentiation of 17 novel pear varieties by targeting microsatellites using PCR and high-resolution melting curve analysis

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Pears (*Pyrus* spp.) are known for their health-promoting benefits, including anti-inflammatory properties, and for providing essential nutrients such as dietary fibre and bioactive compounds like antioxidants. For these reasons, they are widely cultivated and valued for both their economic and nutritional importance and are consumed worldwide in fresh form as well as in processed products such as juices and jams [1,2].

Breeding programs aim to develop new pear cultivars with enhanced fruit quality and visual appeal, improved storage performance and shelf life, and increased resistance to pests and diseases. The aim of this study was to investigate whether newly developed pear cultivars sharing the same maternal and/or paternal parent could be distinguished by targeting microsatellite regions (simple sequence repeats, SSRs) using polymerase chain reaction (PCR) followed by high-resolution melting (HRM) analysis. To address this objective, 15 previously established primer sets were evaluated for their ability to differentiate among pear cultivars [3-5].

The study included 17 newly developed pear cultivars obtained through crosses between the maternal cultivars Abata, Fetel, Conference, Williams Christ, Dita, or Dicolor and the paternal cultivars Bunte Julibirne, Winterdechantsbirne, Forellenbirne, Dicolor, Carmen, Sanguinole, Fondante de Charneuses, Norma, Vereinsdechantsbirne, Winterdechantsbirne, or unidentified paternal cultivars. Genomic DNA was extracted from pear leaves using the NucleoSpin Plant II kit (Macherey-Nagel). The extracted DNA was amplified by PCR, and the resulting PCR products were subsequently analysed by HRM. Data evaluation was performed by comparing the melting curve profiles and their derivatives obtained for the novel pear cultivars with those of the corresponding maternal and paternal cultivars.

Using the SSR primer pair CH01f12, most pear cultivars could be successfully differentiated including those sharing the same maternal or paternal parent, although differentiation was not always possible for closely related cultivars. Overall, 91 % of the varities could be differentiated with this primer pair.

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[P 14] Application of Real-Time PCR and High-Resolution Melting for Authentication of Honey

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This study aimed to evaluate the potential of real-time PCR coupled with high-resolution melting (HRM) analysis for the authentication of various types of honey available in Austria and other European countries. Reliable determination of honey origin is of increasing importance due to frequent cases of mislabeling and food fraud. Our approach was based on the amplification of a polymorphic region of honey bee (*Apis mellifera*) DNA by real-time PCR, followed by the discrimination of subspecies based on differences in the melting behavior of the resulting amplicons. According to the literature, the presence of DNA from specific honey bee subspecies is associated with the geographic origin of honey. (1)(2)(3)

DNA was extracted from honey using the DNeasy mericon Food Kit (Qiagen), according to the manufacturer's instructions. As reference material, DNA was also extracted from honey bee specimens collected in Austria, North Macedonia, Croatia, and Bosnia and Herzegovina. Primer pairs for the amplification of honey bee DNA were selected from the literature and tested in silico. The BEE2 primer pair, originally designed by Honrado et al. (1), targets a region of the cytochrome oxidase I (COI) gene. This region contains several single nucleotide polymorphisms (SNPs), as confirmed by BLAST analysis, resulting in the generation of subspecies-specific amplicons that can be distinguished by HRM analysis (1).

By designing a novel primer BEE2_1, a shorter amplicon than previously reported in the literature was generated, thereby improving the resolution of HRM analysis. Pyrosequencing of the BEE2_1-derived amplicons enabled the assignment of specific melting profiles to the genotypes of distinct honey bee subspecies, thus validating the HRM-based discrimination approach. The method was applied to 56 honey samples from Austria and other European countries.

