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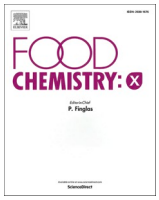

Foodomics: A sustainable approach for the specific nutrition and diets for human health

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ABSTRACT

Foodomics is an interdisciplinary field that integrates various omics technologies to explore the complex relationship between food and human health in depth. This approach offers valuable insights into the biochemical, molecular, and cellular composition of food by employing advanced omics techniques. Its applications span the food industry and human health, including efforts to combat malnutrition, provide dietary recommendations, and ensure food safety. This paper critically examines the successful applications of foodomics across areas such as food safety, quality, traceability, processing, and bioactivity. It highlights the crucial role of metabolomics, proteomics, and transcriptomics in achieving a comprehensive understanding of food components, their functions, and their interactions with human biology.

1. Introduction

The evolving consumption habits reflect a shift in how people perceive food—not just as a source of energy but as a means to promote health and reduce disease risk. Consequently, food science and nutrition research have transitioned from traditional approaches to more advanced, systems-level studies, with food omics playing a pivotal role. Food omics integrates four key disciplines—genomics, transcriptomics, metabolomics, and proteomics—along with chemometrics and bioinformatics (Shi et al., 2024). First defined in 2009, foodomics explores food and nutrition by leveraging advanced omics technologies to improve consumer health, well-being, and trust. The concept of the "Foodome" soon followed, representing the complete set of compounds in a food sample or interacting biological system at a given time. Foodomics primarily focuses on food constituents, involving both qualitative and quantitative data analysis (Capozzi & Bordoni, 2013). It assists researchers in identifying the specific effects of food on human health and nutrition (Valdés et al., 2021; Zheng & Chen, 2014).

Moreover, foodomics has proven its value in addressing food safety, enhancing quality and traceability, and revealing the molecular bioactivity of food. Advances in high-throughput technologies and biostatistics have made foodomics critical for biomarker development and dietary analyses, drawing significant attention from research institutions, regulatory bodies, and the food industry (León et al., 2018).

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For instance, foodomics has been instrumental in identifying dietary biomarkers (Scalbert et al., 2014) and deepening our understanding of dietary patterns (Fitó et al., 2016). These biomarkers complement traditional dietary assessments (Olarini et al., 2022), offering a more comprehensive view of food consumption (Pujos-Guillot et al., 2013). This growing interest in foodomics parallels a shift in medicine and biosciences toward proactive disease prevention through informed dietary choices and the development of functional foods (García-Cañas et al., 2012).

Foodomics has also found successful applications across various food science domains. These include the analysis of milk proteins (Le et al., 2017), studies on lactic acid bacteria and probiotics (Vinusha et al., 2018), compositional assessments of durum wheat (Saia et al., 2019), identification of triacylglycerols and polar lipids in olive fruit (Alves et al., 2019), and the study of emerging technologies and quality factors in meat products (López-Pedrouso et al., 2019; Munekata et al., 2021). It plays a crucial role in understanding the presence, bioavailability, and biological characteristics of key molecules in different food matrices (Cifuentes, 2009). These molecules possess the capacity to impact one or more metabolic processes, ultimately playing a role in enhancing overall health. They showcase a diverse array of chemical structures and can be classified into numerous groups, such as alkaloids, bioactive peptides, capsaicinoids, carotenoids, glucosinolates, phytosterols, polyphenols, polyunsaturated fatty acids, polysaccharides, terpenoids, tocopherols, and triterpenes (Câmara et al., 2020).

This review highlights significant advancements in health-related disease prevention, food safety, and quality, focusing on areas such as traceability, processing, and bioactivity. It underscores the contributions of genomics, transcriptomics, proteomics, and metabolomics to these fields while discussing the challenges faced by foodomics. Additionally, the integration of AI, a rapidly evolving aspect of the field, presents new potential for future advancements (Fig. 1).

2. Omics tools for foodomics

Genomics is the systematic study of the structure and function of genomic genes in an organism, including sequencing, assembly, and analysis. In genomics, tools like complementary DNAs (cDNAs) are the most potent and adaptable instruments. DNA arrays are a group of interconnected DNA spots that correspond to individual genes and are immobilized to a solid surface by covalent or electrostatic interaction with appropriate chemical matrices (Mendes-Ferreira et al., 2017). Another tool is the next-generation sequencing (NGS) technique.

In contrast to DNA arrays, NGS technology can conduct millions of sequencing reactions concurrently without needing a sequence library, often known as massively parallel sequencing. NGS accelerates obtaining DNA sequence data and decreases the expenses associated with sequencing. Similarly, single-molecule sequencing is an appealing method for investigating genomes (Zhang et al., 2021).

Transcriptomics is the comprehensive analysis of RNA data from an individual cell or a cluster of cells. It is a crucial method for inferring the functional components of the genome (Pareek et al., 2011). Transcriptomics uses techniques like gene expression microarrays (GEM) and RNA sequencing (RNA-Seq). GEM is an extensively employed technique in high-throughput research. Based on the nature of the microarrays, they can be classified into two types: microarrays on flat substrates and microarrays on particle substrates (Valdés et al., 2017). However, GEM analysis has several limitations due to its reliance on acknowledged sequences, which renders the characterization of unfamiliar RNA sequences unattainable. Hence, it is unattainable to achieve a thorough and accurate description of the transcriptome (Valdés et al., 2013a). RNA-Seq enables the examination of the qualitative and quantitative properties of various types of RNA, such as microRNAs, messenger RNAs (mRNAs), small interfering RNAs (siRNAs), and long noncoding RNAs. Because it sequences the whole transcriptome, the RNA-seq technique is suitable for genome-wide high-throughput transcriptomics (Wang et al., 2009). Using transcriptomic-based fingerprinting helps to clarify the molecular processes of metabolic changes and functions in food

