

Application of Multi-omics in Food Safety Detection

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Abstract A primary objective of food science is to ensure food quality and safety. While detection techniques for known hazards are well-established, significant challenges remain in identifying unknown and potential sources of food safety risks and determining their composition and origin. These challenges encompass complex issues such as food authenticity verification, adulterant identification, and allergen tracing. Multi-omics approaches enable a transition from qualitative identification to precise quantitative analysis, from targeted detection to non-targeted screening, and from multi-component to comprehensive whole-component analysis. Consequently, multi-omics strategies offer a more accurate and efficient means to identify and validate the safety of food components, demonstrating unique advantages in addressing food adulteration, authenticity confirmation, and allergen screening. More importantly, these approaches establish a critical link to personalized diet, enabling the transition from general food safety to individualized health optimization. This review summarizes the fundamental concepts and strengths of multi-omics technologies, including genomics, transcriptomics, proteomics, and metabolomics. It further elaborates on the current applications and future prospects of multi-omics in food safety detection, with a specific focus on key areas such as food authenticity verification, adulteration detection, and allergen analysis. The aim is to establish a theoretical foundation for the application of multi-omics in the food sector and to effectively advance the development of food safety detection methodologies.

Key words Multi-omics; Authenticity; Detection; Adulteration; Allergen

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With the continuous growth of the global population and the improvement of living standards, public concern regarding food safety has increased significantly, leading to a growing demand for rapid and sensitive detection of potentially harmful substances in food. On one hand, incidents of foodborne illnesses occur frequently, posing substantial risks to public health. In recent years, excessive residual contaminants and emerging foodborne pathogens have been frequently detected in dairy products^[1], meat products^[2], and aquatic products^[3], presenting significant hazards to consumers. On the other hand, food fraud practices such as false labeling^[4], ingredient adulteration^[5], and substandard quality^[6] seriously compromise food safety. Such deceptive practices undermine public trust in the food system and damage the credibility of the entire food industry^[7]. Furthermore, the lag in the development of food traceability and information platforms has also become a latent concern.

Traditional food safety detection methods primarily rely on monitoring single components, which often fail to reflect systemic changes in the food system or identify unknown hazardous factors. With the advancement of food adulteration techniques, conventional approaches have become increasingly inadequate for detecting food fraud, presenting a regulatory challenge in global food safety governance.

Multi-omics, as a vital component of systems biology, in-

tegrates data from multiple molecular levels such as genomics, transcriptomics, proteomics, and metabolomics to comprehensively investigate the structure, function, and dynamics of biological systems. This approach utilizes high-throughput technologies, including gene sequencing, mass spectrometry, and nuclear magnetic resonance, along with bioinformatics tools, to enable holistic analysis of biological processes. In the field of food science, multi-omics has been widely applied to assess food quality, functional components^[8], and the safety of genetically modified foods^[9–11], offering a systematic perspective for elucidating food properties and underlying biological pathways^[12]. More importantly, this integrative multi-omics approach establishes a critical link to personalized diet (Fig. 1), enabling the transition from general food safety to individualized health optimization. Fig. 2 illustrates the research pathway of systems biology based on integrated multi-omics approaches.

Concept and Advantages of Multi-omics

In the field of food science, multi-omics refers to the application of multiple omics technologies, such as genomics, transcriptomics, proteomics, and metabolomics, to analyze food composition, safety, and the relationship between food and health. This approach offers a comprehensive view of food components and their mechanisms of action, enabling a deeper understanding of the molecular complexity of food. It thus contributes to improving food quality, enhancing food safety, and developing new functional foods. By accurately analyzing genes, proteins, metabolites, and other components in food, multi-omics aids in identifying specific constituents, such as nutrients, pathogenic factors, or functional ingredients. Understanding how these components affect human health supports the design of foods that promote health and prevent diseases.

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The application of multi-omics technologies allows for more precise detection of microorganisms and contaminants in food, thereby improving food safety. It is also used in monitoring food quality to ensure consistency and compliance throughout the

production process. Genomics, transcriptomics, proteomics, and metabolomics have been widely employed in relevant research. Depending on the study objectives, the omics strategies and the technical methods employed vary accordingly (Fig. 3).