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[P 15] Determination of Chloramphenicol Residues in Shrimp Products using LC-MS/MS

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Chloramphenicol is a broad-spectrum antibiotic used for treatment and prophylaxis in aquaculture worldwide. Therefore, residues are detected in aquaculture products, e.g. in shrimps imported from Southeast Asia. On the downside, chloramphenicol impacts both the environment and human health. Antibiotic residues in food can lead to the development of drug resistance, hypersensitivity, and aplastic anemia. The European Medicines Agency concluded that acceptable daily intake (ADI) for chloramphenicol cannot be established, and a maximum residue limit (MRL) cannot be calculated. This means zero tolerance for chloramphenicol residues in food, and thus, it has been banned from food production in the European Union. From an analytical point of view, chloramphenicol has a known tendency to cause carry-over effects and strict adherence to good laboratory practices are required.
Within an ASEA-UNINET (European Academic University Network) cooperation project between vetmeduni Vienna and Khon Kaen University in Thailand, an LC-MS/MS method for the determination of chloramphenicol in shrimps was adapted. After homogenization of the samples, a subsample was spiked with the internal standard (d_5-chloramphenicol) and extracted multiple times with ethyl acetate. Following sample evaporation, a solid phase extraction (Strata X) was performed. For separation a Kinetex C18 column with a water-acetonitrile gradient was applied on a 1290 Infinity II UHPLC system (Agilent Technologies, USA). Detection was performed in multiple reaction monitoring mode on a QTRAP 6500+ (Sciex, Canada). In total 23 samples from Thailand and Austria were collected. While none of the wild shrimp samples were contaminated, seven farmed shrimp samples were classified as suspicious and one sample contained chloramphenicol above the limit of quantification (0.09 µg/L).
The study showed that although chloramphenicol is banned, it is still used in aquaculture facilities around the world.

This research project was supported by European Academic University Network (ASEA-UNINET)

[P 16] Herbivore-Induced Volatiles in Cowpea (Vigna unguiculata) Pods: Differential Emission in Response to Infestation by Riptortus dentipes and Nezara viridula

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Plants emit volatile organic compounds (VOCs) as a constitutive and induced defense mechanism against herbivorous insect pests. Cowpea (*Vigna unguiculata*), a vital crop providing rich dietary proteins, vitamins, and income for subsistence farmers, is highly susceptible to pod-sucking bugs, which can cause yield losses ranging from 30 to 70%. This study aimed to characterize and compare the chemical profile of headspace VOCs emitted by intact pods of the Padituya cowpea variety and those infested by two major pod-sucking bug species, *Riptortus dentipes* and *Nezara viridula*. Headspace volatiles were collected from three treatments: undamaged control pods, pods infested with *R. dentipes*, and pods infested with *N. viridula*. Each entrainment was conducted over a 96-hour period. The collected volatiles were analyzed using gas chromatography-mass spectrometry (GC-MS). Analysis revealed that undamaged cowpea pods emitted a blend of compounds including 1-octen-3-ol, 3-octanol, 2-nonanone, oleic acid, octadecanoic acid, and dodecanoic acid. Infestation by *R. dentipes* induced the emission of a distinct VOC profile, characterized by hexanoic acid, (E)-3-hexenoic acid, (E)-2-hexenyl hexanoate, 2-tridecanone, 1-(4-ethylphenyl)ethanone, and eicosanoic acid. Conversely, infestation by N. viridula induced the emission of 4-hydroxy-4-methyl-2-pentanone, 3-ethylbenzaldehyde, 1-(4-ethylphenyl)ethanone, and (E)-2-decenyl acetate. With the exception of the shared compound 1-(4-ethylphenyl)ethanone, the cowpea plant exhibited a differential volatile response, releasing distinct VOC blends specific to the attacking herbivore species. These identified semiochemicals represent promising candidates for synthesis and application in integrated pest management (IPM) strategies, such as push-pull systems or monitoring lures, to mitigate yield losses in cowpea production.

Keywords: Herbivore-induced plant volatiles, Gas chromatography-mass spectrometry, *Vigna unguiculata*

[P 17] Authentication of acacia, lime, and chestnut honey by plant DNA barcoding and NMR analysis

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Unifloral honeys, including acacia, lime, and chestnut honey, are defined by a predominant botanical origin and are associated with characteristic sensory and chemical properties. Due to their higher market value, reliable authentication of these honeys is essential for consumer protection. However, verification of botanical origin remains analytically challenging, particularly for honeys with low pollen content, where traditional approaches such as melissopalynology may yield ambiguous results.
In this study, DNA barcoding assays targeting fragments of chloroplast DNA were developed and evaluated for their suitability to identify the botanical origin of acacia, lime, and chestnut honey. Different DNA extraction strategies were compared, and a kit optimized for extracting cell-free DNA resulted in higher DNA yields. Primers targeting a fragment of the *rbcL* (ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit) gene containing multiple single nucleotide polymorphisms (SNPs) enabled amplification of plant DNA from honey samples. Subsequent pyrosequencing allowed differentiation of acacia, lime, and chestnut honey. The selectivity of the DNA barcoding approach was evaluated with respect to relevant forage plants.
Honey samples were also analyzed by nuclear magnetic resonance (NMR) spectroscopy, yielding chemical profiles reflecting the overall composition of the samples. The results demonstrate that DNA barcoding and NMR profiling are complementary tools for the authentication of unifloral honeys.