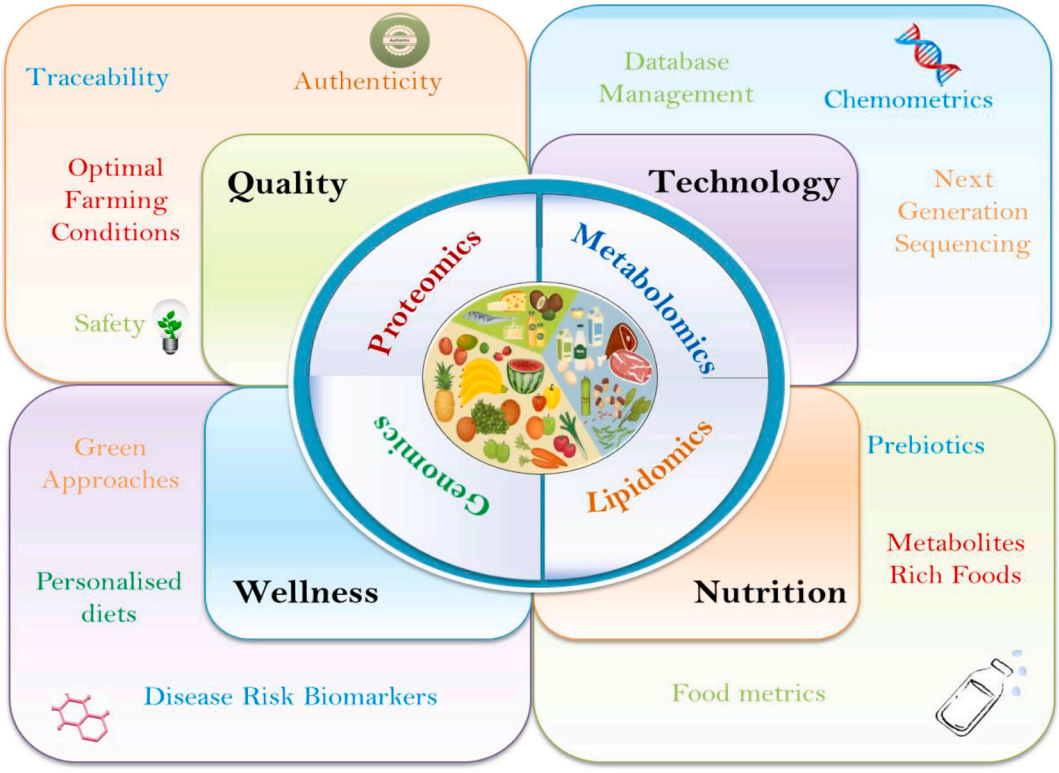

Fig. 1. Foodomics implementation throughout the food system for food safety, quality, technology and nutrient availability for human nutrition health.

fermentations. It illustrates the impact of dietary nutrients from consumed foods (Valdés, García-Cañas, et al., 2013).

The field of proteomics serves as a valuable addition to genomics and transcriptomics by providing accurate biological insights for foodomics. Furthermore, proteomics examines the chemical structure and functionality of proteins. It explores the impacts of protein modifications, quantitative measurement of protein abundance, protein interactions, and the investigation of their intracellular mechanisms (Aebersold & Mann, 2016). Mass spectrometry (MS) coupled with chromatography-based methods detect and identify protein components in food (Balkir et al., 2021). In this technique, peptides are isolated from protein using liquid chromatography (LC) and then sent to MS to detect the separated peptides (Monaci et al., 2018). Techniques like HPLC (High-Performance Liquid Chromatography) tandem ion trap MS are promising for eliminating the isolation and purification step (Picó et al., 2019). The processes involved in proteomics encompass protein extraction and separation, protein hydrolysis into peptides, MS analysis, and subsequent qualitative and quantitative protein analysis. Generally, protein isolation and separation in proteomics can be achieved using two-dimensional electrophoresis (2-DE) and multi-dimensional liquid chromatography. The 2-DE technique for protein isolation and separation relies on the separation of proteins by isoelectric point (pI) and molecular mass using 2-DE on polyacrylamide gels. This is followed by image analysis to categorize all visible spots in the image, which serves as a reference for future scholarly investigations (Zhang et al., 2021).

However, the 2-DE method for protein extraction and separation has certain limitations. The extraction and separation of high-molecular or low-molecular-weight proteins exhibit inadequate performance and require significant time (Chandramouli & Qian, 2009). Hence, the technique of multi-dimensional liquid chromatography (LC-MS/MS) has been devised to extract and separate proteins using LC connected to tandem MS. At present, the primary methods employed for proteomic analysis to describe protein samples are MS, namely matrix-assisted laser desorption/ionization-time of flight (MALDI-TOF) and electrospray ion trap (ESI-IT) MS. Both methods initially ionize proteins and subsequently examine them using mass spectrometry (Ferranti, 2018).

Metabolomics technology is used to qualitatively and quantitatively probe small molecule metabolites (<1000–1500 Da) to compare sample variations. Metabolomics research aims to discover biomarkers, which are compounds that directly influence an organism's metabolism or metabolic pathways. Metabolomics workflows typically consist of the following stages: identification of target metabolites tailored to research objectives; selection of analytical instruments and preparation of samples; on-board testing of samples; data collection; and utilization of analytical tools for analysis and detection (Valdés et al., 2017). Bioinformatics and chemometrics are analytical techniques employed mainly to analyze metabolomics data (Cevallos-Cevallos et al., 2009). Nuclear magnetic resonance (NMR), LC-MS, gas chromatography-MS (GC–MS), and capillary electrophoresis-MS (CE-MS) are the most commonly employed data acquisition platforms in metabolomics (Miggiels et al., 2019). However, NMR technology was most prevalent in the initial metabolomics investigations. NMR is a highly effective analytical method for measuring metabolites and examining structural characteristics. It necessitates a minimal sample size and does not require intricate sample preparation methods, such as separation or derivatization.

Nevertheless, the technique of NMR analysis is limited by its somewhat low sensitivity in detecting metabolites (Emwas, 2015). Metabolomics methods based on MS offer unique advantages. They are mainly employed for identifying unidentified chemicals and quantitatively analyzing metabolites (Raji et al., 2013). The notable benefits of MS analysis technology include its minimum sample volume need, exceptional sensitivity, and rapid separation speed (Liu et al., 2015). LC-MS is the predominant MS technology. Utilized in most metabolic profiling investigations, this method is highly effective in quantifying compounds and precisely determining their structural information. The main objective of GC–MS technology is to analyze volatile, non-polar, and thermally stable compounds with optimal separation efficiency and reproducibility. This enables the analysis of complex metabolic mixtures. GC–MS remains highly valuable despite the introduction of CE-MS (Kohler & Giera, 2017). The introduction and use of CE-MS technology serve as an additional enhancement and refinement to LC-MS and GC–MS procedures. CE-MS necessitates a minimal sample volume and straightforward sample processing, achieving excellent separation efficiency, exceptional repeatability, and elevated sensitivity, making it suitable for analyzing highly polar or charged substances (Zhang et al., 2021).

The various omics approaches have distinct advantages, and integrating many metabolomics analysis technologies will provide complimentary analytical findings (Table 1).

Table 1
Advantages and disadvantages of foodomic techniques.

Techniques	Advantages	Disadvantages	References
Gene Expression Microarrays	• Evaluates cellular transcriptome. • Facilitates the detection of alterations in gene expression. • Standard approach of data submission • Inexpensive	• Analyzes only pre-defined sequenses. • High variance for low expressed genes. • Specialized knowledge needed for interpretation	Martin et al. (2016)
RNA-Seq	• Sequence analysis of any RNA • No requirement to have prior knowledge of the sequence • Broader sensitivity	• Expensive • Not suitable for small sample sizes • Complex computational analysis • More storage space needed	Martin et al. (2016)
NGS	• Detect genome abnormalities • Higher sensitivity	• Expensive • Expertise required for interpretation • More storage space needed	Badalian-Very (2014)
2-DE	• 100–1000 polypeptides can be analyzed at once • Proteins can be separated • Polypeptides can be probed with antibodies	• Manual work is needed • Salt ions could interfere with protein separation • Limited reproducibility	Baskin and Yigitbasi (2010)
MS	• High sensitivity • High throughput experiments • Suitable for coupling with other methods	• Identification of protein is less direct • Manual work is required • Low protein identification rate (<10 %)	Baskin and Yigitbasi (2010)
MALDI-TOF-MS	• High sensitivity • Rapid	• Requires relatively pure samples • More ambiguity in identification • Exact or homology protein must be present in the database	Baskin and Yigitbasi (2010)
LC-MS	• Automation • Multi-dimensional • High sensitivity	• Time-conusming • Sensitive toward interfering compounds • Restricted mass range	Fliser et al. (2007)
CE-MS	• Automation • High sensitivity • Rapid • Inexpensive • Low sample volume	• Not suited for larger proteins (>20 kD)	Fliser et al. (2007)

3. Foodomics for human health and diseases

The primary goal of Foodomics is to deepen our understanding of how nutrients and metabolites influence human health and contribute to disease prevention (Fig. 2). By promoting healthy eating habits and the development of functional foods, Foodomics closely collaborates with medical science. A key challenge is uncovering the molecular functions of food compounds, including their interactions with genes and their effects on proteins and metabolites. This knowledge could inform dietary strategies to regulate cellular functions and significantly improve overall health (Andersen et al., 2014). To achieve this, Foodomics must integrate data from transcriptomics, proteomics, and metabolomics, which, although essential, presents considerable challenges. The field must evolve toward clinically relevant methods, such as personalized nutrition, to fully realize its potential. This evolution is crucial for translating Foodomics insights into practical applications that positively affect individual health (García-Cañas et al., 2012).