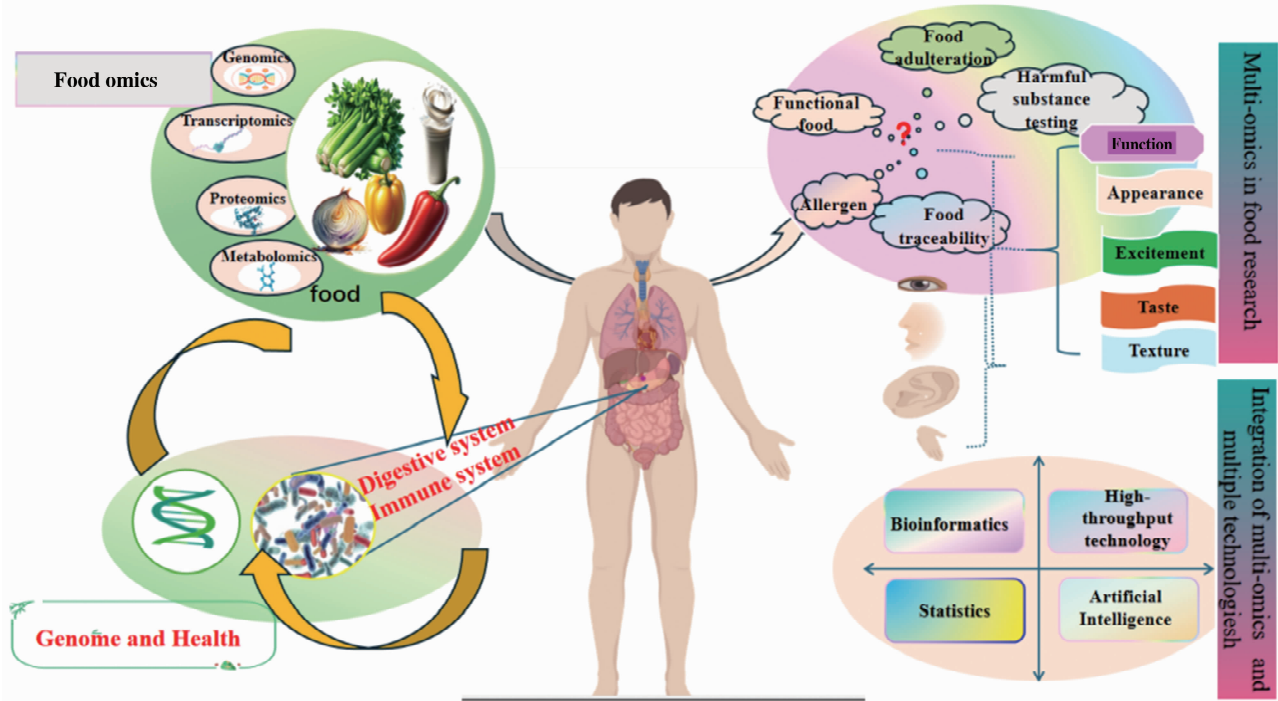


Fig. 1 Through the link between multi-omics strategies and personalized diet

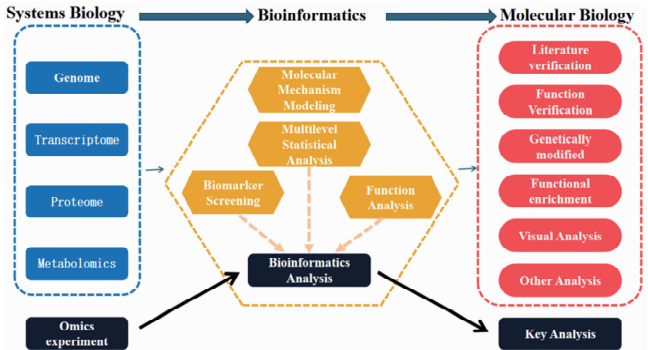


Fig. 2 Research pathway of systems biology based on integrated multi-omics approaches

Genomics

The genome refers to the complete set of genetic information carried by a specific organism, including both coding genes and non-coding DNA sequences. Genomics is a discipline that systematically studies the structure, function, expression regulation, and evolutionary patterns of genomes. By integrating high-throughput sequencing technologies and bioinformatics methods, it elucidates the molecular mechanisms linking genetic information to phenotypic traits in organisms.

