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Foodomics: A new approach in food quality and safety

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ABSTRACT

Background.

The progress in the analytical methods in food science and technology brought about a novel and modern approach concerning human health and food quality and safety. Foodomics is a recently coined term and is an integration of relevant omics disciplines. The constituent omics approaches have extensively been applied in biology and medical domains so far. Recently, food and nutrition scientists have also been interested in these omics research.

Scope and Approach.

Foodomics is a powerful tool in determining the food constituents and nutrients at the molecular level. Lately, researches in the food area have been fuelled by using the analytical techniques through different omics disciplines like proteomics, metabolomics, lipidomics, nutrigenomics, metagenomics and transcriptomics. Numerous research papers address the use of different omics technologies separately or in combination not only in analysing the food constituents but also in food authentication and evaluation of food safety and quality. It is evident that using the advanced analytical techniques in omics research has empowered the scientists looking into food and nutrition science at a broad perspective.

Key Findings and Conclusions.

This review discusses the recent developments in the analytical methodologies used in each "omics" discipline and how foodomics approach elucidates the arguments concerning food quality, food safety, the origin of food, human nutrition and relatedly human well-being.

1. Introduction

The term "Foodomics" was first denominated in 2009 and defined as "a discipline that studies the food and nutrition domains through the application and integration of advanced omics technologies to improve consumer's well-being, health, and confidence" and it is a combination of different related *Omics* technologies such as transcriptomics (mRNA), nutrigenomics (nutrients), proteomics (proteins), metabolomics (metabolites) and genomics (detection of genes) (Bordoni et al., 2014; Cifuentes, 2017). The connotation of the suffix *-Omics* should be clearly understood to interpret the term of Foodomics. The word "Omics" is a derivation of the Latin Word "omne" which means everything, totality, wholeness, entirety even referring to the interactions between the disciplines that it is used as a suffix. The meaning of "omics" fundamentally involves the determination of actions and roles of molecules that generate cells (Williams & Anderson, 2018).

Since there has only been a decade that the term "Foodomics" was coined, these omics technologies have highly attracted attention in recent food, nutrition and health researches (Herrero, 2018). These omics technologies are related to analysing food composition, food quality, food authentication, the activity of food proteins and peptides, identification of food allergens, toxins, genetically modified foods as well as deciphering of the human genome and find application area in understanding the effects of food at the genetic level, enabling a higher level of understanding of new functions of food and process technologies (Pinu, 2015; Schasteen, 2016; Andjelkovic & Josic, 2018).

Food is known to be rich in various macro- and micronutrients; proteins, lipids, carbohydrates and minerals, vitamins, phytochemicals, antioxidants, which do not have single functions in the human body. The same omic technologies are considered in both food science and nutrition science, but the samples can be different. The reliability and reproducibility of the analytical methods are of key importance to ensure food quality and food safety. These analytical methods are also used for the detection of some exogenous compounds which have a

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harmful impact on human health and the chief concern for food safety (Fasoli & Righetti, 2015; Zhang et al., 2015). Foodomics produced reliable results in determining the food allergens (Andjelkovic et al., 2015) and nutritional elements in milk-based infant formulas (Azcarate et al., 2017) which directly linked to human health. Several papers mention the adaptation of green technologies in foodomics. According to "Green foodomics", green techniques in extraction, sample preparation, analysing and development of novel foods are considered concerning environmental sustainability (Castro-Puyana et al., 2013). The green analytical chemistry employs the following principles; a) replacement of toxic reagents by safer counterparts, b) elimination or reduction of the usage of chemicals in the analytical methods, c) the assessment and reduction of the energy used, d) minimizing the waste volume. There is no doubt that this concept is also integrated into each of the above-mentioned omics disciplines (Gilbert-Lopez et al., 2017).

Besides research reports and reviews, there exist some book chapters focusing on foodomics. To better understand the term "Foodomics", all constituent "*omics*" disciplines must be examined thoroughly.

1.1. Proteomics and metaproteomics

Proteomics, which is connected to the protein-coding section of a genome, is widely used in food technology. Proteins play a key role in living organisms and processes like splicing, protein processing are significant modifications considered from the biological point of view and accordingly, which means that proteomics not only deals with protein sequences but also all biological sciences. Peptidomics is the sub research field of proteomics, investigating the characteristics of peptide sequences and interactions of peptides. The human genome includes 20 000 proteins which are far over the number of 500–5000, that a proteome method can detect (Bendixen, 2013). Numerous researches address the use of mass spectrometry (MS) coupled with chromatography based methods as the most common methods that allow detection and identification of many protein components in various food samples, as well as acquiring fingerprints used to detect food adulterations (Angel et al., 2012). This mechanism is explained as MS-based proteomics can detect and define any covalent changes in a protein after translation (Doll & Burlingame, 2015). In this technique, peptides are separated from the protein sample generally by liquid chromatography, then ionized and sent to MS which is confident in detecting the amino acid sequence and separated peptides (Monaci et al., 2018).