Foodomics role in health and disease spans several critical areas. It investigates genetic variations among individuals in response to specific dietary patterns, aiding the development of personalized nutrition (Bertram & Jakobsen, 2018; Mancano et al., 2018). It also aims to identify genes associated with early disease stages, potentially discovering molecular biomarkers. Additionally, Foodomics examines the gut microbiome's roles and its influence on health (Trimurtulu et al., 2015). As an integrative tool, Foodomics assesses the health impacts of food compounds by combining various omics technologies. Proteomics and bioactive peptides—sequences within proteins that become active through hydrolysis—are gaining significant attention. This approach involves analyzing the interactions between diet, nutrition, and host-microbiome health. Researchers combine genomic and transcriptomic data from microbiomes with proteomic or metabolomic data from host stool samples to assess how gene expression in microorganisms interacts with dietary metabolites and proteins (León et al., 2018). Foodomics provides critical insights into malnutrition and the biochemical, molecular, and cellular effects of food biomolecules, helping to clarify both beneficial and harmful health outcomes (Ahmed et al., 2022). While Foodomics is crucial for understanding individual health, it also plays a pivotal role in promoting sustainable dietary practices.

3.1. Foodomics for sustainable diets

Foodomics is at the forefront of a data-driven transformation aimed at enhancing nutritional, health, and environmental outcomes related to food. By leveraging comprehensive foodomics data, researchers are now better equipped to precisely identify the biomolecular components of both unhealthy and healthy diets, offering deeper insights into the complex interactions between the environment, diet, and health. This approach is revolutionizing food product development by incorporating biomolecules that promote health and sustainability, without compromising sensory and quality attributes. For instance, peptidomic research has successfully identified a specific peptide in gluten responsible for inflammation in individuals with Celiac disease. This discovery has paved the way for innovative solutions, such as the development of gluten-free wheat varieties and real-time therapies that neutralize this peptide in the stomach. Similarly, foodomics has facilitated the discovery of natural alternatives to synthetic food dyes. A notable example is the identification of a unique anthocyanin from red cabbage, capable of replacing synthetic blue dye in food products (Ahmed et al., 2022).

Beyond product innovation, foodomics plays a vital role in preserving the biocultural diversity of Indigenous Peoples' food systems. Collaborative efforts, whether spearheaded by communities or in partnership with Indigenous groups, can harness foodomics to authenticate the biochemical, sensory, and health properties of traditional foods. For example, Lin et al. (2020) investigated the microbiological and biochemical transformations during the ripening process of Laowo dry-cured ham, a traditional Indigenous fermented food. This study highlights foodomics potential to protect and validate the quality and health advantages of such traditional foods.

Foodomics is also proving to be a valuable tool in linking dietary components to specific health outcomes. Srinivasan (2020) investigated the correlation between brain health and omega-3 fatty acid levels in red blood cells (RBCs). In this study, the fatty acid composition of over 100

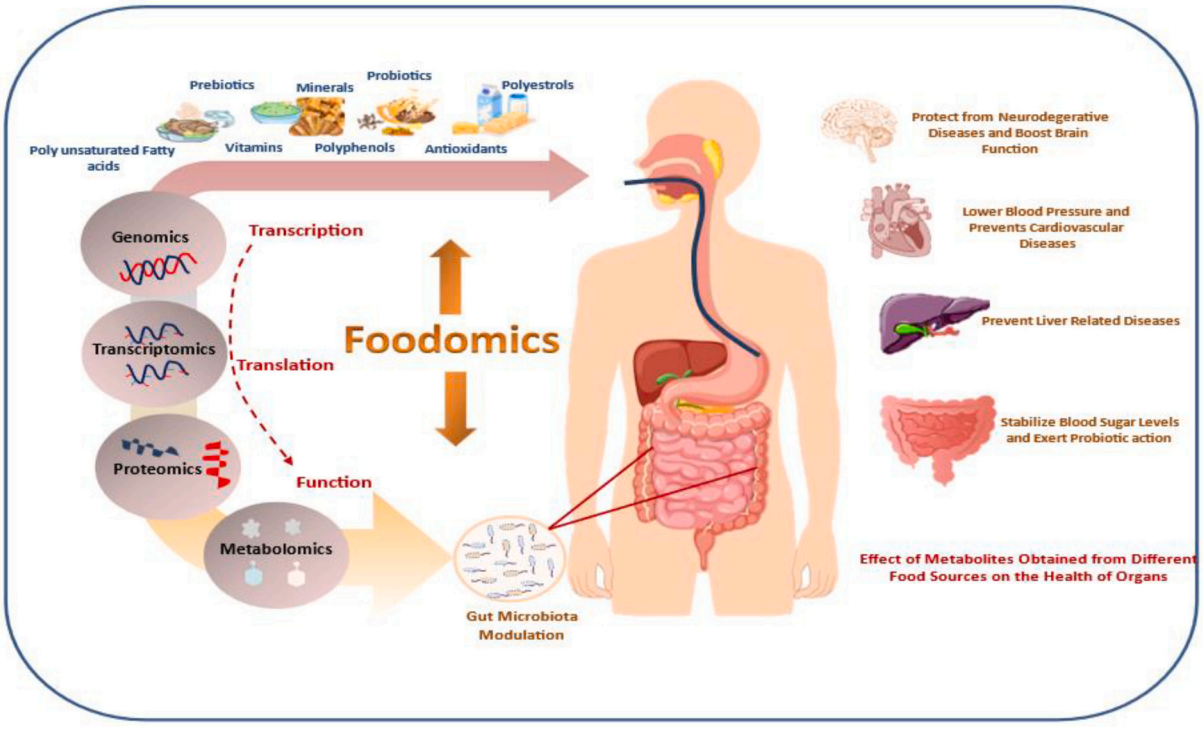

Fig. 2. Dynamics of Foodomics for nutrients and metabolites availability in various organs and tissues for human health.

RBC samples was analyzed using GC–MS and subsequently linked to brain MRI data, revealing insights into the structural and functional organization of the brain. This type of research underscores the complex interplay between diet and health, where antagonistic or synergistic interactions between food components further complicate the analysis (Braconi et al., 2018).