In the field of food science, the application of genomics is primarily focused on addressing three key aspects: First, it concerns food safety and authenticity assessment. Genomic techniques

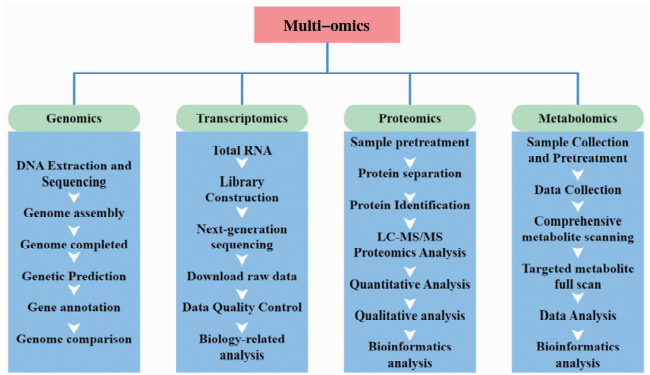


Fig. 3 Multi-omics analysis workflows and methods

are used to identify suitable biomarkers at the DNA level, providing a novel indicator for evaluating the safety and authenticity of food. This approach renders the assessment process more precise and rational, ensuring that consumers receive reliable and truthful food information^[13]. Second, it covers efficacy evaluation of functional foods. The application of genomics not only aids in identifying appropriate biomarkers to measure the effects of functional foods, but also facilitates the development of novel, targeted, and effective functional food products. By utilizing genomic technologies to discover biomarkers for evaluating the efficacy of functional foods, and based on these, developing new targeted and effective functional foods, their effectiveness and market value can be

enhanced, thereby contributing to consumer health^[14]. Third, it involves personalized genotype-based nutrition strategies. These strategies optimize health and nutrition based on individual genetic profiles^[15]. By identifying genes associated with disease development, personalized dietary plans can be formulated to promote individual health, prevent and manage chronic diseases, and provide tailored nutritional support. Fig. 4 illustrates the strategy for developing personalized diets.

Metagenomics, functional genomics, and nutrigenomics collectively form an integrated research framework spanning from fundamental analysis to end-use applications. Metagenomics analyzes the genetic material of microorganisms within samples to decipher the structure of microbial communities in food. It is widely employed in fermented food technology to monitor microbial dynamics at different fermentation stages, thereby simplifying the characterization of quality or spoilage biomarkers and improving the control of fermentation processes^[16]. Functional genomics delves into gene functions, utilizing high-throughput technologies to clarify key genes and their mechanisms related to food quality, flavor, and other traits^[17]. It enables the isolation of genes associated with food quality to optimize food processing techniques, enhance nutritional quality, and develop new functional foods. Nutrigenomics connects genomic information with human health needs by studying the interactions between dietary components and individual genes, thereby providing a scientific basis for developing personalized nutrition plans^[18].

Transcriptomics

The transcriptome refers to the complete set of RNA molecules within a biological organism, primarily composed of messenger RNA (mRNA), ribosomal RNA (rRNA), transfer RNA (tRNA), and various non-coding RNAs (ncRNA). Transcriptomics is a technology used to study the behavior of microorganisms under different environmental conditions. mRNA represents the link between genotype and phenotype and is crucial for understanding the functional elements of the genome and the molecular composition of cells, thereby holding significant value in biological research. These technologies employ high-throughput transcriptomic tools, such as RNA sequencing (RNA-Seq) and microarrays, to assess the survival of foodborne pathogens under various conditions within the food production chain. Transcriptomic studies are essential for fully understanding the resistance mechanisms and metabolic pathways of foodborne pathogens, aiding in the development of new control strategies. For example, transcriptomics has been applied to evaluate the survival of foodborne pathogens under conditions such as biofilm formation, food matrix and its environment, heat treatment, acid tolerance, biocides, and food preservatives^[19].

Furthermore, transcriptomics has also been applied in various plant tissues through techniques such as single-cell/nucleus RNA sequencing (scRNA/snRNA-seq), single-cell/nucleus assay for transposase-accessible chromatin (scATAC/snATAC-seq), and spatial transcriptomics sequencing. The rapid development of single-cell RNA sequencing (scRNA-seq) methods enables researchers

to study plant organs with high resolution and throughput. Existing studies have integrated transcriptomics with functional enrichment analysis to reveal the multi-target mechanisms of rosemary polyphenols in colon cancer, providing a paradigm for anticancer research on dietary polyphenols^[20].

Proteomics

Proteomics is closely associated with the protein-coding portion of the genome and is widely applied in food technology. Proteins play key roles in biological organisms and processes such as splicing, and protein processing represents important modifications from a biological perspective. Therefore, proteomics encompasses not only protein sequences but also broader aspects of biological sciences. Peptidomics, a branch of proteomics, focuses on characterizing polypeptide sequences and studying interactions among peptides^[21]. This mechanism can be understood as mass spectrometry (MS)-based proteomics enabling the detection and definition of any covalent modifications in post-translationally modified proteins^[22]. A large number of bioactive peptides derived from fermented milk and its hydrolysates have been identified using high-performance liquid chromatography (HPLC) coupled with ion trap MS, offering a promising approach that avoids time-consuming and complex steps during isolation and purification. Matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) MS is employed for qualitative analysis and characterization of proteins/peptides^[23]. MALDI-TOF MS has been successfully applied to determine the content and molecular weight of Ginkgo seed proteins treated with high hydrostatic pressure^[24]. In proteomic research, two-dimensional polyacrylamide gel electrophoresis (2D-PAGE) is an efficient and reliable method for separating proteins based on both mass and charge^[25]. Proteomics also serves as an important and powerful tool in nutritional science. The combinatorial peptide ligand library (CPLL) method is a reliable analytical technique that enhances signals from trace components to achieve broader proteome identification via MS, and has been applied in numerous studies on fruits and fruit ripening^[26].