In proteomic studies, chromatographic techniques are usually coupled with MS-based methods. A large number of bioactive peptides derived from fermented milk and its hydrolysate were identified by HPLC tandem ion trap MS, which is a promising procedure for eliminating the time-taking and troublesome steps for isolation and purification processes (Picó et al., 2019). Matrix-assisted laser desorption and ionization time-of-flight (MALDI-TOF) MS technique is employed for rather qualitative analyses and characterization of protein/peptides (Monaci et al., 2018). MALDI-TOF MS could successfully determine the content and molecular weight of high hydrostatic pressure treated ginkgo seed protein (Zhou et al., 2016). Proteomic analyses conducted by LC-MS and MALDI-TOF/TOF MS in parasite proteins gave valuable data in the early detection of the foodborne parasite, which is promising for future treatment and diagnosis of specific parasites (Toledo et al., 2011). Proteomics is also an important and robust tool in nutrition, in screening metabolic pathways with some nucleic acid sequencing technologies. The reflection of this can be seen in many studies conducted on fruits and fruit ripening (Fasoli & Righetti, 2015).

Metaproteomics is also a recent term and can be described as the proteomics at the microbial level (Wilmes et al., 2015) and it is applicable in microbial studies by revealing the total protein abundance for beneficial and spoilage or pathogenic microorganisms in food systems under different stress or growth conditions (Almeida et al., 2014). Foods are biological systems and microorganisms mediate some metabolic transformations by breaking down the macromolecules in the processes like fermentation and ripening. Siragusa et al. (2014) investigated the proteomics of *Lactobacillus plantarum* in food materials. This approach gave an opportunity to explain the growth behaviour and microbial performances of the bacterium, making the adaptation of the strains possible in food biotechnology. De Angelis et al. (2016) gathered a large number of works in which the biotechnological characteristics, metabolic pathways and interactions between different environments of *Lactobacillus* sp, that are widely used in fermented dairy, meat, sourdough and vegetable foods, are elucidated by using metaproteomics. Integration of bioinformatics was suggested to understand these interactions by reconstructing the metabolic pathways. In Chinese fermented fish, *Siniperca chuatsi*, 2175 proteins were identified by shotgun metaproteomics methods. Likewise, the presence of 63 amino acid degradation proteins in *Streptococcus* sp., *Bacillus* sp., *Escherichia* sp. and *Pseudoalteromonas* sp. suggested that these microbial strains could be responsible for aroma formation in fermented fish (Ji et al., 2017).

1.2. Metabolomics

Metabolomics stands for a discipline related to the study of dynamics, composition, interactions of intracellular metabolites and their reactions to the changes in any living organisms and is highly related to nutritional research and also called as metabolome analysis, metabolic profiling or metabonome (Mozzi et al., 2013).

Metabolomics researches dominated in the clinical and pharmaceutical in vitro and in vivo studies first. Food and nutrition scientists have recently been interested in this discipline and metabolomics analyses in food and nutrition research have been optimised over the past decades. Metabolomics has a wide range of applications in food and nutrition science and one of these scopes is physiological monitoring in food intervention or diet challenge studies alongside food component analysis, food quality assessment, shelf life, effects of food processing and food consumption monitoring. The intake of over 25000 metabolites by food consumption enhances the complexity of metabolomics and various researches have been done lately in a wide range of food materials (Chin & Slupsky, 2013; Scalbert et al., 2014).

Metabolomics is regarded as a useful tool for improving sensory and beneficial attributes of cereal-based fermented products. Ferri et al. (2016), used metabolomics approach to determine the flavour and antioxidant profiles characteristic of different *Lactobacillus plantarum* strains in sourdoughs of durum wheat and KAMUT® Khorasan wheat and found that *L. plantarum* fermentation significantly affected sensorial and health beneficial compounds in both types of wheat flours.