The influence of diet on gene expression, especially through epigenetic mechanisms, is another area where foodomics is making significant strides. With its focus on sustainable diets, foodomics aims to unravel the molecular mechanisms behind dietary interventions and to identify biomarkers associated with food intake, nutrition, and health or disease status (Putignani & Dallapiccola, 2016). A key study by Andersen et al. (2014) exemplifies this approach. They applied untargeted metabolomics to assess compliance with specific dietary regimes, using UPLC-qTOF-MS to analyze urine samples from individuals following either the Average Danish Diet (ADD) or the New Nordic Diet (NND). The study revealed that specific urinary metabolites could accurately reflect dietary adherence, with greater diagnostic accuracy for ADD. This underscores the potential of metabolites as indicators of dietary compliance, although the development of targeted, quantitative models is necessary for practical application (Andersen et al., 2014).

Despite its promise, foodomics faces several limitations. The high cost of conducting multi-omics studies in large populations, along with computational challenges, continues to be a barrier (Braconi et al., 2018). In the context of sustainable diets, one of the primary challenges is improving our understanding of how complex food matrices influence health at the molecular level. This includes deciphering the interactions between genes and metabolites within these matrices. Such knowledge is crucial for the rational design of dietary strategies that modulate cellular functions, ultimately contributing to improved health outcomes.

3.2. Foodomics for allergen detection

A food allergy (FA) occurs when the immune system reacts to certain components in food, known as food allergens. Currently, 1–10 % of the global population is affected, and the prevalence continues to rise. FAs pose a significant health risk, as even minute amounts of allergens can quickly trigger severe or life-threatening reactions. These allergies also create anxiety and uncertainty for both those affected and those around them. To address this, several food processing methods aim to reduce the allergenic properties of foods. Most food allergies are triggered by proteins or their breakdown products. Although any food can potentially cause an allergic reaction, the majority are linked to proteins found in eight major allergens: peanuts, tree nuts, eggs, milk, fish, shellfish, wheat, and soy.

For detecting and measuring allergens in complex food systems, mass spectrometry (MS)-based proteomic methods offer greater sensitivity, reliability, and precision compared to antibody or nucleic acid-based techniques (Anđelković et al., 2015). A novel research direction in allergenomics applies proteomic methods to study the in-vitro degradation of peanut digests in simulated gastric and intestinal environments. Through this research, stable allergens such as Ara h 2 and 6 have been identified as potential immune triggers, making them candidates for serological assays to detect allergens in patient blood. While challenges remain in analyzing peanut allergen residues after ingestion, antibody-based methods have shown promise. Combining proteomic and metabolomic approaches may aid in endotyping peanut allergies and discovering biomarkers for phenotype prediction (Czolk et al., 2021).

Certain cereals, such as wheat, rye, and barley, contain gluten proteins that can trigger hypersensitivity in many individuals. Hajas et al. (2018) analyzed proteins from 23 wheat cultivars and identified five suitable for developing gluten reference materials. Peanuts, widely used for their protein and oil content, are another major source of allergic reactions due to proteins like Bet v 1, profilins, and nonspecific lipid transfer proteins. Traditional allergen detection methods such as ELISA and LC-MS remain widely used, while newer techniques, like flow cytometry (xMAP technology), allow for the rapid identification of multiple allergens (Pedersen et al., 2017). Additionally, targeted proteomics using Multiple Reaction Monitoring (MRM) and labeled peptides enables precise allergen quantification in crops like soybean, wheat, and maize (Jain et al., 2019; Rogniaux et al., 2015).

Data-Independent Acquisition Mass Spectrometry (DIA-MS) is particularly well-suited for detecting multiple allergens simultaneously, which is critical for assessing the risk of cross-contamination in food processing environments. Bottom-up targeted proteomics has also been employed to detect and quantify various food allergens in complex matrices. Techniques such as LC-SRM/MRM assays using QQQ or QTRAP instruments have been successfully applied to accurately measure allergens like peanuts, hazelnuts, walnuts, milk, and eggs in food products. In a recent study, a rapid detection method for the primary fish allergen, β-PRVBs, was developed using heat-based protein purification, accelerated digestion with High-Intensity Focused Ultrasound (HIFU), and biomarker monitoring via LC-MS/MS SMIM/PRM. This approach allows β-PRVBs to be identified in under two hours across various food products, including cooked and processed items. Notably, this is the fastest reported method for β-PRVB detection and has been successfully applied to quickly identify the allergenic protein Ani s 9 from Anisakis species (Carrera et al., 2016; Carrera et al., 2024).

3.3. Foodomics for food bioactivity

Bioactive compounds in foods, also known as nutraceuticals, offer health benefits beyond basic nutrition, such as enhancing well-being or reducing the risk of disease. These compounds exert their effects by directly or indirectly interacting with the human genome, altering gene expression. They function as signals that modulate gene expression through transcription factors or by interacting with proteins, thereby influencing their levels and functions. Omics technologies are crucial for analyzing gene expression, protein levels, and metabolite abundance, which allows for a deeper understanding of signalling pathways and cellular processes. These technologies are mainly applied for three purposes: (i) to elucidate the mechanisms of action of bioactive compounds by identifying regulated cellular pathways at the molecular level; (ii) to pinpoint specific tissues and organs affected by these compounds, facilitating the development of targeted nutritional interventions; and (iii) to discover biomarkers associated with compound exposure, bioactivity, effects, and related risks (Ortea, 2022).

Omics technologies allow researchers to thoroughly evaluate how dietary components influence gene expression by examining hundreds of genes, proteins, or metabolites within a single sample. For instance, in studies on in vitro anticancer activity, polyunsaturated fatty acids (PUFAs) like docosahexaenoic acid (DHA) and arachidonic acid (ARA) showed different mechanisms of action. Using quantitative proteomics, which identified 1882 proteins across various samples, it was found that ARA suppressed cellular DNA replication by downregulating the helicase complex, whereas DHA mainly inhibited proteasome proteins (González-Fernández et al., 2019; Ortea et al., 2018). Investigating molecular targets of bioactive compounds is another common application of omics. Terms like “nutritargeting” and “therapeutic targeting” are often used interchangeably in this context. Phytochemicals provide an excellent case study for researching molecular targets, as they demonstrate anti-tumor activity at various stages of cancer development (initiation, promotion, and progression) (Afrin et al., 2020). Modern omics techniques enable the detailed investigation of specific transcripts, proteins, or metabolites that are either up- or down-regulated by bioactive compounds, while also offering a broader view of their mechanisms of action. This level of precision allows researchers to identify, for example, whether a substance with anti-inflammatory properties targets cyclooxygenase or lipoxygenase within the eicosanoid biosynthesis pathway (Trimurtulu et al., 2015).

Proteomics, particularly through the use of mass spectrometry (MS),

is also used to explore how polyphenols interact with the gastrointestinal tract by analyzing changes in protein expression. Valdés, Ibáñez, et al. (2013) applied this approach to examine the effects of a polyphenol-rich rosemary extract on HT-29 human colon cancer cells over 2, 6, and 24 h. By employing nano-LC/MS and stable isotope dimethyl labeling, they quantitatively assessed protein changes, finding that the rosemary extract improved intestinal health by reducing protein aggregation and enhancing autophagy. This showed anti-proliferative effects on HT-29 cells. In a separate study, Di Nunzio et al. (2018) integrated proteomics and transcriptomics to investigate the impact of dietary quercetin on the distal colon mucosa of F344 rats, revealing that quercetin inhibited colorectal cancer by increasing the expression of tumor suppressor genes, cell cycle inhibitors, and genes related to xenobiotic metabolism, while also suppressing the MAPK pathway (Zhang et al., 2021).