Metabolomics

Metabolomics is the discipline concerned with the dynamics, composition, interactions of metabolites within cells, and their responses to changes in any organism. It is highly relevant to nutritional research and is also referred to as metabolomic analysis, metabolic profiling, or metabonomics. Metabolomic analysis is typically categorized as either targeted or untargeted. Targeted analysis primarily involves the multiplexed analysis of known metabolites, including the absolute qualitative and quantitative analysis of target substances using standards. Untargeted, comprehensive metabolomics aims to gather information on as many substances as possible, offering broad coverage of metabolites. Metabolomics is applied in food science through two distinct approaches. Firstly, the metabolic profiling of food can serve as a reference to reflect its status. For instance, untargeted metabolomics and volatile aromatic compounds have been used to predict the sensory attributes of beef jerky as evaluated by both experts

and consumers. Both metabolites and volatile aromatic compounds showed close correlations with aging, quality grade, and degree of doneness. Metabolomics was able to differentiate quality grades and aging times, which aids in creating flavor distinctions. Untargeted metabolomics can be used to differentiate and characterize the sensory profiles, consumer preferences, and volatile aromatic compound features of beef jerky. When combined with volatile aromatic compound data, it accounted for 86% of the variation in scores from expert and consumer sensory panels^[27]. Secondly, food safety can be assessed by examining the impact of food on endogenous metabolites within organisms^[28]. Fig. 5 illustrates the application of multi-omics in food science.

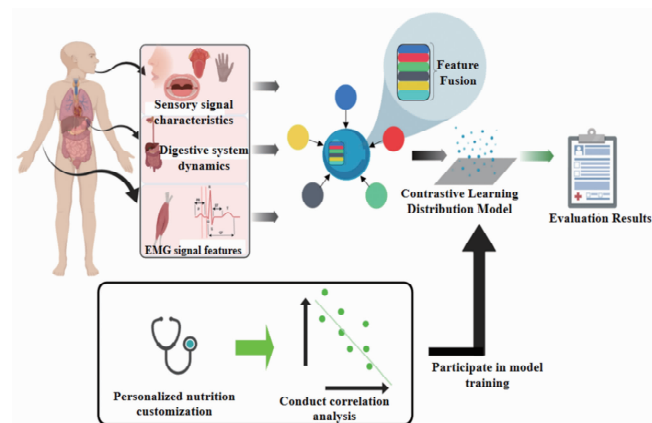


Fig. 4 Strategy for developing personalized diets

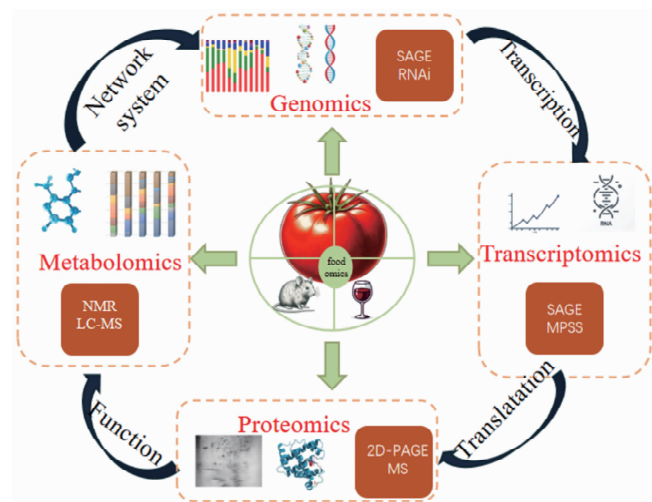


Fig. 5 Application of multi-omics in food science

The core strength of multi-omics research lies in its systematic integration capability, which overcomes the limitations of traditional single-omics analyses. While a single omics layer can provide information in a specific dimension, it often fails to capture the dynamic regulatory networks of interactions among genes, transcripts, proteins, metabolites, and microbial communities within complex food systems. It is precisely these cross-level, non-linear interactions that constitute the core mechanisms driving the evolution of food quality, the emergence of safety hazards, and