In metabolic profiling, the most applied techniques are gas chromatography/mass spectrometry (GC/MS), liquid chromatography/mass spectrometry (LC/MS), capillary electrophoresis/mass spectrometry (CE/MS), near-infrared spectrometry (NIR), Fourier transform infrared spectrometry (FTIR), direct infusion MS and nuclear magnetic resonance (NMR) (Onuh & Aluko, 2019). In metabolomics research GC, LC and CE methods are generally collocated with MS or MS/MS (Hu & Xu, 2013). Lack of standardized procedures and nutritional intervention in metabolite identification are the challenging aspects of MS technique. However, MS-based studies surpassed NMR-based studies because of the high sensitivity and selectivity and spectral information in metabolite identification. MS technique allows the quantification of metabolites at pico- and nano-molecular levels whereas NMR can only quantify them in the micromolecular range (Cajka & Fiehn, 2015). Several authors with its pros and cons discussed NMR technique in metabolomics analysis. The major advantages of NMR technique in metabolomics research were reported to be the minimal sample preparation and user interaction, ease of quantification, non-destructivity and suitability for biofluids, cells and tissues in both in vitro and in vivo (Gowda & Raftery, 2017). Although NMR techniques are known to be the most sensitive compared to ^{31}P, ^{13}C, ^{17}O and ^{15}N, the sensitivity of ^{1}H NMR is reluctant and is limited to evaluate maximum around 60 metabolites in biological samples (Laghi et al., 2014). Despite that, there is evidence indicating

the successful application of ^{1}H NMR in metabolic profiling of fermented foods. ^{1}H NMR coupled with multivariate data analysis was efficiently used in determining the quality change and freshness of fermented crab paste (Chen et al., 2016). ^{1}H NMR together with headspace solid phase micro extraction-gas chromatography/mass spectrometry (SMPE-GC/MS) produced significant findings facilitating the selection of suitable starter strain combinations in set-type yoghurt produced with *S. thermophilus* and *Lb. delbrueckii* subsp. *bulgaricus*. The selection of the starter strains and the cooperation between them are two important factors that affect the organoleptic quality of yoghurt and data evaluation through biostatistics was recommended to make the discrimination of yoghurt samples possible based on metabolite profiles (Settachaimongkon et al., 2014). In a two-laboratory comparative work, olive oil was classified by 70% of integrity by using ^{1}H NMR (Piccinonna et al., 2016).

The application of Gas chromatography/time-of-flight mass spectrometry (GC/TOF-MS) technique in metabolomics analyses is scarce. Ochi et al. (2012) administered this method in metabolic profiling of Cheddar, Gouda and Parmigiano-Reggiano cheeses demonstrating that Parmiggiano-Reggiano cheese was unique and the maturation had an important influence on cheese flavour. HPLC/MS technique may provide some advantages over GC/MS with minimal sample preparation and rapid analysis of metabolite profiles. In a work done by Roullier-Gall et al. (2014), Ultra high-performance liquid chromatography coupled with quadrupole time-of-flight mass spectrometry (UHPLC-QTOF-MS) method in metabolic profiling of red and white wines from Burgundy region yielded accurate identification of the chemical composition of wine samples. The identification of mass formula and molecular structure for unknown molecules would also be possible by combining these two methods. Gil-Solsona et al. (2016), successfully discriminated extra virgin Spanish olive oil samples from six different regions by employing Ultra high-performance liquid chromatography coupled with quadrupole time-of-flight mass spectrometry (UHPLC-QTOF-MS). Twelve different compounds were precisely identified whereas seven of them were doubtfully identified. Quantification of the detected compounds with a simple MS/MS equipment was offered to promote quality control in oil manufacturing. Lately, capillary electromigration techniques have been boosted in metabolomics as well as proteomics and transcriptomics researches (Alvarez et al., 2018).

1.3. Lipidomics

Lipids are responsible for a vast amount of biochemical functions owing to variations in their chemical structure and physicochemical properties. Lipidomics was issued in 2003 and expressed as the subcategory of metabolomics and is a strong tool for characterizing lipids and other lipophilic compounds, which are vital for cellular membranes. Within around the last two decades, considerable progress in lipid characterization at the molecular level has been made thanks to lipidomics (Lam et al., 2017; Lee and Yokomizo, 2018). Lipids are the cause of some metabolic diseases and lipidomics has extensively been used in data validation for human health studies as obesity, atherosclerosis, metabolic syndrome and cancer (Wang et al., 2019).

