**METABOLOMICS AND PROTEOMICS IN FOODS**

Selcen GÜÇLÜa1\*, Berika HAYOĞLUb2, İbrahim HAYOĞLUa3

a\*Food Engineering Department, Engineering Faculty, Harran University, 63000, Sanliurfa, Turkiye, **1**<https://orcid.org/0009-0002-0147-3873>

bNutrition and Dietetics Department, Health Sciences Faculty, Acibadem University, Istanbul, Turkiye, **2**https://orcid.org/0009-0003-2671-8715

**3**https://orcid.org/0000-0002-6358-8302

|  |  |  |
| --- | --- | --- |
| ***Keywords*** |  | **ABSTRACT** |
| *Omic, Metabolomics, Proteomics, Biomarker, Mass Spectrometry (MS), Food Quality*  |  | The discovery of the human gene sequence by analysis has started a new era called omics technology. Omic technologies; Nutrition offers a future in the study of the complex relationship between food and metabolism. In recent years, a wide variety of omics sub-disciplines have emerged, and each branch of science has its own specific applications. Allowing new areas of research to emerge, omics technologies include mass spectrometry and many other techniques that allow high throughput analysis.Metabolomics and proteomics are omics technologies; they have unparalleled advantages in understanding physiological and pathological activities in food science. Metabolomics and proteomic analyses in the food industry; It is used to determine food quality, product production, traceability of food, how the processes during storage affect the structure of foods, and biomarkers that cause food allergens and the relationship of biomarkers with nutrition. Studies in this field allow detailed examination of the changes in foods thanks to the developments in the field of chromatography. In this study, the areas of metabolomics and proteomics technologies used for foodomics and their future status are discussed. |

**Introduction**

The term omics, derived from the Latin suffix -ome, means 'many' and is accepted as a broad expression of the 'whole' of the terms it represents according to the names to which it is added. For this reason, in omics technology, not only one or a few measurements can be made in the matrix examined, but many measurements can be made in the entire matrix. Omics technology was expressed by Hans Winkler in the 1900s with the word genome and emerged with the term genomics in the 1980s. Genomics technology draws attention to the study of genomes as a whole, unlike genetics, which examines genes or variants one by one. Especially in the early 2000s, it was associated with the development of various branches of science in omics technology and with these developments, it has many fields of study such as nutri-genomics, transcriptomics, proteomics, metabolomics, lipoproteinomics, immunomics. However, only genomics, nutri-genomics, transcriptomics, proteomics and metabolomics technologies are used in food science (Davies, 2010).

Genomics, which is one of the most studied omics technologies in recent years, is a branch of science that examines the structure of DNA, which carries the genetic information of all cellular organisms, in detail. (Ordovas & Corella, 2004) Omics technologies are interconnected and follow a certain order. In this evaluation; transcriptomics, which is a continuation of genomics, is the branch of science that examines the mRNA produced in a cell in a certain time interval; Proteomics is the branch of science that examines the synthesis, structure, functions of proteins produced in a tissue, their relationships with other proteins; metabolomics, on the other hand, is defined as the branch of science that examines the profiles of metabolites produced as a result of biochemical reactions in cells (Elaine et al., 2006; Carbonaro, 2008; Kahraman & Bozkır, 2020). While metabolomics continues to work on the cause-effect relationship, proteomics technology is result-oriented (Yılmaz & Özpınar, 2019).

Protein: It is of Greek origin and is derived from the word proteios, which means 'in the first place', 'important', 'of primary importance'. Since proteins form the basic building blocks of the functions that occur in the organism, they have formed the basis of many research, especially omics technologies (Sevimli & Özçelik, 2013; Cristea et al., 2004). Proteome is defined as the sum of all the different proteins that the cell or organism has and expresses at a certain time and region. 'Different proteins' here also include not only peptide/polypeptide structures synthesized and encoded by genes but also the modifications and combinations that occur after synthesis. The expression 'region' also indicates the location of the same/different proteins and, the same/different cell types (Özcengiz, 2007). The term biomarker is expressed as a molecule used in the biological identification of cells, cell communities or large organisms. With the combined use of omics technologies, it is among the assumptions that new biomarkers can be discovered in food science, as well as healthier new food products can be produced by using them in R&D studies. In addition, it is stated that new biomarkers discovered as a result of recent studies can be used in the control of personalized nutrition programs used in disease types such as celiac, lactose intolerance, obesity, cardiovascular, diabetes and cancer (Cristea et al., 2004). Proteomics technology provides us with the knowledge of 'what could be' and metabolomics technology provides us with the knowledge of 'what happened in reality' (Coşkun, 2007). According to metabolomic information and food molecular content; researchers have found that more nutritious foods can be obtained with the changes that will occur as a result of food processing. In this context, the use of metabolomics techniques contributes to the development of food consumption patterns, the benefits of any diet, and the improvement of physiological responses. There are many studies on this subject in the fields of food science and nutrition, food quality and food safety, and food processing (Moco et al., 2006). For the reasons mentioned above, omics technologies; contribute to the world of science on issues related to public health in terms of nutrition, food safety and quality (Wenk, 2005).

Methods used for metabolomics and proteomic research today are mentioned below;

 High-Pressure Liquid Chromatography (HPLC)

* Liquid Chromatography Mass Spectrometry (LC/MS)
* Matrix Coupled Laser Desorption Ionization (MALDI)
* Gas Chromatography-Mass Spectrometry (GC/MS)
* Nuclear Magnetic Resonance (NMR)
* Electrospray Ionization Mass Spectrometry (ESI/MS)
* Time-of-Flight Mass Spectrometry (TOF/MS)
* Mass spectrometry (MS) (Rapoport et al., 2011)

**Metabolomics**

Today, with the increasing awareness of consumers about healthy nutrition, their tendency to foods with more physiological and metabolic benefits has started to increase rather than meeting the basic food components needed (Sakin & Tanoğlu, 2016; Taşdemir, 2017). With the increase in the world population, various food quality and safety issues such as the emergence of new food pathogens, food adulteration, risk assessment in genetically modified foods and detection of chemical contaminants have become one of the most important issues in food analysis, attracting increasing public attention. With the increasing demand for high standards in food quality assurance, metabolomics technology has been developed to comprehensively evaluate the quality and safety aspects of foods and provide valuable insights into the quality and authenticity of food products (Garcia-Carnas et al., 2012; Garcia-Carnas et al., 2014; Aru et al., 2018; Shubo et al., 2021; Kathuria et al., 2024).

'Metabol' is a word of Greek origin that means 'to change'. '-ome' means set. The entire metabolism in a cell, organelle, or organism is referred to as metabolomics, and studies of metabolomes are referred to as metabolomics (Gibney et al., 2005). Metabolites; oligonucleotides, sugars, peptides, nucleotides, organic acids, ketones, aldehydes, amines, amino acids, lipids, steroids, alkaloids and chemical compounds such as drugs (Başaran et al., 2010).