nutritional health effects. The maturity and widespread application of the multi-omics concept have been facilitated by the rapid advancement and cost reduction of omics technologies, such as high-throughput sequencing and high-resolution mass spectrometry, making the simultaneous acquisition of multi-level data a reality. Concurrently, progress in computational biology methods data integration algorithms, network analysis, and statistical modeling provides crucial support for processing, correlating, and interpreting these vast, heterogeneous, and complex datasets. Leveraging this integrative analytical capacity, multi-omics strategies demonstrate powerful predictive potential. They can systematically map the dynamic trajectories of key quality indicators flavor, texture, shelf-life, enable earlier identification of potential risk factors/hazard signals, and provide in-depth insights into the intrinsic mechanisms through which food components modulate health effects by influencing the molecular networks of the host and its symbiotic microbiota. This establishes multi-omics as an indispensable core research paradigm for understanding and predicting the behavior of food throughout its lifecycle.

Application of Multi-omics in Food Safety Testing

Identification and characterization of functional factors

Functional foods refer to nutritional products that confer at least some beneficial effects on human physiological functions, thereby improving health or reducing the risk of disease. As interest in enhancing human health grows, functional foods are gradually enabling people to achieve more stable and healthy development in terms of bodily metabolism^[29]. Metabolomics and multi-omics integration strategies are profoundly transforming the paradigm for the identification and characterization of functional constituents. Compared to traditional single-indicator detection methods such as high-performance liquid chromatography with ultraviolet detection (HPLC-UV), metabolomic techniques integrating high-resolution mass spectrometry (*e.g.*, UPLC/Q-TOF-MS) and nuclear magnetic resonance spectroscopy (HR-MAS NMR) have increased analytical throughput by 50 to 100 times. This successfully overcomes the limitations of traditional analytical methods and marks a shift from single-component detection to multi-dimensional bioactivity assessment. This technological system not only enables the high-sensitivity (reaching ng/ml levels) dynamic tracking of the transformation of ginsenosides during the processing of ginseng products^[30], and comprehensively elucidates the evolution patterns of 124 sulfur-containing metabolites during the aging stages of black garlic^[31], but also accurately evaluates the impact of heat treatment on the phytochemical profile of black raspberries via untargeted analysis, revealing the stability of its key functional factors (quercetin, phenolic acids) and the dynamic changes of anthocyanin degradation products^[32]. More importantly, the multi-omics integration strategy has achieved a leap from component identification to functional verification. Whole-genome sequencing precisely identified the probiotic functional gene clusters

in *Bifidobacterium longum* BLB2-01, and subsequent systematic phenotypic analysis successfully verified its key functions, including gastrointestinal tolerance, antioxidant activity, and cholesterol-lowering effects^[33]. Furthermore, this strategy has elucidated the mechanisms of action of functional components. Multi-omics correlation studies have confirmed that green tea extract activates the skin glutathione metabolic pathway by modulating the abundance of intestinal bifidobacteria, providing molecular evidence for the "gut-skin axis" theory^[34]. This signifies that research on functional factors has moved from static compositional analysis to a new stage of systematic functional verification^[35]. The identification and characterization of functional factors have thus entered a new era. Modern metabolomics has increased analytical throughput by 50–100 times, enabling the efficient and sensitive identification of complex functional constituents. Meanwhile, multi-omics correlation strategies, such as genomics-metabolomics integration, have shifted the research perspective from static compositional analysis to dynamic functional verification, truly achieving a closed loop from detection of presence to confirmation of function. In the future, with the integration of more innovative omics technologies and bioinformatics tools, the identification and characterization of functional factors will become more precise and efficient, providing an inexhaustible driving force for the scientific design and personalized application of functional foods.

Application in food adulteration

Food adulteration compromises food quality, while the application of omics technologies enables rapid and accurate adulteration detection, thereby safeguarding public health. Milk serves as a vital source of human protein. Some manufacturers may use whey as a partial substitute for milk in cheese production to reduce costs^[36]. Whey exhibits high thermal stability and is also a major allergen in dairy products. In proteomic analyses, β -lactoglobulin can serve as a biomarker for whey, facilitating adulteration detection with a sensitivity as low as 10%^[37].

Milk fat globule membrane (MFGM) proteins are crucial nutritional components in infant formula. Galani *et al.*^[38] developed a targeted proteomics method capable of absolutely quantifying four MFGM proteins, demonstrating excellent precision and accuracy. This method is well-suited for large-scale, multi-batch testing within the infant formula industry, aiding in the elevation of industry standards and assisting in the prevention of adulteration.