Keywords: unifloral honey, authentication, plant DNA barcoding, NMR spectroscopy, acacia honey, lime honey, chestnut honey

[P 18] INVESTIGATING COWPEA, VIGNA UNCUICULATA, RESPONSE TO DIFFERENT HERBIVORE FEEDING

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Cowpea, *Vigna unguiculata*, is an important crop in Ghana and provides an accessible source of protein. Crop yield is reduced by many biotic factors, especially the pod-borer Maruca vitrata that can cause up to 80% losses. When plants are damaged by herbivores, they release blends of volatile organic compounds (VOCs) referred to as Herbivore-Induced Plant Volatiles (HIPVs), which attract natural enemies and/ or deter herbivory attack. The induced VOCs can also be perceived by neighboring plants to activate their defensive mechanisms for possible attack. The signal provides the potential to deter pest attack and to increase predator populations around the crop. Understanding the role of these signaling compounds is important in the development of affordable pest management strategies for cowpea production on smallholder farms. We examined the volatile chemistry produced before and during herbivory, response to mechanical damage and also the specificity of the plant-insect interactions. VOCs were collected by air entrainment from Ghanaian cowpea cultivar plants that were challenged with *Maruca vitrata*, *Aphis craccivora*, *Latoia vivida* and *Myzus persicae* and induced signals compared to mechanically-damaged cowpea plants. In a behavior assay, *Apanteles taragamae* a larva parasitoid of Maruca vitrata was exposed to synthetic compounds induced *by M. vitrata* in a Y-tube olfactometer (behaviour) bioassay. Floral VOCs were also collected from an intact cowpea flowers and exposed to female *M. vitrata* in a GC-EAG bioassay. VOCs were collected using air entrainment and analysed using GC/GCMS.

Keywords: *Vigna unguiculata*, *Maruca vitrata*, Herbivore-induced plant volatiles, Natural enemies, Crop protection

[P 19] Histamine Degrading Enzymes for Biotechnological Applications

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Histamine is a biologically important biogenic amine and has emerged as an intensively investigated field, driven by its increasing relevance in biomedical diagnostics and food-safety monitoring. Food intolerances are estimated to affect at least 1 in 5 individuals and histamine intolerance in detail is associated with a wide range of nonspecific clinical symptoms [1]. In parallel, histamine serves as a critical indicator of food spoilage, particularly in protein-rich and fermented products, further underscoring the importance of robust detection strategies [2].
Enzyme-based approaches have attracted sustained interest due to their inherent specificity and compatibility with biotechnological applications. The enzymes most prominently studied to date include diamine oxidase (DAO), a group of histamine oxidases (HOD), and histamine dehydrogenase (HDH). These biocatalysts differ substantially in terms of reaction mechanism, cofactor dependence, substrate specificity, and operational stability, yet all have been characterized at the biochemical level and successfully produced in recombinant form. Current limitations are associated with enzyme production, stability, and integration into practical systems. Improvements in heterologous expression, protein engineering, and process design are therefore required to fully exploit their potential. While clinical applications, such as supplementation or diagnostic use, continue to be explored, enzyme-based histamine detection offers particularly strong prospects for biotechnological implementation, especially in food quality control and safety assessment, where robustness, scalability, and operational simplicity are critical.

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[P 20] Robustness and performance evaluation of a GC-HRMS workflow for exposomics

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The totality of environmental exposures across the lifespan of an individual is defined as the exposome. Because environmental factors are estimated to be responsible for up to 90% of overall chronic disease burden, the exposome is a major public health determinant. Among the large variety of environmental contaminants, exposure to persistent organic polluters (POPs) leads to particularly adverse health outcomes, with dietary intake constituting the dominant source. Although human exposure to POPs peaked in the 1970s, and they were banned globally under the Stockholm Convention in 2004, they remain a public health concern today due to their persistent nature. As shown in the 2015-2016 National Health and Nutrition Examination Survey (NHANES; n = 1989) DDT metabolites were detected in nearly all U.S. serum samples.