Metabolomics; small molecule metabolites that occur with lipids, carbohydrates, vitamins, hormones and other cell components in cells, tissues or physiological fluids within a certain period, especially MS-based; NMR is determined using high-speed and efficient technologies such as GC-MS and LC-MS (Hamad, Alma, Gulcin, Yilmaz, & Karaogul, 2017; Eyyüp Karaogul, Kirecci, & Alma, 2016; Koyuncu, Gönel, Temiz, Karaoğul, & Uyar, 2021; Nedjip & Karaogul, 2021), and expressed by measuring their quantities (Goodacre, 2005). Metabolomics offers the opportunity to examine foods in more detail. All food ingredients, natural and unnatural, are often referred to as "food metabolomes". The food metabolome provides important information for the complex interactions between nutrition and health (Rubio et al., 2012). Metabolomics technology in food safety control, foods during critical stages such as production, processing, transportation and storage; It can be contaminated with many foodborne agents such as pathogens, biotoxins, man-made physical and chemical toxic substances (pesticides and metals) and thus lead to foodborne illness or poisoning or even death (Resetar et al., 2015; Alothman et al., 2017). According to the World Health Organization, unsafe food can cause more than 200 diseases, from diarrhoea to cancer, and an estimated 600 million people die each year after consuming contaminated food, almost 11% of the world (Havelaar et al., 2015; Chen et al., 2020). Nevertheless, with the increase in the diversity of the modern food industry and the physical and chemical hazards that threaten food safety and quality, it may take weeks to detect biological and chemical pollutants in some biochemical analyzes (Resetar et al., 2015; Jadhav, 2019). Considering the shelf life of food products, metabolomics-based methods have been appropriated to identify microbial biomarkers with different levels of microbial contamination, demonstrating great potential for rapid and reliable detection of microbial contamination in the early stages (Xu et al., 2014). Jadhav (2019) used GC-MS to characterize three important foodborne pathogens (E. coli O157:H7, L. monocytogenes and S. enterica), and stated that as a result of the study, biomarkers specific to the potential pathogen were identified, giving sensitive, fast and reliable results between non-contaminated foods and contaminated foods. To determine toxicity in food, Christopher & Haselssen. (2008) used NMR technology to determine the types of aflatoxin produced by A. Flavus, A. Parasiticus, and A. Nomius, known as the three species of Aspergillus. As a result of the analysis, the selectivity and rapidity of the method were especially noted. Cevallos & Rodrick (2009) observed E. coli-contaminated spinach from freshly harvested spinach using MALDI-TOF-MS technology. Although the study does not aim to determine the exact amount of E. coli, the technique used shows us that it can detect pathogens quickly in food analysis. In general, foodborne biotoxins can be classified into two categories: (1) non-zoonotic, such as amatoxins, lectins, and phytotoxins, (2) bacterial exotoxins and endotoxins, such as mycotoxins, neurotoxins, and enterotoxins. With the development of pathogens in inadequately sterilized or contaminated foods, various toxins are secreted out of the cell and are the second cause identified as the source of foodborne illnesses or deaths (Chen et al., 2018). Metabolomics technology is used to provide the earliest stage of profiling and identification of metabolites related to microbial contamination to ensure food safety by using NMR and MS technology in combination (Castro-Puyana et al., 2017). Food adulteration is known as the production of foodstuffs or food contact substances and materials with the addition of low-quality or unauthorized food or ingredients. This situation poses a health risk to consumers by catching the quality defects of the food (Cubero – Leon et al., 2014; Kendall et al., 2018). Therefore, food originality; for the food industry and consumers, the nutritional value of food is of great importance in terms of securing the city/country of origin and production processes. However, it is often difficult to distinguish between adulterated or pure products using traditional sensory evaluation and quality indicators, such as the iodine value and saponification value of edible oils. With analytical advances, metabolomics-based approaches are expected to complement the methods required to distinguish between pure and adulterated foods, detect adulterated foods, and trace geographical origin (Hou et al., 2017).

Food analysis; It consists of determining components such as protein, fat, carbohydrate, fiber, mineral, dry matter and ash. By detecting the metabolomes that make up the food thanks to the metabolite profiles, it was determined whether the food was imitated-adulterated, and the quality of the food was determined. In one study, metabolite profiling of tomatoes and tomato juice was obtained using LC/MS and NMR devices. As a result of the analysis, more than 60 non-polar and low amounts of polyphenols were determined and used to determine the origin of the tomato. (Gibney et al., 2005) Detailed metabolite and biomarker profiles of overconsumed foods such as milk, beer, fruit juice, and grapes have been obtained (Gibney et al., 2005; Ghosh & Poisson, 2009; Singh et al., 2024). Thanks to metabolomic research, it allows the detection of imitation-adulteration by extracting special profiles of foods whose metabolite profiles cannot be determined by other traditional methods. In a study, the accuracy of the method was proven by testing the speed and sensitivity of the method using NMR technology in 92 different fruit juice varieties (59 oranges, 23 grapes, 10 mixed) (Hu et al., 2007; Almeida et al., 2006). Genetically modified foods have an important potential in many areas such as increasing the nutritional value of food, increasing food diversity in the food industry and extending the shelf life of food. For example, genetically modified seeds may require less herbicide or pesticide application, less irrigation, and may contain more of the compounds or nutrients needed by human metabolism. With the development of the systems used by genetic engineering and the combined work of other engineering units, the popularity of genetically modified products has started to increase due to the inability of the agriculture/food industry to meet the supply/demand balance of the increasing world population, the long shelf life of these products, and the belief that they have more nutritional value (Gao, 2018; Chen et al., 2018). However, the unexplored health risks of genetically modified foods cause concern for consumers (Chao & Krewski, 2008). It is not possible to evaluate these risks with traditional technologies, and it is of great importance according to the scientific world to evaluate the risk of these foods using metabolomics technologies (Shubo et al., 2021). Chang et al. (2012), in a comparison of genetically modified rice and regular rice. Using HPLC-Q-TOF-MS, they investigated the effect of genetics and environmental factors on these two samples at the metabolite level. They determined that the method they used was reliable according to the results they obtained, that tryptophan, linolenic acid, 5-hydroxy-2-octaadenoic acid levels decreased by 15%, 6% and 30%, respectively, and that the planting dates were effective in the values of these metabolites together with temperature. Food traceability is an important issue in food analysis, and is closely linked to food quality, food safety and human health and is defined as 'farm to fork' (Kaufmann, 2014). In this process, it is essential to record all critical control points with the farmer, production, processing, packaging (E. Karaogul, 2019; Karaoğul & Alma, 2019), storage, transportation and final point of sale, and it is of great importance to ensure food safety, which is the purpose of traceability (Gaulitz et al. 2018). Metabolomics technology can provide useful information about the composition, originality and processing of foods by providing information about food metabolites and their changes in these metabolites depending on the genotype of the food and the growing/production conditions (such as soil, climate, heat treatment, fermentation, storage), their effects on health, and the desired/undesirable effects during pretreatment and processing, such as the formation of new compounds formed during the process (Rubert et al., 2015). Wishart (2008) used GC-MS and LC-MS to compare the produced whole wheat and regular pasta in terms of phytosterols, unsaturated fatty acids, amino acids, carotenoids and mineral compounds. According to the results of the analysis, although whole meal pasta is richer in terms of many components, it has been determined that more than one metabolite is transformed during pasta production under the applied processing conditions.