Food authenticity detection technology is undergoing a paradigm shift from single omics to integrated multi-omics approaches. Regarding meat adulteration, while traditional elemental analysis can discriminate offal tissues^[39], it faces limitations in resolving mixed samples. Genomics technologies, utilizing DNA barcoding (with a detection limit of 0.1%)^[40] and 16S rRNA sequencing^[41], enable species-specific identification. In the field of edible oil adulteration, traditional fatty acid profiling is limited by the loss of minor metabolites in refined oils^[42]. In contrast, four-dimensional metabolomics, employing trapped ion mobility spectrometry coupled with liquid chromatography and high-resolution

mass spectrometry (TIMS LC HRMS), expands metabolite coverage to approximately 1 200 compounds. When combined with machine learning models, this approach achieves a detection limit for refined olive oil adulteration as low as 1%, representing a fivefold increase in sensitivity compared to DNA barcoding technology^[43]. For high-value spices, hydrogen-1 nuclear magnetic resonance (¹H NMR) spectroscopy combined with partial least squares discriminant analysis (PLS-DA) models achieves 100% discrimination of adulteration types. Its chemometric algorithms enhance the coefficient of determination (R^2) for quantitative prediction to 0.99, significantly outperforming the benchmark value of 0.85 associated with traditional chromatographic methods^[44]. Honey is highly valued for its rich nutritional composition and medicinal properties. Some suppliers substitute premium honey with cheaper honey or sweeteners for profit. Manuka honey, derived from *Leptospermum scoparium*, is globally marketed for its numerous health benefits, but this popularity has also led to widespread adulteration. Traditional methods for analyzing Manuka honey composition, such as measuring methylglyoxal and dihydroxyacetone content, are often insufficient for effective adulteration detection. Proteomics studies have identified characteristic proteins in Manuka honey that serve as unique biomarkers, aiding in its authentication and verification^[38]. As summarized in Table 1, biomarkers and indicators discovered through multi-omics technologies have proven effective in assessing food authenticity and safety.

Faced with complex food matrices and sophisticated adulteration practices, single-omics approaches often prove inadequate. In contrast, the synergistic effect of multi-omics can break through these bottlenecks. When genomics is limited by DNA degradation, peptide markers from proteomics and elemental fingerprints from metabolomics can corroborate each other, enabling high-resolution analysis of mixed samples. More importantly, bioinformatics facilitates in-depth mining of vast, multidimensional datasets through algorithms such as machine learning, constructing predictive models that simultaneously consider gene sequences, protein expression, and metabolite concentrations. This process can uncover novel risks hidden within the data. This new paradigm of untargeted discovery and systemic diagnosis, by building intelligent identification systems that are faster-responding, broader-coverage, and deeper-insight, ultimately provides unprecedented technological support for ensuring the transparency and safety of the global food supply chain.

Application in food traceability

The core challenge in food authenticity verification lies in establishing a precise raw material traceability system, which involves species identification, geographical origin authentication, and processing method recognition. However, it is often limited to the analysis of predetermined indicators, making it difficult to counter complex adulteration practices. The groundbreaking advances in omics technologies have provided multidimensional solutions for this field: genomics enables species-specific identification, metabolomics deciphers characteristic metabolites associated

with geographical origin, and proteomics can trace processing histories.

Taking the geographical origin authentication of ginger as an example, while traditional methods including isotope ratio mass spectrometry (IRMS) and multi-element analysis can distinguish among seven major production regions in China, they carry the risk of characteristic overlap^[54]. Untargeted metabolomics, utilizing liquid chromatography quadrupole time of flight mass

spectrometry (LC QTOF MS), identifies multiple groups of differential metabolites (such as phenolic and flavonoid compounds). This approach significantly enhances discrimination efficacy compared to traditional isotopic analysis ($P < 0.05$) and reveals the influence of environmental factors on metabolic profiles^[55]. This technology overcomes the single-dimension limitation of traditional physicochemical analyses, achieving traceability analysis at the level of metabolic pathways.