Here, we present a GC-HRMS workflow to quantify >100 environmental contaminants, especially POPs, in human plasma samples. The robustness and performance of the workflow were evaluated and refined. A quantification transition list was created using reference libraries, including the NIST library. Furthermore, the performance of different extraction solvents (isooctane, isohexane, cyclohexane, and hexane) was evaluated of which isooctane exhibited the best performance, yielding the highest average apparent recovery of 80%. The limits of quantification (LOQ) were estimated by the injection of matrix matched calibration curves. Of 107 analyzed analytes 102 exhibited LOQs ≤ 2 ng/mL. The robustness of the GC-HRMS workflow was assessed in 13 full acquisition sequences each analyzing 78 human plasma samples and three aliquots of the NIST standard reference material 1958 (Organic Contaminants in Fortified Human Serum Freeze-Dried), over a total of >1800 injections. Of the 38 analytes fortified in the SRM 1958, which overlapped with the analytes of the targeted method, 28 could be quantified. The RSD of the normalized area of the SRM 1958 remained <30%. Absolute and relative errors will be presented in the poster. The results demonstrate that the workflow provides low LOQs, underlining the sensitivity of the workflow. Further consistent results of the quantification of analytes fortified in the SRM 1958 with low RSD, confirm the robustness of the workflow.

[P 21] A novel extraction method for *Prymnesium parvum* toxins from whole algal cultures

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Aquacultures worldwide are threatened by harmful algal blooms (HABs) leading to massive fish kills. One of these HAB species is the haptophyte *Prymnesium parvum* which for example caused a massive fish killing event in the Odra/Oder River in Poland/Germany in summer 2022. The ichthyotoxins believed to be responsible are known as prymnesins (PRMs) and unlike other toxic algae are primarily retained in the biomass while release mechanisms are still unclear.
The detection of PRMs remains challenging due to a lack of analytical standards, stability issues, and losses in conventional extraction methods. Therefore, in a systematic approach we assessed the effects of ultrasonic treatment, freezing, and different media on PRM stability. Furthermore, the PRM recovery for the three most common extraction methods for microalgae was re-evaluated: solid-liquid extraction (SLE), liquid-liquid extraction (LLE) and solid-phase extraction (SPE). Finally, a novel method applying a 50% methanolic extract to the SPE was developed.
The results of the sonication experiments showed a negative impact of sonication in whole culture samples regarding the total PRM yield. Stability experiments over a whole week under cooled conditions revealed stable signals for the methanolic solutions while degradation in aqueous media occurred. The novel 50% methanolic extract SPE approach outperformed LLE and SLE. It offers advantages for saltwater samples through desalination and reduces PRM losses by eliminating reconstitution and evaporation steps. Furthermore, it offers the potential of real-time assessments without the risk of PRM degradation.

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[P 22] HRM and Pyrosequencing-Based Identification of *Apis mellifera carnica* mtDNA in Honey for Product Authentication and Subspecies Conservation

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Honey is susceptible to fraud, including false declarations of origin. Since honey contains environmental DNA (eDNA), molecular approaches can be used to assess its authenticity. In particular, *Apis mellifera* DNA recovered from honey provides information on the entomological source of the product, can indirectly indicate its geographic provenance, and is relevant for the protection of native honeybee subspecies [1,2]. Mitochondrial DNA (mtDNA) is especially suitable for this purpose due to its high copy number, stability, maternal inheritance, and high mutation rate [3].

This study aimed to develop a method to identify *A. mellifera* subspecies in honey, with particular focus on A. m. carnica, a subspecies native to Austria and protected in four Austrian federal states [4-7]. Honey samples were selected to represent diverse geographic origins and subspecies distributions, focusing on Austrian honeys, as well as relevant European and non-European reference samples. Bees specimens were also collected for analysis and used as a reference. DNA extraction was optimized for both honey and bees, including the Alpine and Pannonian variants of *A. m. carnica*. Highly variable mtDNA regions were then investigated. In the ND4 gene, a region containing six diagnostic SNPs was identified and targeted using a newly designed primer pair, the BEE 3_2 assay, with a biotinylated reverse primer to enable pyrosequencing (PSQ). Quantitative PCR followed by high-resolution melting (HRM) analysis was conducted, with subsequent PSQ to confirm and refine the results.