Lipid molecules show broad chemical diversity; therefore, a single method may not be comprehensive enough to exhibit the lipid profile of a cell or tissue (Wei & Wu, 2020). In high-throughput quantitative lipidomics research, chromatographic techniques that are also recognized as separation-based techniques, namely thin layer chromatography, gas chromatography, liquid chromatography, supercritical fluid chromatography, two dimensional chromatographic techniques, capillary electrophoresis, nuclear magnetic resonance and several MS-based techniques or their combinations have been the most prevalent methods used in fat authentication in biological systems (Chen et al., 2017; Jurowski et al., 2017). NMR-based lipid analytical technique is considered to have lower sensitivity and to be more challenging (Li. et al., 2017). Rustam and Reid (2018) stated that the number of lipidomics research based on NMR had been continuously decreasing since 2014. Compared to the other techniques, MS is the most preferred method regarding selectivity and sensitivity. The advantages of MALDI-MS technique in lipidomic research were also discussed by Ng et al. (2015) as having high quality and high reproducibility. Another MS-based technique, electrospray ionization mass spectrometry (ESI-MS) was reported to be one of the most robust technologies used in lipidomics. On the other hand, the accurate quantification of lipids, notably in the lipid mixtures, by this method is still compelling (Hsu, 2018).

Some studies focused on detailed profiling of milk fat and alteration of milk fat lipids throughout lactation by using, GC, LC and MS techniques separately or in combination and valuable results, which allow the design of new dairy products, were attained (Liu et al., 2018; Li et al., 2019). Besides, some frauds and adulterations in vegetable oils and milk of different animal breeds were disclosed by using MS alone or MS tandem HPLC technique (Ferranti, 2018). A research conducted by Pinto et al. (2014) proven the efficiency of hydroxyapatite-based chromatography in searching the polar groups of lipids from chicken egg yolk and buttermilk. Mi et al. (2019) successfully discriminated three types of fowl eggs having different lipidome data correlated to different nutritional quality, by employing liquid chromatography-mass spectrometry/mass spectrometry-based lipid profiling and least square discriminant analysis. MS and NMR based techniques used in lipidomics and other omics studies in recent papers were gathered in Table 1.

In lipid authentication, several databases are also used. The most prominent reference databases date back to late 2000s and were reported to be LipidDAT, Lipidbank and LIPID MAPS Structural Database (Sud et al., 2007). By considering some limitations of these existing databases, Foster et al. (2013) developed a new database called LipidHome, providing theoretically generated lipid molecules and useful metadata. Machine learning methods, random forest, support vector machine, a radial basis function kernel, C5.0, model-averaged neural network and k-nearest neighbour classifiers algorithms were used in combination with direct infusion mass spectrometry in the detection of the adulteration made into Korean rice. Lysoglycerophospholipid profiling together with random forest and support vector machine showed the highest performance in discriminating the different rice species of different geographical origins (Lim et al., 2017).

1.4. Nutrigenomics

Nutrigenomics, or nutritional genomics, is considered as the future of nutrition science and is described as analysing the nutrients at the molecular level concerning human health by using “systems biology” approach that is an integration of genomics, proteomics and metabolomics. Nutrigenomics aims to explain the human body’s response to food through this approach (Braicu et al., 2017).

In a comprehensive review authored by Verma and Verma (2019), the scopes of nutrigenomics were pointed out based on the items as follows:

1. Common dietary chemicals acting directly or indirectly on the human genome, thus altering the genetic structure.
2. Diet can be a critical risk factor for numerous diseases under specific conditions.
3. Diet-regulated genes play a role in initializing or progress of the chronic diseases.
4. The extent to which diets affect the balance between healthy state to malady may depend on the individual’s genetic background.
5. Dietary intervention in relation to nutritional status can be used to prevent or cure the diet-related disease.

Nutrigenomics is interested in searching the reactions of certain diets applied to individuals or a group of people (Sales et al., 2014). A great number of published research reports indicated that there was a strong

Table 1
Examples of applications of MS and NMR based omics in food researches.