Metabolites found in food affect organisms through proteins and enzymes. In a study, it was observed that there was a difference in the composition of the nerve membranes compared to that of other animals, especially in animals whose diet was predominantly fatty acids. It has been observed that the difference in the composition of the membranes affects the shape, structure, size, flexibility and functions of the cells (Budak & Dönmez, 2012). Carbohydrates, fats and proteins constitute the majority of the metabolites that make up the food, but the analysis of water-insoluble lipids of this class by metabolomic techniques is called lipidomics. Lipidomics are determined in metabolomics analyses because they have different properties from lipids. Studies based on lipidomics technology, aim to develop appropriate analysis methods to monitor the inadequacy and excessive consumption of people in their diet, taking into account the ratio of omega-3 fatty acids to omega-6 fatty acids (Lindon et al., 2004). Thanks to metabolomic studies, metabolites in food components, physiological fluids and biological structures are determined quickly and with high efficiency, these metabolites are evaluated in terms of physiological, psychological, biological and gastroenterology, and the effects of nutrition programs on human metabolism are also investigated (Zhang et al., 2008). Important studies have been carried out by scientists and nutritionists to develop food products with higher nutritional value for the development of human health. In addition, personalized diet programs and food supplements such as minerals and vitamins, which are deficient in their treatments, have been recommended to individuals (Mashego et al., 2007). In recent years, the increase in obesity has been considered a serious public health problem, and the underlying problems of the disease have not been fully understood by biochemical methods. However, the identification of obesity-related biomarkers with metabolomics approaches helps to identify these mechanisms. In a study, considering obesity problems; branched-chain amino acids (BCAA) (valine, leucine, isoleucine), unesterified fatty acids, organic acids, and phospholipids have been identified as potential biomarkers using NMR technology (Ghosh & Poisson, 2009; Heuberger et al., 2010; Bayram & Gökırmaklı, 2018). Although the use of Chinese weight loss tablets, which are known to help rapid weight loss, is very common among consumers, in a study, it was determined by metabolomic studies that the aristolochic acid used in these weight loss tablets is very harmful at the gene level in the bone marrow of rats, and in another study, this acid is associated with gene mutation (Yaman, 2015).

**Proteomics**

Macromolecules formed by the bonding of amino acids with peptide bonds are called proteins. Each protein has its own special amino acid sequence and properties depending on this sequence. Various proteins are obtained by binding 22 different amino acids to each other differently. In order to identify the protein, it must first be removed from its environment and broken down according to its physical and chemical properties. (Peng & Gygi., 2001). Proteome refers to all proteins found in organisms or physiological fluids (Marko, 2004). Proteomics is a branch of science that has become very popular in the last 20 years, which examines the identification, identification and characterization of proteins at a certain time and region in cells, organisms and tissues, their changes, interactions with each other and their resulting breakdown products using different proteolytic separation methods. In addition, proteomics technology is also referred to as the quantitative analysis of proteins/peptides present in cells, tissues, or body fluids under variable conditions (O'Farrell, 1975). In the food industry, proteomics technology is used to determine the quality of foods, imitation-adulteration, and changes that may occur in allergens that have emerged or may occur in production, storage, transportation and R&D studies (Smith, 2009). Apart from these, the effects of the processes applied during product production and storage on the characteristics of foods are the subject of proteomic research (Han and Wang, 2008). Since proteins play a decisive role in tissue and cell structures, proteomes also interact against the effects of the internal and external environment. Thus, the changes that occur in organisms occur at the level of proteins. In addition, biomarkers used in the identification of pathogens that cause food spoilage and foodborne diseases are determined by the science of proteomics (O'Flaherty & Klaenhammer, 2011). Due to their complex structure, no analysis method identifies the proteins or peptides in the suspended samples in a single trial or determines their doses. For this reason, before the analyzes that define the proteins, fragmentation is performed using various methods, and then measurements are made by combining these methods with MS which has high sensitivity. One of the most powerful strategies of this branch of science has been the use of 2D gel electrophoresis and highly sensitive mass spectrometry technologies, which have a very high separation technique, of proteomics technology, which has been in studies for the last 20 years (Bantscheff et al., 2007).

Two methods are used to separate complex samples using proteomics technology: electrophoretic and chromatographic techniques. Proteins; it is separated into peptides and amino acids using high-performance liquid chromatography (HPLC), ion exchange chromatography (IEX), size sieving chromatography (SCX), capillary electrophoresis (CE) and nuclear magnetic resonance (NMR). The separation of protein or peptide mixtures according to physical and chemical methods is an advantage of electrophoretic and chromatographic techniques (Kiran & Osmanağaoğlu, 2013).