Table 1 Biomarkers identified by multi-omics techniques for food authenticity evaluation

Food type	Characteristics	Omics methods and techniques	Biomarkers	References
Mare's milk	Adulteration of mare's milk	Proteomics and metabolomics	Osteopontin (OPN) and serotransferrin (TF)	[45]
Goat's milk	Goat's milk adulterated with cow's milk	Proteomics and metabolomics	Choline and N-formyl amino acids, lactate and 4-aminobutyric acid	[46]
Linseed oil	Adulteration of linseed oil	GC-MS analysis and chemometrics	Phytosterols	[47]
Olive oil	Adulteration of olive oil	UPLC-QTOF-MS	Triacylglycerols	[43]
Pomegranate juice	Adulteration of pomegranate juice	GC × GC-MS	Terpinen-4-ol, α-terpineol, 1-octen-3-ol, linalool, terpinene, bergamotene, nonanal	[48]
Grapefruit juice	Adulteration	Untargeted metabolomics	Neohesperidin and naringin	[49]
Sichuan pepper	Adulteration of Sichuan pepper	Metabolomics combined with chemometrics	Sn-3 triacylglycerols	[44]
Wine	White wine	Proteomics	Cystatin and lipid membrane ATPase	[50]
Beef tallow	Adulteration	NMR and metabolomics	Monoglycerides	[51]
Cocoa butter	Adulteration	Untargeted metabolomics by HPLC-MS	Flavonoids, fatty acids, terpenoids, and lysophospholipids	[52]
Lamb	Adulteration	Untargeted metabolomics	Lysophospholipids	[53]
Pork	Adulteration with lymph nodes	Metabolomics	Amino acids; blood lipids; nucleic acids; organic acids; sugars; vitamins	[5]

To address the adulteration challenges of high-value foods, proteomics technologies demonstrate unique advantages^[56]. In the field of honey origin authentication, a novel method for geographical traceability of honey that does not rely on plant reference databases has been developed. By integrating metagenomics with machine learning, this method achieves high-precision, high-resolution discrimination of honey geographical origins^[57].

Detection of harmful substances

Food contamination is categorized into biological, chemical, and physical types, with biological contamination being the most common in daily life. Pathogenic microorganisms can infect hosts through various pathways such as water, air, and food, exerting adverse effects on the host organism. Infections caused by pathogenic bacteria represent a common route of transmission, and food poisoning incidents induced by such pathogens frequently occur.

Inorganic arsenic exposure constitutes a major global public health concern. Proteomics-based research enables the detection of proteins in food affected by arsenic. During rice growth, plants absorb not only nutrients but also arsenic present in the soil. The World Health Organization classified arsenic as a carcinogen in 2017, with arsenic trioxide being a common arsenic compound. The arsenic absorbed by rice ultimately resides within the grains and may alter their protein composition. Long-term ingestion of inorganic arsenic can induce various cancers, skin diseases, cardiovascular diseases, neurotoxicity, and diabetes^[58]. Therefore,

proteomics-based research methods can effectively detect changes in proteins in rice and other foods under arsenic influence^[59]. For instance, major proteins in rice and maize include cysteine synthase, S-adenosyl-L-methionine, jasmonic acid, antioxidant-related proteins, ATP synthase, succinyl-CoA synthase, cytochrome P450, malate dehydrogenase, Rubisco, chloroplasts, and formate dehydrogenase^[60].

Salmonella is a primary foodborne pathogen posing significant risks to food safety and public health. Specifically, non-typhoidal *Salmonella* is a leading cause of foodborne illnesses globally associated with meat products. Comparative genomic analysis of *Salmonella* isolates from various retail meats has been conducted to identify genomic features and determinants of antibiotic resistance, thereby contributing to enhanced food safety^[2]. Through metagenomics, information regarding the genomic content of different members within a microbial community can be obtained^[61]. A crucial aspect of aquatic product quality is the rapid and accurate identification of bacterial species. From this perspective, omics technologies have proven to be effective techniques for assessing the quality and safety of seafood. These technologies can pinpoint and detect low-level contamination by pathogenic and spoilage bacteria and can be used to study the impacts of seafood processing and storage. Integrating food processing with monitoring microbial properties using traditional microbiological analyses, supplemented by molecular techniques, can establish a baseline for developing

faster, more sensitive, and more reliable screening methods for seafood safety^[62]. Proteomics has been applied to detect and identify bacterial species in aquaculture products, whether by directly detecting bacterial species in fish products or by isolating and cultivating bacterial species in different media^[63]. Innovative rapid targeted proteomics workflows have demonstrated their utility for the swift detection of fish parasites and microorganisms in aquaculture^[64].