Proteomics	Sample	Method	Reference
Protein identification	Gingko seed protein	MALDI-TOF MS MDLC	Zhou et al., 2016
	Wheat flour hydrolyzed (WFH) Whey milk (WM) Tomato juice (TJ)	MALDI-TOF-MS/MS LC-nano-ESI-MS/MS	Siragusa et al., 2014
Metaproteomics			
Understanding of microbial metabolic modes	Chinese fermented fish	2D nano LCeMS/MS	Ji et al., 2017
Metabolomics			
Determination of the flavour and antioxidant profiles	Cereal-based fermented foods	SPME-GS–MS	Ferri et al., 2016
Determination of the quality change and freshness	Fermented crab paste	^{1}H NMR	Chen et al., 2016
Identification of volatiles and non-volatile polar metabolites	Set-yoghurt	SPME-GC/MS ^{1}H NMR	Settachaimongkon et al., 2014
Cultivar classification	Olive oil	^{1}H NMR	Piccinonna et al., 2016
Metabolomics-based component profiling	Cheese	GC/TOF-MS	Ochi et al., 2012
Identification of the chemical composition	Wine	UHPLC-QTOF-MS	Roullier-Gall et al., 2014
Identification of the geographic origin	Spanish Extra Virgin Olive Oils	UHPLC-QTOF-MS	Gil-Solsona et al., 2016
Lipidomics			
Determination of the lipid composition	Donkey milk	UHPLC-QTOF-MS	Li et al., 2019
Searching the polar groups of lipids	Egg yolk Buttermilk	MALDI-TOF MS Nano-ESI-Q-TOF MS MS/MS	Pinto et al., 2014
Profile (characterization) of the lipids in the egg yolk	Fowl eggs	LC-MS/MS	Mi et al., 2019
Verification of the authenticity	Rice	DI-MS	Lim et al., 2017

2D Two-dimensional
DI-MS Direct infusion mass spectrometry
GC/TOF-MS Gas chromatography/time-of-flight mass spectrometry
MALDI-TOF MS Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry
MDLC Multidimensional liquid chromatography
nano-ESI Nano-flow-electrospray ionization
NMR Nuclear magnetic resonance
SPME-GS–MS Solid phase micro extraction-gas chromatography–mass spectrometry
UHPLC-QToF-MS Ultra-High Performance Liquid Chromatography coupled with Quadrupole Time-of-Flight Mass Spectrometry

relationship between nutritional habits and some degenerative diseases, such as cardiovascular diseases, diabetes and cancer (Lucini et al., 2020). Naturally occurring gene variants, rather than mutations, are responsible for the production of any chronic disease by causing the change in DNA (Nunes et al., 2018). With the advent of nutrigenomics, new genomics-based phenotypical biomarkers are referred in the early identification of the onset of the diseases which can be reversed by planning a personalised diet (Neeha & Kinth, 2013). Fig. 1 illustrates the *Omics* disciplines making up Foodomics and how they act upon human health.

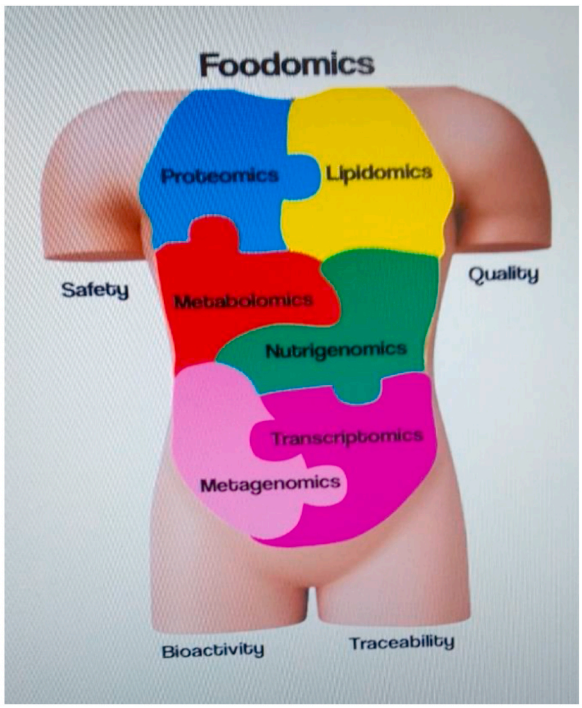
According to Kato et al. (2011), nutrigenomics is a combination of mainly transcriptomics, proteomics, metabolomics and other omics disciplines based on epigenetics and micro RNA, connected with a database. Analytical methods in determining the metabolic effects of ingredients and foods which will designate the nutritional program for sustaining the health status and preventing diseases were discussed in detail by Puiggros et al. (2011). Proteome profiling of a genome also enables the identification of new biomarkers of the nutritional state depending on the diet, facilitating managing diet regulation (Picó et al., 2019). Some researchers made a series of work to reveal the roles of amino acids and proteins in preventing or triggering some metabolic diseases, which were compiled by Chou, Affolter, & Kussmann, 2012. MS-based amino acid and principle component analysis identification methods discovered that obese subjects could be discriminated from the lean ones based upon a combination of branched-chain amino acids, methionine glutamate/glutamine, phenylalanine and tyrosine, C3 and C5 acylcarnitines.