Studies in proteomics technologies have two main objectives. The first main purpose is to determine the proteins/peptides obtained from cells, food or physiological fluids, and the second main purpose is to determine the amounts of defined proteins/peptides. The best tool to achieve both of these goals is mass spectrometry (MS) (DeBruyne et al., 2011). In comparative proteomics technology, it is obligatory to separate the protein/peptide to be identified from other macromolecules before the determination of the proteins is made. The methods used to separate proteins are numerous. These methods are 2D gel electrophoresis, two-dimensional differential gel electrophoresis (2D DIGE), one-dimensional liquid chromatography (1D-LC) and two-dimensional liquid chromatography (2D-LC). The 2D gel electrophoresis method is one of them (Nenni et al., 2020). In separating proteins, 2D gel electrophoresis has the same basic electrophoresis technique. The first part, in which proteins are separated according to their isoelectric points (pl), isoelectric focusing (IEF), and sodium dodecyl sulfate-polyacrylamide gel electrophoresis, in which proteins/peptides are separated according to their weight, constitute the second part. Separated proteins/peptides are identified in high-tech instruments such as mass spectrometry (MS) (Issaq, 2001). In 2D gel electrophoresis, silver staining, organic or fluorescent dyes are used to make the gels more visible to make the proteins more visible. (Ong & Pandey., 2001). Ionizable tryptic peptides are analyzed using MALDI-TOF (Matrix Assisted Laser Desorption Ionization Time-of-Flight Mass Spectrometry) and peptide mass fingerprint similarity (Rabilloud, 2002). In studies in proteomics technology, MALDI-TOF is used for the identification of proteins, while two-dimensional gel electrophoresis (2-DE) is used to separate proteins. However, the disadvantage of two-dimensional gel electrophoresis; in addition to proteins/peptides that are not present in sufficient amounts in the sample, proteins with high hydrophobic, acidic or basic characteristics cannot be detected (Rabilloud et al., 2010). In the case of more sensitive detection of some proteins/peptides or if the molecular masses do not match as a result of previous detection, MS-MS (Tandem MS) is defined (Wittmann et al., 2006). Due to the complex structure of foods or the physical and chemical changes that occur during the production of foods, many problems are encountered in the detection of allergen proteins by biochemical and DNA determination methods. However, the increase in R&D studies in the food sector and the development of the techniques used, brings with it the continuity and necessity of studies on allergens. Proteomics technologies, which continue to develop over time with sensitive, fast, accurate and highly efficient technical tools, have become one of the most preferred methods in recent years due to the determination and identification of the ratios of food allergens due to the advantages they provide. Ansari et al. (2012) targeted the result of hazelnut-specific biomarker peptide sequences with LC-MS/MS and first identified 8 marker peptide sequences for Cor a 8, Cor a 9 and Cor a 11 hazelnut allergens. Later, the BLAST program was used to check the selectivity of peptides and it was reported that peptide sequences were also found in other nuts. Planque et al. (2016) aimed to detect milk, casein and whey, egg (white and yolk), soybean and peanut allergens in complex food matrices by UHPLC-MS/MS after trypsin breakdown and purification of proteins and determined the minimum detection levels of allergen proteins by selecting chocolate, ice cream, tomato sauce and biscuit matrices in the study. The detection limits of allergen proteins were expressed as 2.5 mg/kg for casein (0.5 mg/kg), whey (5 mg/kg), egg white (3.4 mg/kg), 29 egg yolks (30.8 mg/kg), soy (5 mg/kg) and peanuts. For the detection of egg, milk and peanut allergens in biscuits, egg, milk and peanut allergens by LC-MS/MS (Boo et al. (2018) examined protein/trypsin levels and different breakdown times in the range of 2-16 hours. The optimum breakdown time for all allergen peptides was determined to be 4 hours. With the use of proteomics technology in gastroenterology, proteomic profiles of microorganisms that have an important role in intestinal flora are revealed. As a result of these researches, it is estimated that the treatment of gastroenterological disorders and personalized diets can be created in the future (Han & Wang., 2008). Studies have been conducted on the human health effect of healthy nutrition for many years. Nutritional peptidomics, which is one of the sub-branches of proteomics technology, is used to enrich the content of food and to provide easier access to the basic nutrients needed by the body (Prasad et al., 1998). With the development of recombinant DNA technology, modified foods, which are popular among consumers, need to be investigated in terms of public health. With the advent of modified foods, proteomics technologies have started to gain more importance. Proteomics technology is used in this field to compare the structures of modified and natural products and to determine the side effects of unknown properties (Wimmers et al., 2010).