Foodomics plays a pivotal role in examining the bioavailability and bioaccessibility of bioactive compounds in food (Dima et al., 2020). In vitro gastrointestinal digestion models are commonly employed to assess the bioaccessibility of various food matrices. For example, extra virgin olive oil (EVOO) was subjected to in vitro gastrointestinal digestion, and an untargeted metabolomics approach using UHPLC-Q-TOF MS/MS analysis was used to track changes in its bioactive components. This method identified 219 sterols and 67 polyphenols in the EVOO samples, showing that undigested EVOO contained higher levels of total sterols and tyrosol (Rocchetti et al., 2020).

4. Foodomics for food safety, quality and processing

4.1. Foodomics for food safety and quality

The global expansion of the food supply chain, along with the rising demand for ready-to-eat, minimally processed, and preserved foods, has introduced new challenges to both food safety and food processing. These challenges are further complicated by increasing microbial resistance, shifts in climatic conditions, and human errors in food handling, all of which constrain the effectiveness of global food safety management systems (Josić et al., 2017). The discovery of unforeseen contamination, product degradation, diverse functionalities, and untapped potential in food materials and by-products has fueled interest in the foodomics approach. This methodology is gaining significance in ensuring food safety, authenticity, quality, and traceability by offering extensive data across various fields, including nutrition, food science, and health (Muguruma et al., 2022). Foodomics, which employs omics technologies to analyze and quantify biomolecules in food, holds great promise for improving well-being by addressing food composition needs, authentication, and quality assessments (Balkir et al., 2021), providing new insights (Ahmed et al., 2022) throughout the entire food production and distribution process (Rodríguez-Carrasco, 2022).

The adoption of foodomic techniques capable of identifying and assessing novel food hazards and toxins at various points in the production chain is crucial, as issues of adulteration and fraud demand immediate attention (Rodríguez-Carrasco, 2022). During the critical stages of production, processing, transportation, and storage, food items are prone to contamination from pathogens, biotoxins, as well as chemical and physical pollutants such as pesticides and metals, all of which contribute to foodborne diseases (Rešetar et al., 2015). To mitigate foodborne diseases and ensure food safety, increasing focus has been placed on sensory attributes, quality, traceability, and regulatory compliance, alongside the implementation of high-tech analytical methods (Fallahzadeh et al., 2018).

Recent literature on the role of foodomics in food safety highlights significant advancements, particularly over the last two years, with a focus on understanding the effects of pathogens on food composition (Lou et al., 2021). Furthermore, “metabolomics,” a key aspect of foodomics, has made considerable progress in enhancing food safety, enabling traceability, and detecting adulterants (Chang et al., 2021). In modern food analysis, metabolomics based on MS/NMR has become the leading technique for identifying and quantifying pathogens, environmental pollutants, banned substances, and naturally occurring toxins (Castro-Puyana et al., 2017).

Lou et al. (2021) studied the deterioration of fish products, such as fish sticks and broths, typically caused by microbial activity. By introducing *Shewanella baltica* strains into sterile fish sticks and broths, they sought to investigate the changes in metabolic profiles. After storing the samples for 10 days at 4 °C, metabolites were extracted using a methanol/water solution (1/2; *v*/v) three times, freeze-dried, and reconstituted in deuterated water for NMR analysis. Harmful biogenic amines from amino acids, along with inosine and hypoxanthine, products of adenine nucleotide breakdown, were observed in both matrices.

In a separate study, Wu et al. (2021) evaluated the effectiveness of inactivating *Listeria monocytogenes* on salmon using a combination of electrolyzed water and mild heat treatment. Their metabolomics approach, involving NMR analysis, identified 43 metabolites extracted with phosphate buffer saline and acetonitrile, followed by cold sonication. The synergistic effect of these antibacterial treatments resulted in a 55 % bacterial inactivation. Jadhav et al. (2018) applied matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-ToFMS) for proteomics and gas chromatography–mass spectrometry (GC–MS) for metabolomics to detect three pathogens—*L. monocytogenes*, *S. enterica*, and *E. coli O157*—in red meat. Their methodology enabled species-level identification within 18 h for *S. enterica* and *E. coli O157*, and within 30 h for L. *monocytogenes*.

Similarly, Christodoulou et al. (2015) established a multi-residue detection system for pesticides using LC-MS/MS, targeting 172 pesticide residues in 27 commercial wines. Their cost-effective method was validated for pesticide determination. Another notable study by Bellassi et al. (2021) applied metabolomics and proteomics to evaluate the effect of *Pseudomonas fluorescens* contamination on cold-stored milk. They employed two pretreatment methods—liquid-liquid extraction with methanol/formic acid or dichloromethane/formic acid—before conducting untargeted UHPLC-Q-TOF-MS metabolomic analysis, which identified phosphatidylglycerophosphates and glycerophospholipids linked to contamination levels.

Li et al. (2016) conducted parallel studies using UHPLC-HRMS/Targeted methods to quantify pesticides, antibiotics, and steroids in honey, presenting a rapid and accurate technique for measuring xenobiotic residues in honey and detecting 157 compounds within 15 min. Rees et al. (2017) explored volatile compounds released by the pathogenic bacterium *Klebsiella pneumoniae* in Lysogeny broth using GC-TOFMS/Untargeted analysis, expanding the catalog of *K. pneumoniae*-associated volatile molecules from 77 to 150, providing early insights into the pathogen's volatile metabolomic profile. Fig. 3 illustrates the role of foodomics in metabolite analysis and its implications for human health.

4.2. Foodomics for understanding complex matrices

Scientific literature often investigates the activity and efficacy of pure bioactive molecules from foods or extracts. However, it's important to consider that food consumption involves complex matrices, where bioactive molecules interact with other substances that may enhance or hinder their effects. For example, Danesi et al. (2016) studied the cholesterol-lowering effects of dill and kale, both containing the same major bioactive molecule but differing in overall composition. They observed similar results but noted minor differences, emphasizing the importance of considering the whole food matrix in foodomics studies. The complexity of food matrices also affects digestion and bioavailability, as advanced techniques now allow researchers to study food bioaccessibility and simulate digestion and absorption processes. Foodomics approaches have been applied to understand the digestion of starch, cheese proteins, and meat, contributing to a better understanding of how diet impacts human health (Braconi et al., 2018).