On the other hand, some recent papers have emphasized the level of food processing and health consequences. Nutrients are merely considered as the cause of some diseases, however, a more holistic approach is needed by regarding the degree of food processing on food matrix and food composition for human and animal health and our planet (Fardet & Rock, 2018). A study in a cohort showed that consumption of ultra-processed food highly correlated with body fat during childhood and adolescence (Costa, Del-Ponte, Assunçao, & Santos, 2017). Some processed foods contain high amounts of pro-inflammatory stimulants of Toll-like receptor-2 and TLR4 (pathogen-associated molecular patterns) which were proven to be responsible for cardiometabolic diseases (Herieka et al., 2015). Leo and Campos (2020) stated that higher consumption of ultra-processed food prepared with refined substances such as simple sugars, salt, fat and some additives and lower consumption of fibre and vegetables together with environmental factors correlated with chronic metabolic diseases and suggested that ultra-processed foods should be strictly restrained by further searching their negative effects on human health.

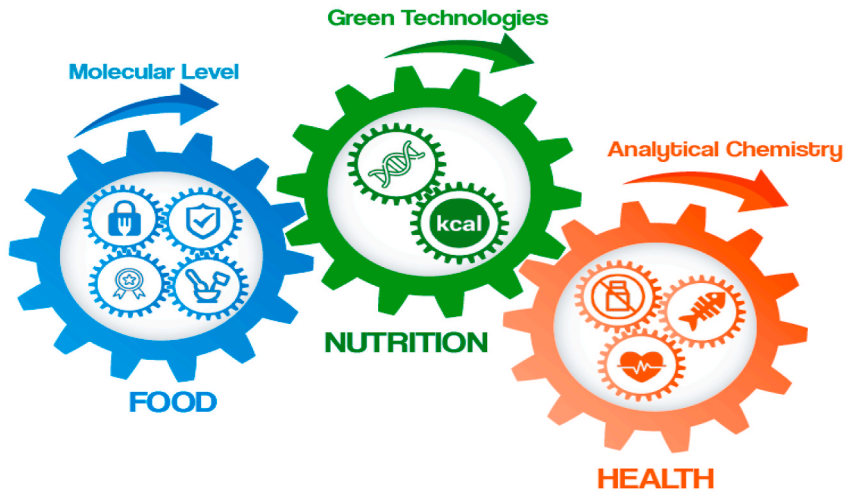
To understand the nutritional health impact at the molecular level, the interactions between the genomes of food, the gut microbiome and the human host must be investigated (Kussmann & van Bladeren, 2011). Lately, by considering the effect of food processing and design on host microbiome and internal digestion, a novel omics, namely “enginomics” that is a combination of engineering and omics (*e.g.,* genomics, proteomics, metabolomics, transcriptomics (mRNA), epigenomics, microbiomics) was offered (Saguy & Taoukis, 2017; Saguy, 2019). This new discipline is very recent and needs to be developed.

1.5. Metagenomics

Metagenomics is a high-throughput sequencing technology and is widely used in fermented food products technology to monitor the microbial dynamics at different stages of fermentation, which simplifies the characterization of biomarkers for quality or spoilage and the control of fermentation process (De Filippis et al., 2017). Conventional microbiological methods require much time, labour and cost. New techniques and databases permitted the identification of more than 1000 microbial genomes (Sayers et al.,). In the last decade, metagenomics studies have soared up because of the higher availability of



(a)



molecular level	green technologies	analytical chemistry
FOOD	NUTRITION	HEALTH
Authentication	human genome	allergen
Constituents	nutritional elements	toxins
Quality		well-being
Safety		

(b)

Fig. 1. *Omics* disciplines which make up Foodomics and their impact on human health.

sequencing centres, reasonable costs and advanced platform of bioinformatics and biostatistics (Ferrocino & Cocolin, 2017). Scholz et al. (2016) developed a pangenome-based phylogenomic analysis ensuring a comprehensive insight into the functionality and the potential of the organisms, identification of novel strains, source and strain tracking by profiling the complex communities through the genomic and transcriptomic approach.

The performance of metagenomic analysing and data processing on microorganisms was proven by many types of research conducted on the microbiota of various fermented food products. A recent work conducted by Xie et al. (2019) supported this by revealing the predominant species of a Chinese traditional fermented soybean product as

Enterobacter, *Enterococcus*, *Leuconostoc*, *Lactobacillus*, *Citrobacter* and *Leclercia* species. Metagenomics and metaproteomics approaches together were suggested to be used in the determination of key enzymes in the fermentation of soy and functional genes of fermented products. In understanding the sourdough fermentation process and the microstructure of yeast and lactic acid bacteria, metagenetics gave the most reliable and precise data, among other *omics* disciplines (Wecx et al., 2019).