As a measure of meat quality, crispness, juiciness, color, and odor are related to the biological, genetic and nutritional aspects of the animal. For example, the fat content in the tissues increases the taste and structural properties of the meat. Proteomics technology plays a major role in improving meat quality by allowing the investigation of the gene that controls the accumulation of fat between tissues. (Zapata et al., 2009) In addition, crispness is affected by the reactions that occur in the cells during the transformation of muscle into meat. Although these reactions are not very understandable by analyses at the cellular level, they enable groundbreaking research to be carried out in this field by using proteomics technology (Pedreschi et al., 2010). With the help of protoemic technology, it is preferred to establish a link between important properties such as the modification of milk proteomes and their interaction with other proteins (O'Donnella et al., 2004). Especially used for fermented milk products Lactococcus lactis, Streptococcus thermophilus, Lactobacillus delbrueckii ssp. lactis, Lactobacillus acidopbilus and Propionibacterium freudenreichii This technology has been used to reveal the proteomic maps of many microorganisms. At the same time, studies have been carried out on the sensitivity of these microorganisms to the digestive system, their durability, and their adaptation to food (Roncada et al., 2012). Another area where proteomics technology is used in dairy technology is the investigation of the proteolysis mechanism that gives the cheese its specific texture and taste. Investigating the changes in casein, which is a milk protein, during maturation in different types of cheese makes important contributions to the understanding of proteomics (Manso et al., 2005). Kim et al. (2007) tried to compare the effect of Pseudomonas on proteinases and the effect of Penicillium caseicolum and P. Roqueforti on caseins. While the changes of α-casein in Gouda cheeses were examined in terms of proteomes, the relationship between rennet, plasmin and P. caseicolum in Camembert cheese was revealed. Mastitis is an important type of disease in terms of both animal and public health. By using proteomics techniques, it is aimed to investigate the source of the disease and make an early diagnosis. With the biomarkers to be obtained, the disease will be diagnosed early, so that significant benefits will be obtained in terms of animal health and milk quality by using appropriate antibiotics (Green et al., 2007). In addition, egg, which is a valuable food, is on the agenda of proteomics studies due to its nutritional aspect and allergenic effect. Apart from these issues, proteomics technology is an indispensable technique to examine how the metabolites it has during shelf-life change at the protein level and their effects on human health in terms of nutrition (Omana et al., 2011). Calvano et al. (2013) developed a novel method using proteomics technology to detect the components of powdered milk mixtures from both raw and processed milk. It is especially stated in the study that the same results can be obtained using 2-DE-based proteomic analyses, but MALDI-TOF-TOF technology is a much faster, safer and more efficient method for this process. In this research, it has been stated that peptides that define milk powder with very high sensitivity have been brought to the scientific world. In an analysis conducted with LC-MS/MS for the detection of sesame allergens in processed food products, Ma et al. (2020) performed a breakdown process using trypsin enzyme for 0.5-16 hours and compared with the areas of peptides determined as biomarkers. According to the results of the analysis, the fragmentation time was 8 to 12 hours, and after the fragmentation, the areas of the peptides were the same therefore the sample preparation time was determined as four hours. Celiac disease is known for the hypersensitivity of the organism to gluten protein, and the consumption of wheat, barley and rye proteins triggers allergenic responses in the body. The most common gluten proteins; are glutenins and gliadins. These proteins, also known as prolamins, are the main source of celiac disease. Various proteomic analyses have been developed to identify and quantify gluten proteins obtained from processed foods (Bromilow et al., 2017; Prasad et al., 1998). Many analyses have been carried out to identify and determine the gluten proteins that may be released during the processing of gluten-free foods. Akagawa et al. (2007) used two-dimensional gel electrophoresis and MALDI-TOF for the detection of gluten allergens in 3 Japanese wheat varieties. As a result of the analysis, they identified 18 wheat allergens. Proteomic technologies have been used to clarify issues such as quality safe fish production and fish welfare. In these studies, zebrafish is the species that has been determined as the target. In addition to this species, trout is also the subject of proteomics technologies (Forne et al., 2010). Listeria monocytogenes is a foodborne pathogen that causes disease in humans. It takes 4-5 days for L. monocytogenes to be detected by the traditional method. An easy and sensitive technique has been developed for the detection of L. monocytogenes directly from the medium. In the study, it was shown that L. monocytogenes in the amount of 1 cfu/ml can be detected within 30 hours via MALDI-TOF-MS (Jadhav et al., 2014). Liu et al. (2012) used 2-DE and MALDI-TOF to investigate the flavors of commercial and village chickens in breast and leg meat. 7 different proteins were found in the breast meat of two types of chickens and 9 different proteins were detected in the leg meat. Since the high protein variety in village chicken can directly affect the meat flavor, it has been suggested that proteomic studies can play an active role in determining the difference between the taste and quality of meat. A comparison was made using whey obtained from healthy cow's milk and whey obtained from cow's milk with mastitis MALDI-TOF MS and 2-DE. As a result of the study, it was observed that there was an increase in the amount of blood serum-derived proteins in mastitic whey compared to normal whey, but the concentrations of α-lactalbumin and β-lactoglobulin, which are basic whey proteins, decreased (Hogarth et al., 2004). Donkey milk and goat milk are widely used in newborn and infant nutrition because they are less allergenic and have a higher nutritional value than other types of milk. In order to determine imitation-adulteration in these sensitive diets, in a study, the results of the analysis were compared using MALDI-TOF/MS in five different milk varieties (female donkey, goat, cow, sheep and buffalo), first in pure form and then mixed with it. It has been specifically stated that this technique gives much more precise and faster results than the techniques used before (Girolamo et al., 2014). Its use as a biomarker for comparison with other genetically modified and non-modified foods is emphasized with the information obtained by identifying important allergen species and anti-nutrient proteome profiles (Natarajan et al., 2009). Studies have shown that food bioactive components are associated with genetics in the prevention of diseases. In the studies, it is aimed to prevent the formation of tumors in the organism thanks to the diet recipes prepared using proteomics technology. It is especially stated that it may be effective in modifying the steps that play a role in tumor formation by enriching the components of foods that are essential / not essential in terms of the nutritional content of the body by using various techniques (Gallardo et al., 2013). In particular, studies have shown that the consumption of foods rich in beta-carotene, vitamins C and E and fiber reduces the risk of developing some types of cancer. In addition, in vitro and in vivo systems of fish oils rich in n-3 fatty acids, it was explained that these fatty acids prevent tumor formation and cardiovascular diseases (Forne et al., 2010). The goal of food safety is to prevent foodborne diseases that may occur in consumers. Although the most important problem in protecting the safety of food is known as food poisoning due to pathogens that may develop at certain stages in the product, contamination with biological/non-biological substances, changes at the molecular level during the heat treatment phase, food allergens that are/may occur, and imitation-adulteration in foods are serious problems that threaten the safety of food (Levin, 2009). Identifying, identifying and verifying pathogens and their toxicity in foods is very important for the protection of public health. Proteomics technologies offer their analysis to the scientific world in terms of faster identification of microbial contaminants and toxins (Piras et al., 2016; Kim, 2007). When it comes to the detection of microorganisms used in various foods, two basic approaches have been designed using proteomics technologies. The first approach is to proteome profiling bacteria in specific places, times and conditions. In a study conducted for this purpose, the proteome map was defined by determining the Bifidobacterium longum NCC2705 strain as a reference and presented to the scientific world (Yuan et al., 2006). The second basic approach is based on the changes that may occur in microorganisms exposed to different environmental conditions and analysis by comparison. This is the most preferred and up-to-date approach today (Levin, 2009; Aires et al., 2010). In recent years, the stress responses of bacteria against different environmental conditions have been examined in detail under proteomics technologies, and the progress of studies has accelerated as proteomics technology continues to develop. The food industry, which needs to increase the shelf life of foods, has become increasingly popular to identify starter cultures that can provide resistance to various conditions and to understand the stress mechanisms that may occur under these conditions. For this subject, important proteomic studies are carried out, especially on species belonging to the genera Enterococcus, Lactobacillus and Lactococcus. (Serrazanetti et al., 2009; Hörmann et al., 2006; Wu et al., 2009). Bifidobacterium longum strains of human origin were compared at the proteome level and proteins involved in carbohydrate metabolism, cell wall and membrane synthesis were revealed based on strains (Aires et al., 2010). With the analyzes performed, 2-DE and MS techniques allowed the identification of the proteins involved in the adhesion of the Lb. plantarum strain and proteins that could act as biomarkers for probiotic selection were revealed (Izquerdo et al., 2009). The presence of mycotoxins in foods poses a threat to the preservation of food quality, and proteome and metabolite-based studies are carried out using proteomic techniques to detect the presence of mycotoxins. In addition to the use of proteomics technologies, immunochemical and chromatographic methods, especially the combination of LC and MS/MS, have become widespread in recent years (Capriotti et al., 2012; Seng et al., 2009). In food technology, the production, processing and observation of microbial contamination in the final product can be easily realized with the developments that have occurred. The identification, verification and quantification of bacteria and bacteria-derived toxins in foods is important for public health. Proteomics technologies offer more sensitive, advanced and specific methods for the identification of microbial food contaminants and toxins and the determination of sanitation procedures compared to current technologies (Levin, 2009). Listeria monocytogenes is a ubiquiter foodborne pathogen that causes foodborne illness and death in humans. Cultural identification of L. monocytogenes takes about 4-5 days. According to a study, an easy and sensitive method has been developed for the detection of L. monocytogenes directly from selective enrichment fluid. In the study, it was shown that L. monocytogenes in the amount of 1 cfu/ml can be detected within 30 hours via MALDI-TOF-MS (Jadhav et al., 2014).