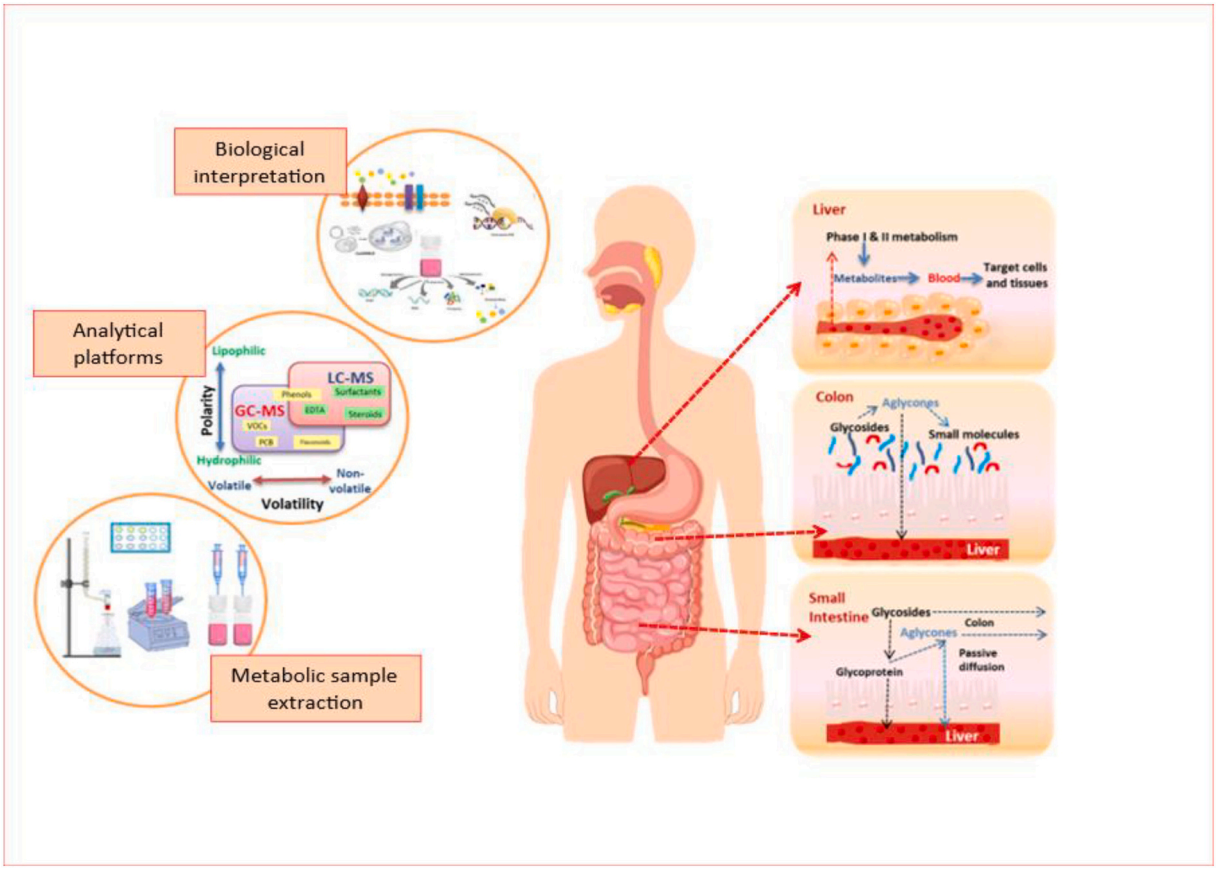

Fig. 3. Various analytical techniques like GC–MS and LC-MS utilized for identifying and quantifying metabolites, as well as evaluating the absorption, distribution, and interaction of crucial biomolecules within the human body.

Foodomics plays a pivotal role in understanding changes in food matrices caused by functional ingredients, especially within complex systems. It enables researchers to analyze these changes impact on human health at the metabolomic level (Ibáñez & Cifuentes, 2014), validating health claims through human intervention trials. These trials are crucial because the health effects of food may not be immediately observable, yet they shape international dietary standards, requiring precision and large sample sizes. Regulatory approval, particularly for health-related product labels, depends on permissible claims like disease risk reduction, therapeutic, functional, and general health claims. The quality of scientific evidence determines regulatory approval, underscoring the vital role of foodomics in ensuring product compliance throughout this process.

Previous studies have demonstrated the bioactivity of compounds derived from food matrices, but it is essential to remember that eating involves the absorption of complex matrices containing bioactive compounds and other molecules that may function synergistically or antagonistically. Understanding how food matrices influence health is an evolving area of research. Danesi et al. (2016) showed that while both dill and kale have cholesterol-lowering effects due to similar bioactive components, their differing compositions led to slight variations in results. This reinforces the need for foodomics research to consider the entirety of the food matrix rather than isolating individual compounds.

The breakdown and digestion of food matrices are equally complex. Novel approaches have been developed to explore food bioaccessibility and demonstrate digestion and absorption processes (Braconi et al., 2018). For instance, foodomics techniques have been employed to study protein digestion and the production of functional peptides (Picariello et al., 2013), as well as the digestion of starch (Lopez-Rubio et al., 2008), cheese proteins (Bordoni et al., 2011), and air-dried salted meat (Bordoni et al., 2014). Understanding food metabolism involves exploring the bio transformed components of the food metabolome to enhance our comprehension of how nutrition influences human health.

4.3. *Foodomics for food traceability and authenticity*

Foodomics is critical for ensuring food traceability, providing detailed information about the origin and composition of products throughout the supply chain, from production to retail. These "farm to fork" monitoring procedures enhance food quality, transparency, and accountability. Emerging Foodomics techniques, including metabolomics, proteomics, and genomic technologies, are revolutionizing traceability systems, which are essential for guaranteeing food safety and quality. Product authentication helps combat fraud and certifies a fair food supply by addressing issues related to inaccurate labeling and commercial deceit (Madesis et al., 2014). Authenticity and traceability are fundamental to protecting food safety in the supply chain (Fanelli et al., 2021; González-Domínguez, 2020). Genomic methods, particularly those examining DNA, are vital for developing genetic traceability systems to identify organisms and their products, as highlighted by Theodoridis et al. (2021). DNA-based techniques, which are highly resilient against environmental factors and food processing methods, offer precision in ensuring food authenticity. These methods have effectively traced the source and verified the genuineness of products such as olive oil (Chedid et al., 2020), sheep breeds (Heaton et al., 2014), grapes and wine (Zambianchi et al., 2021), wheat (Silletti et al., 2019), and coffee (Zhang et al., 2020).

Recent advancements have applied metabolomics to assess food traceability and examine molecular changes during food preparation. Metabolites, which are small molecules (less than 1500 Da), include nucleotides, amino acids, carbohydrates, lipids, and organic acids, reflecting cellular regulatory processes and interactions among proteins,

transcripts, and genes (Creydt & Fischer, 2018; Valdés et al., 2021). The metabolome is crucial for discovering bioactive compounds, understanding the effects of agricultural practices and food processing, and conducting authenticity studies (Danezis et al., 2016). In comparison to other omics fields, the metabolome shows a closer connection to the phenotype and is significantly influenced by external factors such as weather, soil composition, and storage conditions (Class et al., 2021).

The metabolome also offers insights into how plants respond to environmental, pathological, and physiological influences (Hamany Djande et al., 2020). Metabolomics acts as a bridge between genotype and phenotype, responding to both genetic and environmental changes (Brunetti et al., 2018). Analytical techniques like NMR (LC-NMR, LC-SPE-NMR, and GC-NMR) are widely used for metabolite characterization. While HPLC and LC are standard, UHPLC, LC-MS, and UPLC-ToF-MS are favored for their sensitivity, precision, and lower costs (Emwas et al., 2021). Combining these techniques provides a more comprehensive understanding of food composition and authenticity. For example, headspace solid-phase microextraction (HS-SPME) with GC–MS is valuable for food fingerprinting due to its high sensitivity and minimal sample preparation (Ch et al., 2021; Ongo et al., 2020).

Ongo et al. (2020) used metabolomics to determine the geographical origin of Arabica and Robusta coffee in the Philippines by analyzing volatile metabolites. Similarly, Putri et al. (2019) conducted metabolite profiling of *Coffea arabica* and *Coffea robusta* from different regions in Indonesia. HR-MS-based metabolomics is also used to investigate meat quality, identifying metabolites that influence processing, ripening, and shelf life. For example, Rocchetti et al. (2021) studied dry-fermented salami production by analyzing the molecular processes induced by microbial starters.