Metagenomics revealed some important new findings in "puer tea", a fermented Chinese tea. Although *Aspergillus*, *Fusarium*, *Penicillium*, *Rhizomucor*, *Trichoderma*, *Cladosporium* and *Mucor*, and yeasts were known to be the microorganisms playing a key role in the fermentation, this modern discipline suggested that the most dominant microorganisms were bacteria and yeast count was overwhelmingly higher than that for moulds. However, the researchers asserted that there was still much work by applying metagenomics to characterize the microbial community in puer tea pile fermentation (Lyu et al., 2013).

Sequencing techniques based on DNA analysis have been used reliably in fermented dairy products and cheese. Impressive results were found by using the parallel-based sequencing approach in kefir. Microbiota of starter grain and kefir milk was considerably different. *Lactobacillacae* dominated in kefir grain while Streptococcaceae was dominant in kefir milk fermentate in bacteriocin (lacticin 3147) producing Irish kefir grain. Pyrosequencing-based techniques were implied to demonstrate symbiosis and complex interactions in kefir microbial community (Dobson et al., 2011). The pyrosequencing approach in analysing the microbiota of artisanal cheeses has also attracted attention. The bacterial population in cheese can considerably differ, which manage the cheese ripening and alter the cheese flavour, surface and rind colour, and other characteristics. In Irish artisanal cheeses, different microbiota for raw milk and pasteurized milk cheeses were examined. *Faecalibacterium*, *Prevotella*, and *Helcococcus* species were detected that were not known to be relevant with that kind of cheese. *Arthrobacter* and *Brachybacterium* species were detected first time in the cheese samples manufactured from goat milk by high-throughput sequencing technique (Quigley et al., 2012). The bacteria responsible for the character and the quality of the Belgian soft cheese were unravelled. Two hundred seven phylotypes were successfully identified and rind microflora of cheeses produced from both raw and pasteurized milk highly varied. The dominant species in the raw milk cheese were found as *Corynebacterium casei* and *Enterococcus faecalis* while *Psychrobacter celer* in the pasteurized milk cheeses (Delcenserie et al., 2014). In Mexican artisanal Poro cheese, the composition and the dynamics of microbial communities were successfully detected during cheese processing by using pyrosequencing, two important issues for standardizing the process and promoting the quality and safety of Poro cheese for local manufacturers. The predominant microflora was *Streptococcus salivarus* subsp. *thermophilus* and *Lactobacillus delbrueckii* and occasionally, *Macrococcus*, *Staphylococcus*, *Enterococcus*, *Streptococcus*, *Lactobacillus* and *Enhydrobacter* were encountered, helping them to standardize process improving quality and safety, as well as to preserve a 10 traditional food that supports the economy of local producers and their families. (Aldrete-Tapia et al., 2014). *Lactococcus*, *Lactobacillus* and *Streptococcus* species were the most abundant bacteria in Danish raw milk cheeses. Other species like *Corynebacterium*, *Halomonas*, *Pediococcus*, *Micrococcus* and *Staphylococcus* were also detected at low levels by 16S rRNA gene sequencing method, which was reported to be the most efficient one in deep sequencing of microbial populations (Masoud et al., 2011). *Lactococcus* and *Streptococcus* species also dominated in the core of Tomme D'Orchies, an artisanal pressed and uncooked French cheese. These starter bacteria were found less than 30% on the surface which was mainly composed of *Corynebacterium*, *Bifidobacteria*, *Brevibacterium* and *Micrococcales* species (Ceugniez et al., 2017).

1.6. Transcriptomics

Transcriptomics is a step forward omics discipline in revealing the effects of different factors that can modify gene expression profiles (Li & Li, 2018). The transcriptome of a living organism is energetic since it can be altered according to the modifying intrinsic and extrinsic factors (Pertea, 2012). Two main techniques, microarrays and RNA sequencing are employed in transcriptomic research (Lowe et al., 2017). Microarray-based techniques are cheaper compared to other technologies used in transcriptomics (Valdes et al., 2013). RNA sequencing caters more complete information thanks to the direct characterization of sequences, which makes it ideal for identifying the full genomic sequence of microorganism. Although transcriptomics has a wide range of applications in the biological research field through RNA sequencing and microarrays, this approach in food microbiology has in its infancy (Lamas et al., 2019).