Using this method alone, the Alpine variant of *A. m. carnica* could be distinguished from the other subspecies commonly used by European beekeepers. In contrast, the development of a second primer pair (BEE 6 assay), targeting a single diagnostic SNP, was necessary for the more challenging discrimination of the Pannonian variant from *A. m. ligustica*. However, the BEE 6 method still requires further validation. The combined HRM and PSQ approach, using these two primer pairs together with another method (BEE 2_1) already established in our research group, showed promising results in distinguishing honey containing only *A. m. carnica* DNA (Alpine, Pannonian, or a mixture of both) from samples containing other subspecies. This approach may therefore support consumer protection, verification of honey authenticity, assessment of geographic origin, and conservation of this protected subspecies.

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[P 23] Evaluation of phytochemical, proximate, antioxidant, and anti-nutrient properties of Corchorus olitorius, Solanum macrocarpon and Amaranthus cruentus in Ghana

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In Ghana, *Corchorus olitorius*, *Solanum macrocarpon* and *Amaranthus cruentus* are green leafy vegetables that are customarily eaten together with a starchy staple food. The present study aimed at assessing the ethanolic leaf extract of *C. olitorius*, *S. macrocarpon* and *A. cruentus* for antioxidant capacity, phytochemical property, nutritional and anti-nutrient content. Method: Phytochemical constituent and proximate analysis were determined using standard protocols. The DPPH scavenging activity was used to determine the antioxidant activity of the ethanolic leaf extracts from the three vegetables. The antinutrients phytate and oxalate were determined by titrimetric methods of analysis. Results: Pytochemical screening revealed the presence of tannins and flavonoids in *C. olitorius*, *S. macrocarpon* and *A. cruentus*. Alkaloids and saponins were present in *C. olitorius* and *S. macrocarpon* but not in A. cruentus. Terpenoids, steroids, carotenoids and coumarins were absent in all the three vegetables. Proximate analysis revealed varying levels of moisture, fat, protein, ash, crude fibre and carbohydrates in the three leafy vegetables. The DPPH scavenging showed 86.71%, 71.72% and 38.86% activity for *S. macrocarpon*, *C. olitorius* and *A. cruentus* respectively. The antinutrient results revealed an oxalate level of 2.7 ± 0.13% for *C. olitorius*, 6.43 ± 0.06% for *A. cruentus* and 12.32 ± 0.13% for *S. macrocarpon*. For levels of phytates, our results revealed a 3.084 ± 0.54%, 1.14 ± 0.26% and 1.71 ± 0.27% for *C. olitorius*, *A. cruentus* and *S. macrocarpon*, respectively. Conclusion: The current study has shown that C*. olitorius*, *A. cruentus* and S*. macrocarpon* possess important phytochemicals, nutrients and significant antioxidant activity, suggesting a potential of these vegetables against diverse disease, if eaten by humans.

[P 24] Optimized Sample Preparation Strategies for Minimizing Carbon-Based Matrix Effects in the Elemental Analysis of Alcoholic Beverages by ICP-MS and ICP-OES

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The elemental analysis of alcoholic beverages, in particular wine and high-proof spirits such as schnapps and whisky, using inductively coupled plasma mass spectrometry (ICP-MS) and optical emission spectrometry (ICP-OES) is associated with substantial analytical challenges[1]. The complex sample matrix, dominated by high ethanol concentrations as well as sugars and organic acids, frequently induces carbon-based matrix effects, which may lead to biased or erroneous analytical results. Nevertheless, accurate elemental determination is indispensable for quality control in the alcoholic beverage industry in order to ensure product safety and compliance with regulatory standards.