Next-Generation Sequencing (NGS)-based metagenomics has become vital for enhancing food safety and quality, profiling microbial communities in food products (Jagadeesan et al., 2019). Advanced technologies like qPCR and 16S rRNA gene sequencing are employed to track microbial populations during food storage. For example, a study on drinkable yogurt assessed microbial community stability over its shelf life, comparing yogurts with traditional *Bifidobacteria*-containing starter cultures to those without. The results showed that yogurts with *Streptococcus* and *Lactobacillus* starters had lower probiotic levels compared to those with added *Bifidobacterium* (Berezhnaya et al., 2021). These developments in Foodomics and advanced technologies offer valuable tools for improving food traceability, quality, safety, and authenticity across various food products.

5. Foodomics challenges

The advancement and application of sophisticated analytical techniques from a Foodomics standpoint have provided new opportunities to augment our understanding in the domain of food science. However, despite the advantages of Foodomics, certain barriers to its application still persist (Table 2). The utilization of analytical methods in Foodomics is expensive, time-consuming, and relatively new (García-Cañas et al., 2012). The current underutilization of omics methods in this sector is attributed to the high cost of equipment, the need for advanced technical skills in method development, software administration, and statistical data analysis. To make Foodomics methods more sustainable and environmentally friendly, there is a call for the development of greener approaches (Khakimov & Engelsen, 2017).

Advancements in mass spectrometry (MS) equipment, coupled with improved separation and fractionation techniques, are poised to enhance proteome, subproteome, and peptidome coverage in proteomics. Despite progress, challenges persist in metabolite identification and quantification in metabolomics, even with innovations like ion mobility analysis. Time constraints limit understanding of metabolic and physiological changes during molecular and cellular processes. Collaboration among scientists is vital for data comparison and sharing to achieve these objectives. It is crucial to further develop analytical

Table 2
Advantages and disadvantages of various Foodomics methods.

Method	Advantages	Disadvantages	References
Genomics	Comprehensive analysis of genetic material	High cost and complexity of data analysis	Herrero et al. (2012); Cifuentes (2014); Valdés et al. (2021)
	Predictive power for traits like allergenic proteins	Requires advanced bioinformatics tools	
	Identification of genetically modified organisms (GMOs)	Limited direct correlation with phenotypic traits	
Proteomics	Analysis of the protein composition of foods	Proteins can be highly dynamic and complex	Capozzi and Bordoni (2013); Cifuentes (2013); Valdés et al. (2021)
	Identification of bioactive peptides and allergens	Requires complex sample preparation	
	Correlation with functional properties of food	High cost and time-consuming	
Metabolomics	Provides a snapshot of the metabolic profile	High variability in sample preparation and analysis	Herrero et al. (2012); Valdés et al. (2021)
	Can identify biomarkers for food quality and safety	Data interpretation is challenging due to the complexity of metabolomes	
	Useful for nutritional studies	Limited by the sensitivity and specificity of analytical techniques	
Transcriptomics	Insights into gene expression changes in response to food components	mRNA levels do not always correlate with protein expression levels	Herrero et al. (2012); Cifuentes (2014); Valdés et al. (2021)
	Can identify pathways affected by diet	High cost and large data sets are difficult to manage	
	Useful for understanding the biological impact of food	Requires high-quality RNA, which can be challenging to obtain	
Lipidomics	Analysis of lipid profiles in food	Lipid extraction and analysis can be complex	Capozzi and Bordoni (2013); Shi et al. (2023)
	Helps in understanding fat composition and its impact on health	Limited databases for lipid identification	
	Can identify lipid biomarkers related to diseases	Sensitivity to storage and handling conditions of samples	
	Provides insights into the role of carbohydrates in health	Requires specialized analytical techniques	
Glycomics	Can be used to study food allergens	Limited availability of standards and reference materials	Afseth and Kohler (2012); Valdés et al. (2023)
	Focuses on the study of carbohydrates and glycoconjugates in food	Glycans are structurally complex and challenging to analyze	
	Provides insights into the role of carbohydrates in health	Requires specialized analytical techniques	
	Can be used to study food allergens	Limited availability of standards and reference materials	

technologies in each omics sector, standardize sample processes, improve computational methods, and establish functional annotated biological databases, among other initiatives.

6. Artificial intelligence (AI) coupled foodomics

Artificial intelligence (AI) algorithms, particularly those encompassing machine learning and deep learning models, have emerged as potent tools in the sector of food science. These algorithms prove invaluable in deciphering intricate patterns within mass spectrometric and spectroscopic data, thereby facilitating the identification of specific compounds, additives, or contaminants associated with various food compositions (Stilo et al., 2021). By correlating this analytical data with sensory attributes, nutritional content, or shelf life, researchers can glean invaluable insights into the quality, safety, and authenticity of food products (Putri et al., 2022).

For instance, a new generation of rapid methods is emerging, utilizing vibrational spectroscopy techniques (such as mid-infrared, near-infrared, and Raman spectroscopy) alongside other sensors like nuclear magnetic resonance spectroscopy and vision technology. Driven by advancements in AI-based analytics and the integration of multispectral/hyperspectral imaging with e-nose technology, these methods can quickly generate highly complex signals that reflect the properties and molecular structures of the foodstuffs being analyzed (Kutsanedzie et al., 2019). Various types of e-nose sensors are available, including organic polymers, metal oxides, quartz crystal microbalance, and even gas chromatography (GC), sometimes coupled with mass spectrometry (MS). These sensors can be used in a non-selective manner, utilizing chemical mass or patterns from a short GC column as an e-nose or "Z" nose. The field of artificial sensing technologies is advancing rapidly, demonstrating the capability to distinguish between different foods and edible products based on aroma, bitterness, and other basic tastes. Additionally, data analysis methods are being developed and applied to these artificial sensing systems, enabling the integration of responses with sensory and chemical data. This also allows for the combination of data from different technologies (such as e-noses and e-tongues) to more accurately mimic the human sensory system (Baldwin et al., 2011).

Moreover, electronic systems that mimic the senses of smell, vision, and taste are gaining significant attention from researchers, with their applications now extending to the evaluation of the quality and shelf life of meat and meat products. The key strength of *E*-nose, E-eye, and E-tongue systems lies in their versatility. They can characterize and differentiate the effects of various preservation techniques (such as chilling, freezing, and irradiation), detect adulteration (including meat from different species and vegetable proteins), grade quality (such as marbling), monitor quality deterioration during shelf life, and detect the presence of toxic microorganisms and compounds—all without the need for complex, time-consuming, labor-intensive, human-based methods (Munekata et al., 2023). For instance, e-nose and e-tongue technologies, along with their combined data, were used to distinguish seasonings from five different brands of instant starch noodles (Ma et al., 2023). Principal Component Analysis (PCA) accounted for over 85 % of the total variance in the e-nose and e-tongue data, indicating that both systems individually could differentiate between the brands. In summary, e-nose and e-tongue systems provide integrated flavor information, making them effective tools for rapid, easy, and accurate food odor analysis that is objective, highly automated, and cost-effective (Ma et al., 2023).