Proteomic and transcriptomic analyses in revealing the characteristics and functionality of probiotic *Lactobacillus rhamnosus* GG were successful with the findings that transcript levels of 316 genes changed significantly and 42 proteins, including both intracellular and surface-exposed proteins, were differentially abundant; suggesting that these proteins facilitated the interactions of the probiotic bacterium with the host mucus in the presence of sublethal doses of bile (Koskenniemi et al., 2011). Transcriptomic analyses allowed the differentiation of starter and non-starter bacteria as well as the quantification of both live and dead cells. It was indicated that with the integration of transcriptomics, proteomics and metabolomics, more detailed information regarding the cheese microflora and thus cheese flavour development which had a key role in directing the processing parameters and cost reduction, was possible (Blaya et al., 2018).

Staphylococcus aureus is a well-known foodborne pathogen forming antibiotic resistant biofilms that makes the treatment harder. Some researchers made works to reveal the biofilm formation and microbial interactions to guide the preservation methods. In a work done by Tan et al. (2015), expression of six genes in biofilm formation was satisfactorily determined through RNA-sequencing, which also suggested that only ursolic acid could inhibit the biofilm formation. Another work investigated the *S. aureus* inhibition by hydrogen peroxide producing lactic acid bacteria. Transcriptomic approach in tracking the growth conditions of two *S. aureus* species; *S. aureus* SA15 dairy strain and MW2 human pathogenic strains under hydrogen peroxide exposure demonstrated that human pathogenic strain was more resistant to hydrogen peroxide (Delpech et al., 2015). Growth conditions of *S. aureus* on chicken meat were investigated in a later work conducted by Dupre et al. (2019), providing valuable data to further work on decreasing the effects of *S. aureus* intoxication. Both metabolic and transcriptomic responses of cultures grown in the autoclaved chicken breast were comparable to those grown in Luria broth agar.

Another well-recognized foodborne pathogen is *Salmonella* causing severe infections. In a multi-laboured work, the dynamic transcriptome of gene-empty regions enabled the identification of 58 wholly undescribed small RNA (sRNA) genes of *Salmonella enterica* serovar *typhimurium* regulating starvation stress response, which suggests that *Salmonella* sRNAs are much more dominating (Amin et al., 2016). The survival of *Salmonella enterica* serovar *typhimurium* in four different food models with a low water activity (milk chocolate, powdered milk, black pepper, dried pet food) was examined. Food composition was found to be the major factor influencing the gene regulation within the first 24 h storage (Crucello et al., 2019).

2. Conclusion

Recent advances in analytical chemistry facilitated the quantification of food constituents and metabolites as well as toxins and allergen compounds at the molecular level. MS-based analytical techniques are the most prominent methods used in omics research followed by

chromatographic techniques. Omics technologies emerged by using these analytical methods, however, they still need to be grown and standardized. Innovations in these techniques will enlarge the omics applications in the food and nutrition domain.

The applications of the omics disciplines; proteomics, lipidomics, metabolomics, metagenomics and transcriptomics that are powerful tools in food authentication, food quality, food safety, detection of adulterations, allergens and toxic matters, and are involved in nutrigenomics research to target human well-being. Metagenomics, metabolomics, transcriptomics and metaproteomics are successfully used in recognition of food microbiota. Understanding the dynamics and pathways of bacteria involved in fermented foods as well as the interactions between the food genome and gut microbiome will help improve the quality and pilot the design of novel functional food products. Furthermore, these techniques allow the inhibition or control of the spoilage microorganisms and pathogen growth, which is a great challenge respecting both food safety and quality.

The literature cited mostly handle the omics research of nutrients and food materials. The effect of various food processing techniques on the molecular level of nutrients and hence health status is an important concern. Ultra-processing of food, which was shown to have a negative impact on the environment and human health is very recently mentioned and the papers on this argument are very scarce. A deeper investigation must be encouraged to elucidate this critical issue.

Prospects include the use of safer, cheaper, sustainable and eco-friendly analytical methods with high sensitivity, accuracy and precision; directly referring to green foodomics. Integration of the bioinformatics and biostatistics to obtain meaningful data from the analytical methods in omics studies is to be another consideration. The database used in the evaluation of the analytical data has made progress over the last two decades and will inarguably proceed along with the improvements in computer software engineering.

It is clear that omics disciplines have interactions and sometimes hard to be distinguished although each is well described. In many cases, the combined use of different omics technologies is more fruitful in food and nutrition research. Food science and technology is a dynamic research field and continuously developing. Further studies at the molecular level and integrations of current technologies will bring about new “omics” terms and research areas in the future.

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