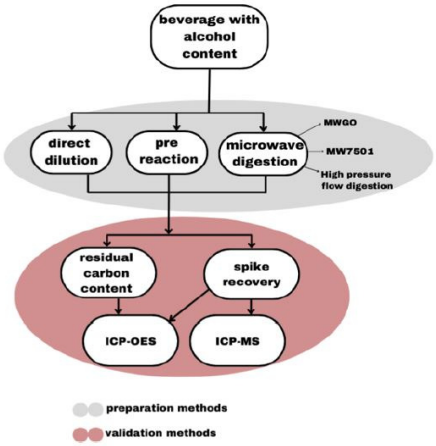

Figure 1: Analytical Strategy for alcoholic beverages analysis

The present study describes the development of an analytical strategy (see figure) aimed at minimizing carbon-based matrix effects through optimized sample preparation. Several approaches were systematically evaluated, including elemental analysis following adequate dilution and mineral acid digestion using an automated high-pressure flow digestion system[2]. The latter approach was demonstrated to represent a time-efficient and effective alternative to conventional digestion procedures, as it minimizes manual handling steps while simultaneously achieving efficient matrix decomposition. The results clearly indicate that a substantial reduction of carbon-based matrix effects can be accomplished by means of targeted sample preparation. Consequently, the proposed methodologies provide a robust and reliable framework for the elemental analysis and quality control of alcoholic beverages.

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[P 25] Can Vegetable Waste in Supermarkets be Reduced by using Innovative Lighting Technologies?

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Food waste has become a topic of increasing concern during the last years. With a European average of 131 kg per capita and year, an incredible amount of food commodities is discarded. Fruits and vegetables account for more than 20% of the wasted food. The increasing awareness for this problem has led to different approaches aiming for waste reduction along the supply chain of different products.

In this study, we investigated an innovative approach to maintain and/or prolong the quality of fruits and vegetables in the retail sector by illuminating the products with optimised light spectra. With the current development of light-emitting diodes (LED), it has become possible to generate light spectra with adjustable distribution and intensity, also changeable over time.

Tomatoes as an important example for climacteric vegetables are illuminated with specific light distributions with the aim to impact the postharvest-ripening processes, and thus, to extend the shelf-life of the product. Specific test chambers were constructed to guarantee controlled conditions in the course of the storage experiments under different illumination spectra. The development of the tomatoes was followed by monitoring colour changes of the surface by spectral imaging but also changes in fruit weight, acidity, soluble solids and texture over time. The impact of light on the formation of flavour compounds was also under investigation. First results demonstrate that ripeness at the time of harvest and the duration of storage on the shelf constitute the main impact factors influencing tomato quality. The selection of the light spectrum shows only a minor influence on the development of tomatoes over the relatively short time on the shelf. Further investigations are required for a better understanding of the effects of specific light spectra on the quality of fruits and vegetables.

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[P 26] Wheat Mycotoxin Monitoring in the Context of Climate Change

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Climate change is altering fungal communities and secondary metabolite formation in agroecosystems, with more frequent extreme weather expected to increase the prevalence and severity of mycotoxin contamination in temperate regions. Long-term, harmonised monitoring in Austria is essential to improve field-relevant risk assessment and reduce contamination-related food and feed losses.

A long-term field trial launched 2024 at BOKU University in Tulln aims to uncover temporal trends of agricultural mycotoxin contamination. Twenty wheat varieties with differing yields and resistance levels are cultivated in eight replicates to minimise varietal and local effects. Half of the wheat plants receive a Fusarium provocation using maize plant material.

Analytically, a broad-spectrum dilute-and-shoot LC–MS/MS workflow is employed, validated for the simultaneous detection of more than 1000 agricultural contaminants to investigate mycotoxin occurrence depending on environmental conditions. In addition to regulated mycotoxins, this method offers a broad screening of fungal contaminants. Mycotoxin data will be linked to weather variables – such as precipitation, temperature, wind, and solar radiation – during critical growth phases to identify climate-contamination relationships. The resulting evidence base will improve the interpretation of weather conditions to predict in-field mycotoxin contaminations. This will guide weather-informed strategic decisions that balance effective plant protection with minimising the ecological impact of agricultural practices.

This work was created within a research project of the Austrian Competence Centre for Feed and Food Quality, Safety and Innovation (FFoQSI). The COMET-K1 competence centre FFoQSI is funded by the Austrian federal ministries BMK, BMDW, and the Austrian provinces Lower Austria, Upper Austria, and Vienna within the scope of COMET - Competence Centers for Excellent Technologies. The programme COMET is handled by the Austrian Research Promotion Agency FFG.