Of noteworthy mention is the rapid evolution experienced by GC × GC–MS, primarily propelled by advancements in AI techniques. Among these, the ROIMCR approach (regions of interest multivariate curve resolution) stands out as a sensitive and versatile technique for identifying and quantifying a diverse array of metabolites in complex samples, notably utilizing comprehensive two-dimensional liquid chromatography (LC × LC) (Gorrochategui et al., 2019; Pérez-Cova et al., 2021). This approach entails the identification of specific regions of interest (ROIs) within mass spectra, effectively highlighting metabolites present at low concentrations, resolving overlapping peaks, and facilitating the discovery of new biomarkers. Moreover, ROIMCR proves instrumental in elucidating metabolic pathways, thus contributing significantly to our understanding of food composition and functionality (Pérez-López et al., 2023).

AI concepts rooted in image processing and computer visualization have proven highly effective in advancing the interpretation of multidimensional data arrays, enabling the extraction of valuable insights and the prediction of sample properties. The intricate compositional makeup of food presents a significant challenge to conventional data processing methods. However, the multidimensional nature of Comprehensive Two-Dimensional Chromatography (C2DC) data presents unique opportunities for computer visualization and augmented visualization techniques.

Robust AI tools demonstrate remarkable capabilities in various domain (Fig. 4):

1. Compensating for Retention-Time Shifts: These shifts can distort images, making comparative visualization and related strategies difficult. AI algorithms adeptly correct for such shifts, enhancing the clarity and accuracy of visualizations.
2. Targeting Unknown-Knowns: AI models are proficient at discerning mass spectral signatures amidst co-elutions and misalignments, effectively identifying unknown compounds within complex data sets.
3. Contamination Source Identification: By analyzing chromatographic fingerprints, AI algorithms can pinpoint the source or sources of contamination within intricate mixtures, aiding in quality control and assurance efforts.
4. Aroma Signature Prediction: AI systematically identifies key food odorants even in the presence of interferents, facilitating the prediction of aroma signatures crucial for sensory evaluation and product development (Caratti et al., 2024).

7. Conclusion and future prospects

Foodomics is a rapidly advancing field that employs multidisciplinary techniques to explore the intricate connections between food components and human health. This innovative approach has transformed our understanding of how food influences the body, offering new strategies for addressing malnutrition and improving overall well-being. Foodomics has proven particularly effective in uncovering metabolic pathways, enhancing dietary quality, and proactively combating diseases. As technological advancements continue, Foodomics is poised to deliver even more precise and comprehensive insights into the impact of food on human health.

The future of Foodomics holds exciting prospects. With the integration of cutting-edge technologies, such as AI and advanced bioinformatics tools, the field is expected to achieve a deeper understanding of the complex interactions between diet and health. These innovations will enable more personalized nutrition strategies, tailored to individual needs, and contribute to the development of functional foods that promote better health outcomes. As Foodomics continues to evolve, it will play a crucial role in shaping the future of nutrition science and public health, offering transformative solutions for improving the quality of life worldwide.

CRediT authorship contribution statement

Dipendra Kumar Mahato: Project administration, Data curation, Conceptualization. **Madhu Kamle:** Writing – review & editing, Supervision, Conceptualization. **Shikha Pandhi:** Writing – review & editing. **Surabhi Pandey:** Writing – original draft, Methodology, Investigation. **Akansha Gupta:** Writing – original draft, Visualization, Validation, Methodology. **Veena Paul:** Writing – original draft, Visualization,

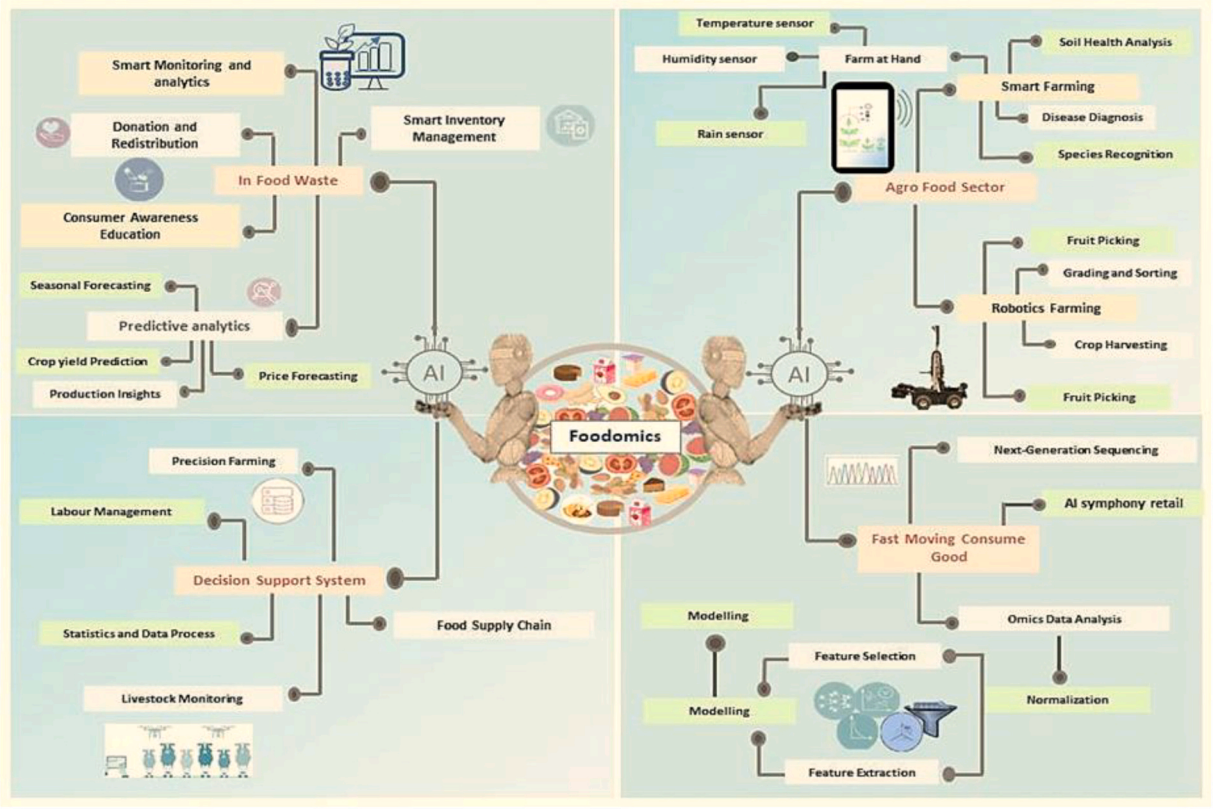

Fig. 4. Artificial intelligence (AI) tools, combined with various advanced technologies and techniques, enhance agriculture farming and food management, leading to improved crop yields, efficient resource use, and better management of food quality for human health.

Validation, Methodology. **Rhythm Kalsi:** Writing – original draft, Validation, Methodology. **Swati Agrawal:** Writing – original draft, Visualization, Methodology, Investigation. **Dawrul Islam:** Writing – original draft, Visualization, Validation, Methodology. **Shubhra Khare:** Resources, Methodology. **Ajey Singh:** Writing – review & editing. **Pradeep Kumar:** Writing – review & editing, Supervision, Formal analysis, Data curation, Conceptualization. **Safia Obaidur Rab:** Funding acquisition, Writing – review & editing. **Mohd Saeed:** Funding acquisition, Writing – review & editing.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

No data was used for the research described in the article.

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