Food allergens and their sensitization mechanisms

Food allergy is a complex and heterogeneous disease that severely impacts the quality of life for susceptible individuals and can even be life threatening. Due to its multifactorial nature involving genetic predisposition, environmental factors, and the microbiome, achieving accurate, rapid, and reliable diagnosis remains a significant challenge^[65]. The rapid development of high throughput technologies and computational methods has positioned omics approaches as effective tools for elucidating the pathogenesis of food allergies. They facilitate the identification of biomarkers associated with specific patient profiles, thereby advancing the development of personalized and precise interventions^[66]. Genomics applications can identify common genetic variants linked to food allergies^[67]. Transcriptome analysis clarifies gene expression differences between allergic and nonallergic subjects^[68], helping to uncover novel immune processes. The application of proteomics to analyze allergenic proteins deepens the understanding of allergens^[69] and elucidates the sensitization mechanisms of various foodborne allergenic proteins. Integrating these findings with clinical data can inform the design of appropriate treatment strategies.

To address this issue, certain food processing methods aim to reduce the allergenicity of foods. Most food allergies are triggered by proteins or their breakdown products. While any food can potentially cause an allergic reaction, the majority are associated with proteins from eight major allergen groups such as peanuts, tree nuts, eggs, milk, fish, shellfish, wheat, and soy. Applying proteomic methods to study the in vitro degradation of peanut allergens in simulated gastrointestinal environments represents a new research direction in allergomics. To evaluate the impact of heating on the structure related allergenic properties of shrimp allergens including tropomyosin (TM), arginine kinase (AK), myosin light chain (MLC), and sarcoplasmic calcium binding protein (SCP), peptidomics and epitope correlation analysis were performed on tryptic digests from raw, fried, and roasted shrimp extracts. Among these four allergens, TM exhibited the most significant changes in released peptides and epitopes. AK provided the epitope matching sequence 331 MGLTEM AVK 340 as a common differential peptide indicative of heat treatment. These results offer new insights into the structural impact of processing on major shrimp allergens and the potential of peptides as processing biomarkers^[70]. Hazelnuts and their byproducts are rich in various bioactive components, primarily polyphenols, which possess antioxidant, antimicrobial, and prebiotic properties. This enhanced functional profile is reflected in an increased prevalence of nut

allergies. Yin *et al.*^[71] developed a sensitive and rapid method based on CRISPR and qPCR capable of detecting trace amounts of hazelnut in processed foods. This detection method, termed CRISPR based Nucleic Acid Detection (Crinac), can identify 1% hazelnut in mixtures and allows for species identification in complex processed samples. The entire detection process can be completed within 60 min. By employing PCR amplification followed by CRISPR/Cas12a activity, endpoint fluorescence measurement for hazelnut quantification is achieved. This approach shortens assay time and eliminates the need for expensive real time PCR instruments. Gao *et al.*^[72] conducted a systematic study on the compositional changes and potential allergenicity of soluble proteins from selenium enriched peanut leaves (SPLPs) using a proteomics approach combined with bioinformatics analysis and molecular docking. They found that low-level selenium treatment enhanced the expression of photosynthesis related proteins by activating the antioxidant system and glutathione metabolism, whereas high level selenium treatment suppressed certain metabolic pathways. Furthermore, the study identified proteins containing Bet v 1 domain as the major allergens in peanut leaves. However, their immunoglobulin E (IgE) binding activity, as validated by enzyme linked immunosorbent assay (ELISA), was significantly lower than that of peanut seed proteins such as Ara h 2, indicating that SPLPs possess low allergenicity characteristics.

Conclusion

Different omics approaches possess distinct advantages in food adulteration detection depending on the type and characteristics of the food. However, most research on specific foods has focused on using a single omics methodology. Some studies have attempted to apply two or three omics techniques simultaneously to the same food sample to better elucidate the relationships relevant to food safety detection from multiple levels and different perspectives. Furthermore, while multi-omics research has made significant progress in food safety and detection, revealing numerous critical biomarkers and related pathways, we continue to face the challenge of effectively managing and analyzing these vast and complex datasets. The rise of artificial intelligence has opened new avenues for the integration and application of multi-omics technologies. Artificial intelligence, particularly machine learning and deep learning algorithms, leverages its powerful data processing and pattern recognition capabilities to transcend the boundaries of individual omics techniques, enabling the fusion and analysis of data from different biological layers. This cross-omics integration not only compensates for the limitations of singular omics approaches, but also uncovers the complex correlations and interactions among various levels within the food biological system. The application prospects of machine-learning-based multi-omics in food safety include fostering stronger interdisciplinary collaboration, developing sophisticated artificial intelligence and statistical algorithms, improving data processing, visualization, and interpretation tools with user-friendly interfaces, and advancing

computational and data management efforts. Progress in explainable artificial intelligence and machine learning, real-time analytical platforms, and the emergence of cost-effective, portable omics tools are likely to drive broader accessibility.

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