[P 27] Identification of carbohydrate-based markers to detect unauthorized adulteration of fruit juices and fruit juice concentrates with sugar syrups

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Adulteration of fruit juices and fruit juice concentrates by adding sugar syrups is financially attractive due to their naturally varying composition, high demand, and raw material shortages. Some analysis methods, such as stable isotope analysis and the GC-FID method according to LOW [1], are commonly used in the routine analysis of sugar addition however these approaches are unable to reliably detect small amounts of added sugar in different matrices. This problem is derived from a lack of systematic investigations, but also methodological limitations, as each method is only suitable for specific matrix and foreign sugar combinations. As a result, a combination of different methods is often necessary to detect adulteration, and if a detection is possible, the detection limits remain relatively high. In addition, certain sugar syrups have not been investigated yet as a potential adulteration. To enable a reliable detection of an adulteration with foreign sugars, a HPLC-MS/MS multi-method with carbohydrate-based marker structures willbe developed. For this, fruit juice concentrates and fruit juices from apples and oranges as well as several invert sugar and starch syrups were examined for their carbohydrate-based minor components.
In order to enable a meaningful comparison of the minor sugar profiles, the minor components were enriched and large portions of the main sugars glucose, fructose, and sucrose were removed by using activated carbon. For this, the method published by Morales et al. in 2006 [2] involving a dispersive system was refined to enable a better removal of the main sugars. Subsequently the samples were analyzed with HPAEC-PAD and the minor sugar profiles obtained were compared with each other. This allowed the identification of compounds, that could potentially be used as markers for the detection of unauthorized adulteration of fruit juices and fruit juice concentrates with sugar syrups.

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[P 28] The Diverse Arsenic Metabolome Found in Penny Bun and Cauliflower Mushroom

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Mushrooms are popular food, yet challenging to cultivate, which is the reason why only a handful of edible mushrooms are commercially available. Many popular mushrooms must therefore be collected wildly, where they are exposed to a wide range of elements at varying levels, resulting in varying elemental metabolomes and nutrient profiles heavily dependent on their natural habitat. Like other organisms, wild mushrooms evolved strategies for the detoxification of arsenic. In most mushrooms, toxic inorganic arsenic is methylated and further metabolized to less toxic organic forms but the arsenic speciation profiles can be heavily dependent on the mushroom species. Characterizing and identifying novel arsenic compounds in edible mushrooms is of great interest for assessing food safety. Herein, we show examples of two common edible mushrooms – penny bun (*Boletus edulis*) and cauliflower mushroom (*Sparassis crispa*) – with strikingly diverse and unusual arsenic speciation profiles where a large number of arsenic compounds are present including many yet-to-be identified. A combination of element-selective and molecular mass spectrometric techniques was used to study the arsenic metabolomes in these edible mushrooms in order to identify and quantify these arsenic compounds including novel natural arsenic compounds that were not previously reported.

[P 29] Targeted LC–QQQ–MS/MS Detection of Blood Plasma Marker Peptides for the Identification of Plasma Adulteration in Salami

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The undeclared addition of blood plasma to meat products represents a potential case of food fraud, as plasma proteins may partially replace higher-value meat proteins and are difficult to detect in thermally processed products from the same animal species. Building on previously described LC–MS/MS methods for plasma protein detection[1)], the present comprehensive large-scale study, led and coordinated by Federal Office of Consumer Protection and Food Safety (BVL) and involving multiple laboratories from several countries, evaluated the applicability of a targeted peptide-based liquid chromatography–triple quadrupole mass spectrometry (LC–QQQ–MS/MS) method to discriminate between low and elevated plasma levels in meat products. The data presented here represent preliminary findings obtained independently of the large-scale interlaboratory validation study using the LC-QQQ-MS/MS method.

Three salami samples prepared with 0%, 0.5%, and 1% plasma protein (w/w) were analyzed using LC–QQQ–MS/MS. The laboratory team was blinded to the plasma protein content. Protein extraction and tryptic digestion were followed by targeted LC-MS/MS analysis using multiple reaction monitoring (MRM) of four plasma marker peptides. These marker peptides were selected based on their specificity, signal stability, and suitability for processed meat matrices.