Today, proteomics technologies have become one of the most preferred methods in studies for the determination of food safety, food safety and food quality due to the preference of proteins in separation-determination analysis, mass spectrometry and many current techniques, and the advances in these techniques. Proteomic technologies are primarily used to determine food quality, as well as to analyze changes in storage, transportation conditions and allergens (Costa & Jongen, 2006). D'Alessandro & Zolla (2012) observed that there was thinning of the egg white structure after 20 days of storage at 22°C to examine both structural and protein changes of egg white with proteomic analyzes under egg storage conditions. It has been noted that there is a significant decrease in the number of proteins that determine nutritional value such as ovalbumin, clustering, ovoinhibitor and ovotransferrin during storage. It has been explained that the decrease can lead to significant changes in the pH of the egg. Eggs were stored at 4, 20 and 37 °C for 15 days in a study examining the changes in egg white proteins, it was determined that the amount of ovalbumin decreased rapidly by using 2-DE and LC-MS after high-temperature storage. In addition, ovotransferrin in determining egg quality. Findings obtained; it is important in terms of the effect of storage temperature on egg white proteins and providing a better understanding of thermally induced biochemical changes that may affect the deterioration process of the egg (Qui et al., 2012). In another proteomics study on eggs, Raikos et al. (2006) identified a large number of protein domains after 2D gel electrophoresis of a mixture of egg whites and yolks and imaged ovalbumin and conalbumin isoforms, and the presence of previously unknown FLJ 10305 and Fatso proteins was also detected and confirmed.

**Future Status**

Proteomic analyzes are becoming increasingly important in order to determine quantitative and qualitative biomarkers and to ensure food quality and safety. Since food quality and safety are two inseparable concepts, if an example of proteomics technology is desired, it can offer faster, more sensitive and more accurate analysis methods to determine the crispness of meat, to determine a problem caused by processing conditions or to determine the factors that may occur from environmental factors (Donna et al., 2009; Rabilloud et al., 2010). In addition, it is recommended to use techniques combined with MS for more precise study (Henzel et al., 2003). On the other hand, food safety is not only a matter of determining the content of a product but also of the degree of edibility of the product from a biochemical point of view, both from a physical, chemical and microbiological point of view (Zhang et al., 2008; Budak & Dönmez, 2012). In addition, the application of mass spectrometry (MS) to the field of microbiology and technological developments in MS devices are expected to contribute more to food safety and protection efforts. This technology also allows for much faster and more accurate identification of bacteria and other microorganisms (Zapata et al., 2009). However, as with all methods and approaches, proteomics technology has its advantages and disadvantages. The most sensitive point in these studies is that proteins have a dynamic structure. For this reason, the standardization of the sample should be done with precision in the analyzes. In addition, results may vary due to technical differences arising from different applications in different laboratories. To overcome this problem, global organizations need to do the necessary work and try to establish globally accepted standards (Seng et al., 2009).

**Conclusion**

Reliable control mechanisms and analysis methods are necessary for safe food production. Determining the quality of the substance and food applied to the food is possible by determining the molecular composition of the food. Today, with the combination of omics technologies and sub-branches, it has become possible to use new and high technologies in food science and analysis. In this context, bioactive nutritional components can be identified, and healthier food formulations can be developed. In addition, with many studies conducted in recent years, it is worthy to indicate that very important steps can be taken in food safety by using omics technologies. It should also be noted that proteins are essential or complementary components of foods. Protemics serve as a compass for scientists on unsolved issues by using proteins in research, which are the most dynamic structure of living things and foods. Today, thanks to proteomics and metabolomics technology, the presence, absence or modification of proteins and metabolites and hundreds of different components can be detected. Thanks to the studies to be carried out on foods using this technology, there will be important developments in the fields of food safety and public health.

**References**

Aires, J., Anglade, P., Baraige, F., Zagorec, M., Champomier-Verge, M. C., & Butel, M. J. (2010). Proteomic Comparison of The Cytosolic Proteins of Three Bifidobacterium Longum Human Isolates and Bifidobacterium Longum NCC2705. BMC Microbiol, 10: 29-36.

Akagawa, M., Handoyo, U., Ishii T., Kumazawa, S., Morita, N. & Suyama, K. (2007). Proteomic Analysis of Wheat Flour Allergens. Journal of Agricultural and Food Chemistry, 55(17): 6863-6870.

Almeida C., Duarte I.F., Barros A., Rodrigues J., Spraul M. & Gil A.M. (2006). Composition of Beer by 1H NMR Spectroscopy: Effects of Brewing Site and Date of Production. J Agr Food Chem 54: 700–706.

Alothman, M., Lusk, K. A., Silocock, P. & Bremer, P. J. (2017). Comparing PTR-MS Profile of Milk Inoculated with Pure or Mixed Cultures of Spoilage Bacteria. Food Microbiology, 64: 155-63.

Ansari, P., Stoppacher, N. & Baumgartner, S. (2012). Marker Peptide Selection for The Determination of Hazelnut By LC-MS/MS and Occurrence in Other Nuts. Anal. Bioanal. Chem., 402(8): 2607–2615.

Aru, V., Khakimov, B., Sorensen, K. M. & Engelsen, S. B. (2018). The Foodome of Bivalve Molluscs: From Hedonic Eating to Healthy Diet. Journal of Food Composition and Analysis, 69: 13 – 9.

Bantscheff, M., Schirle, M., Sweetman, G., Rick, J., And Kuster, B., 2007. Quantitative Mass Spectrometry in Proteomics: A Critical Review. Anal Bioanal Chem, 389: 1017-1031.

Başaran, E., Aras, S. & Cansaran-Duman, D. (2010). General Outlook and Applications of Genomics, Proteomics and Metabolomics. Turkish Bulletin of Hygiene And Experimental Biology. Cx; 67(2): 85-96.

Bayram, M. & Gökırmaklı, Ç. (2018). OMICS: A Journal of Integrative Biology, 177-183.

Boo, C. C., Parker, C. H., And Jackson, L. S. (2018). A Targeted LC-MS/MS Method for The Simultaneous Detection and Quantitation of Egg, Milk, and Peanut Allergens in Sugar Cookies. Journal of AOAC International, 101(1): 108–117.

Bromilow, S., Gethings, L. A., Buckley, M., Bromley, M., Shewry, P. R., Langridge, J. I. & Clare Mills, E. N. (2017). A Curated Gluten Protein Sequence Database to Support Development of Proteomics Methods for Determination of Gluten in Gluten-Free Foods. J. Proteome., 163: 67–75.

Budak, Ş. & Dönmez, S. (2012). New Omics Technologies in Food Science, Food, 37 (3): 173-179.

Calvano, C. D., Monopoli, A., Loizzo, P., Faccia, M. & Zambonin, C. (2013). Proteomic Approach Based on MALDI – TOF MS To Detect Powdered Milk in Fresh Cow's Milk. Journal of Agricultural and Food Chemistry, 61(8): 1609-1617.

Capriotti, A. L., Caruso, G., Cavaliere, C., Foglia, P., Samperi, R. & Laganà, A. (2012). Multiclass Mycotoxin Analysis in Food, Environmental and Biological Matrices with Chromatography/Mass Spectrometry. Mass Spectrometry Reviews, 31(4): 466-503.

Carbonaro, M. (2008). Proteomics: Present and Future in Food Quality Evaluation. Trend Food Sci Tech, 15: 209-216.