The LC–QQQ–MS/MS method enabled clear differentiation between samples containing 0.5% and 1% plasma protein. The negative reference sample (0%) was also correctly identified. Both salami samples with elevated plasma content consistently exhibited marker peptides at significantly higher signal intensities than the negative reference sample. In contrast, the negative reference sample did not display a marker peptide pattern indicative of added plasma, thereby confirming the specificity of the method at low plasma protein levels.

The initial data presented here demonstrate that targeted detection of selected plasma marker peptides using the LC–QQQ–MS/MS method provides a robust analytical approach for distinguishing between low and elevated plasma levels in meat products. The method exhibited high selectivity and practical applicability for routine food control, particularly in the context of food authenticity and fraud detection. Even in complex and processed matrices such as salami, the use of multiple peptide markers enables reliable sample classification.

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[P 30] Oat (*Avena sativa*) as a Central Modulator of Satiety and Energy Homeostasis in Obesity: A Comparative Study with Orlistat

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Obesity remains a critical global health challenge, necessitating novel therapeutic approaches that address its complex pathophysiology. Emerging evidence suggests that central nervous system dysregulation of satiety and energy homeostasis is a key driver of the disease. This study investigated the anti-obesity potential of oat (*Avena sativa*), a nutrient-dense functional food, by evaluating its impact on brain biomarkers in a diet-induced obesity rat model. Sixty adult male Wistar rats were monitored over a 25-week period. The subjects were divided into three control groups and seven treatment groups. The treatment arms received varying doses of oat extracts, which were compared against the standard anti-obesity medication, Orlistat, to assess comparative efficacy in mitigating obesity and its related metabolic complications. Oat supplementation led to significant improvements in metabolic profiles. Central nervous system analysis revealed that oat extracts significantly: upregulated dopaminergic signaling and brain-derived neurotrophic factor (BDNF) levels. Increased brain concentrations of thermogenic and metabolic markers, including UCP-1, irisin, and vaspin. Downregulated the expression of orexigenic neuropeptides, specifically Agouti-related peptide (AgRP) and Neuropeptide Y (NPY) ($P < 0.05$). These findings suggest that oat supplementation acts as a potent modulator of both hedonic (reward-based) and homeostatic (energy-based) satiety mechanisms. By influencing key neurotrophic factors and neuropeptides, *Avena sativa* offers a promising, non-pharmacological framework for obesity management, comparable to conventional treatments like Orlistat.

[P 31] Identification of sulfur compounds in reaction aroma – comparison of two different systems based on comprehensive GC×GC

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According to EU regulation (EC) No 1334/2008, thermal process flavorings are defined as compounds derived from heating mixtures of ingredients with a goal of generating characteristic aroma compounds through controlled thermal reactions [1]. Those reactions are commonly including reducing sugars and amino compounds. These reaction aromas are widely used in the food industry to recreate desirable cooked, roasted, or savory notes, which are closely linked to consumer acceptance and overall sensory appeal of food products. Among the key precursors are sulfur-containing compounds such as cysteine and thiamine, playing a crucial role due to their ability to form highly potent odorants [2].

In general, volatile sulfur compounds (VSCs) are known for extremely low odor thresholds and dramatic influence on the sensory profile of foods. They are present in a wide range of thermally processed foods such as meat, coffee, baked goods, and vegetables. This chemically diverse class includes thiols, disulfides, polysulfides, and sulfur-containing heterocycles, formed mostly through Maillard-type reactions and Strecker degradation pathways. However, analysis of VSCs remains challenging due to their instability, low concentrations, and possible co-elution issues with other volatile compounds [3].

In this study, two comprehensive two-dimensional gas chromatography (GC×GC) systems were evaluated for their performance in analyzing reaction aroma. For that purpose, a model reaction mixture with thiamine as a precursor was employed. A cryogenic modulation GC×GC coupled with time-of-flight mass spectrometer (TOFMS) was compared to a flow-modulated GC×GC system coupled with both TOFMS and sulfur chemiluminescence detector (SCD). The comparative results highlight the strengths of each approach and demonstrate the benefits of combining advanced chromatographic separation with element-specific detection for sulfur containing compounds characterization.

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