Castro – Puyana, M., Perez – Miguez, R., Montero, L. & Herrero, M. (2017). Reprint of: Application of Mass Spectrometry – Based – Metabolomics Approaches for Food Safety, Quality and Traceability. TrAC Trends in Analytical Chemistry, 96: 62-78.

Cevallos, J. & Rodrick, G. (2009). Metabolomic Analysis in Food Science: A Review. Trends in Food Science & Technology, 20 (11): 557-566.

Chang,Y., Zhao, C., Zhu, Z., Wu, Z., Zhou, J., Zhao, Y., Lu, X. & Xu, G. (2012). Metabolic Profiling Based on Lc7mms To Evaluate Unintended Effects Of Transgenic Rice With Cry1ac and Sck Genes. Plant Molecular Biology, 78(4 – 5): 477-87.

Chao, E., & Krewski, D. (2008). A Risk – Based Classification Scheme for Genetically Modified Foods II: Graded Testing. Regulatory Toxicology and Pharmacology: RTP, 52(3): 223-34.

Chen, J., Li, K., Le, X. C. & Zhu, L. (2018). Metabolomic Analysis of Two Rice (Oryza Sativa) Varieties Exposed To 2,2',4,4'-Tetrabromodiphenylether. Enviromental Pollution (barking, Essex: 1987), 237: 308-17.

Chen, L., Zhao X., Wu, J., Liu, Q., Pang, X. & Yang (2020). Metabolic Characterization of Eight Escherichia Coli Strains and Acidic Responses of Selected Strains Revelead By NMR Spectroscopy. Food Microbiology 88: 103399.

Christopher J. & Haselssen J.N. (2008). Metabolic Profiling as A Tool For Understanding Mechanisms of Toxicity. Toxicol Pathol. 36 (1): 140-147.

Coşkun, T. (2007). Nutritional Genomics. Journal of Pediatrics, 50; 47-66.

Costa, A. I. A. & Jongen, W. M. F. (2006). New Insights into Consumer-Led Food Product Development. Trends Food Sci Technol, 17: 457-465.

Cristea, I. M., Gaskell, S. J. & Whetton, A. D. (2004). 'Proteomics Techniques and Their Application to Hematology ', Blood, 103 (10): 3624-3634.

Cubero–Leon, E., Penalver, R. & Maquet, A. (2014). Review on Metabolomics for Food Authentication, Food Research International, 60: 95-107.

D'Alessandro, A. & Zolla, L. (2012). We Are What We Eat: Food Safety and Proteomics, J. Proteome Res., 11: 26–36.

Davies, H. (2010). A Role For ''Omics'' Technologies in Food Safety Assessment. Food Control, 21(12): 1601-1610.

DeBruyne, K., Slabbinck, B., Waegeman, W., Vauterin, P., De Baets, B. & Vandamme, P. (2011). Bacterial Species Identification from Maldi-Tof Mass Spectra Through Data Analysis and Machine Learning. Syst Appl Microbiol, 34: 20-29.

Donna, D., L., Ronci, M., Sacchetta, P., Di Ilio, C., Biolatti, B. & Federici, G. (2009). A Food Safety Control Low Mass- -Range Proteomics Platform for The Detection of Illicit Treatments In Veal Calves By Maldi-Tof-Ms Serum Profiling, Biotechnol. J., 4: 1596–1609.

Elaine, T. M., Cindy, D. & Milner J. (2006). Nutrigenomics, Proteomics, Metabolomics. Pract Dietetics, 106(3), 403-413.

Forne, I., Abian, J. & Cerda, J. (2010). Fish Proteome Analysis: Model Organisms and Non-Sequenced Species. Proteomics, 10: 858-872.

Gallardo, J. M., Mónica, C. & Ignacio, O. (2013). "Proteomics in Food Science." Foodomics: Advanced Mass Spectrometry in Modern Food Science and Nutrition; Cifuentes, A., Ed: 125-165.

Gao, C. (2018). The Future of Crispr Technologies In Agriculture . Nature Reviews Molecular Cell Biology, 19(5): 275-6.

Garcia – Canas, V., Simo, C., Castro – Puyana, M. & Cifuentes, A. (2014). Recent Advances in The Application of Capillary Electromigration Methods for Food Analysis and Foodomics. Electrophoresis, 35(1): 147-69.

Garcia – Canas, V., Simo, C., Herrero, M., Inbanez, E. & Cifuentes, A. (2012). Present and Future Changelles in Food Analysis: Foodomics. Analytical Chemistry, 84: 10150-159.

Gaulitz, J. M., Aceves, C. M., Aksenov, A. A., Aleti, G., Almaliti, J., Bouslimani, A., And Brown, E. A. (2018). Untargeted Mass Spectrometry – Based Metabolomics, Tracks, Molecular Changes in Raw and Processed Foods and Beverages. Biorxiv: 347716.

Ghosh, D. & Poisson, L. M. (2009). "Omics" Data and Levels of Evidence for Biomarker Discovery. Genomics 93(1): 13-16.

Gibney, M. J., Walsh, M., Brennan, L., Roche, H. M., German, B. & Ommen, B. (2005). Metabolomics in Human Nutrition: Opportunities and Challenges. Am J Clin Nutr 82: 497-503.

Girolamo, F., Masotti, A., Salvatori, G., Scapaticci, M., Muraca M. & Putignani, G. (2014). A Sensitive and Effective Proteomic Approach to Identiy She-Donkey's and Goat's Milk Adulterations by MALDI-TOF/MS Fingerprinting. Int J Mol Sci, 15(8): 13697-719.

Goodacre, R. (2005). Metabolomics-The Way Forward. Metabolomics, 1: 1-2.

Green, M. J., Leach, K. A., Breen, J. E., Green, L. E. & Bradley, A. J. (2007). National Intervention Study of Mastitis Control in Dairy Herds in England and Wales. Vet Rec, 160: 287-93.

Hamad, H. O., Alma, M. H., Gulcin, I., Yilmaz, M. A., & Karaogul, E. (2017). Evaluation of Phenolic Contents and Bioactivity of Root and Nutgall Extracts from Iraqian Quercus infectoria Olivier. Records of Natural Products, 11(2), 205-210.

Han, J. Z. & Wang, Y. B. (2008). Proteomics: Present and Future in Food Science and Technology. Food Sci Technol Int, 19: 26-30.

Havelaar, A. H., Kirk, M. D., Torgerson, P. R., Gibb, H. J., Hald, T., Lake, R. J., Praet, N., Bellinger, D. C. & Gargouri, N. (2015). World Health Organization Global Estimates and Regional Comparisons of The Burden of Foodborne Disease in 2010. Plos Medicine 12 (12): E1001923.

Henzel, W. J., Watanabe, C., & Stults, J. T. (2003). Protein Identification: The Origins of Peptide Mass Fingerprinting. Journal of The American Society for Mass Spectrometry, 14(9): 931-942.

Heuberger A.L., Lewis M.R., Chen M.H., Bridge M.A., Leach J.E. & Ryan E.P., (2010). Metabolomic and Functional Genomic Analyses Reveal Varietal Differences in Bioactive Compounds Of Cooked Rice. Plos One, 5: 2915.

Hogarth, C., Fitzpatrick, L., Nolan, A., Genc, F. & Pitt, A. (2004). Eckersall P., Differential Protein Composition of Bovine Whey: A Comparison of Whey From Healthy Animals and From Those with Clinical Mastitis. Proteomics, 4(7): 2094-2100.

Hörmann, S., Scheyhing, C., Behr, J., Pavlovic, M., Ehrmann, M. & Vogel, R. F. (2006). Comparative Proteome Approach to Characterize The High-Pressure Stress Response of Lactobacillus Sanfranciscensis Dsm 20451t . Proteomics, 6: 1878-1885.

Hou, Y., Kamal, G. M., Wang, J., Liu, H., Zhang, G., Hu, Z., Anwar, F. & Du, H. (2017). 1H – NMR – Based Metabolomics for Discrimination of Rice from Different Geographical Origins of China. Journal of Cereal Science, 76: 243-52.

Hu, F., Furihata, K., Kato, Y. & Tanokura, M. (2007). Nondestructive Quantification of Organic Compounds in Whole Milk Without Pretreatment by Two dimensional NMR Spectroscopy. J Agr Food Chem 55: 4307-4311.

Issaq, H. J. (2001). The Role of Separation Science in Proteomics Research. Electrophoresis, 22(17): 3629-3638.

Izquierdo, E., Horvatovich, P., Marchioni, E., Aoude-Werner, D., Sanz, Y. & Ennahar, S. (2009). 2-De and Ms Analysis of Key Proteins in The Adhesion of Lactobacillus Plantarum, A First Step Toward Early Selection of Probiotics Based on Bacterial Biomarkers. Electrophoresis, 30: 949-956.

Jadhav, S. R. (2019). Identification of Putative Biomarkers Specific to Foodborne Pathogens Using Metabolomics. In Foodborne Bacterial Pathogens, ed, A.Bridier, 149-64.

Jadhav, S., Sevior, D., Bhave, M. & Palombo, E. A. (2014). Detection of Listeria Monocytogenes from Selective Enrichment Broth Using Maldi–Tof Mass Spectrometry. Journal of Proteomics, 97: 100-106.

Kahraman, H. & Bozkır, S. (2020). Proteomics Technology and Its Uses in Food Science. Academic Research in The Field of Animal Husbandry, 47-75.

Karaogul, E. (2019). Effects of Asphodel Tuber and Dolomite on the Properties of Bio-hybrid Films Processed by a Twin Screw Extruder. Bioresources, 14(2), 4473-4488.

Karaoğul, E., & Alma, M. H. (2019). Effects of Eremurus Tuber and Dolomite Filler on Several Properties of Poly(Vinylalcohol) Bio-Films. Fresenius Environmental Bulletin, 28(10), 7108-7118.

Karaogul, E., Kirecci, E., & Alma, M. H. (2016). DETERMINATION OF PHENOLIC COMPOUNDS FROM TURKISH KERMES OAK (Quercus coccifera L.) ROOTS BY HIGH PERFORMANCE LIQUID CHROMATOGRAPHY; ITS ANTIMICROBIAL ACTIVITIES. FEB-FRESENIUS ENVIRONMENTAL BULLETIN, 2356.

Kathuria, D., Thakur, S. & Sindh, N. (2024). Advances of metabolomic in exploring phenolic compounds diversity in cereal and their health implications. International Journal of Food Science and Technology, Early View, Online Version, March 2024 https://doi.org/10.1111/ijfs.17056

Kaufmann, A. (2014). Combining Uhplc and High - Resolution Ms: A Viable Approach Fort He Analysis of Complex Samples? TrAC Trends in Analytical Chemistry, 63: 113- 28.

Kendall, H., Naughton, P., Kuznesof, S., Raley, M., Dean, M., Clark, B., Stolz, H., Home, R., Chan, M. Y. & Zhong, Q. (2018). Food Fraud and The Perceived Integrity of European Food Imports Into China. PLoS One, 13(5): e0195817.

Kim, Y., Nandakumar, M. P. & Marten, M. R. (2007). Proteomics of Filamentous Fungi. Trends Biotechnol 25(9): 395-400.

Kiran, F. & Osmanağaoğlu, Ö. (2013). Pretoemic Studies in Lactic Acid Bacteria, Food, 38(1): 55-62.

Koyuncu, İ., Gönel, A., Temiz, E., Karaoğul, E., & Uyar, Z. (2021). Pistachio Green Hull Extract Induces Apoptosis through Multiple Signaling Pathways by Causing Oxidative Stress on Colon Cancer Cells. Anti-Cancer Agents in Medicinal Chemistry- Anti-Cancer Agents), 21(6), 725-737.

Levin, R. E. (2009). The Use of Molecular Methods for Detecting and Discriminating Salmonella Associated with Foods—A Review. Food Biotechnology, 23(4): 313-367.

Lindon, J. C., Holmes, E., Bollard, M. E., Stanley, E. G. And Nicholson, J. K. (2004). Metabonomics Technologies and Their Applications Jadhav S. R., Liuphysiological Monitoring, Drug Safety Assessment and Disease Diagnosis. Biomarkers 9: 1-31.

Liu, X. D., Jayasena, D. D., Jung, Y., Jung, S., Kang, B. S., Heo, K. N., Lee, J. H. & Jo, C. (2012). Differential Proteome Analysis of Breast And Thigh Muscles Between Korean Native Chickens and Commercial Broilers. Asian-Australas. J. Anim. Sci., 25: 895.

Ma, X., Ge, Y., Zhang, J., Huang, W., Han, J., Chen, Y., Li, H. & Sun, J. (2020). Comprehensive Quantification of Sesame Allergens in Processed Food Using Liquid Chromatography-Tandem Mass Spectrometry. Food Control, 107: 106744.

Manso, M. A., Le ́onil, J., Jan, G. & Gagnaire, V. (2005). Application of Proteomics to The Characterisation of Milk and Dairy Products. Int Dairy J, 15: 845-855.

Marko-Varga, G. (2004). Proteomics Principles and Challenges. Pure and Applied Chemistry, 829-837.

Mashego, M. R., Rumbold, K. C., Marjan De Mey, Vandamme, E., Soetaert, W., & Heijnen, J., 2007. Microbial Metabolomics: Past, Present and Future Methodologies. Biotechnol Lett, 29: 1-16.

Moco, S., Bino, R. J., Vorst, O., Verhoeven H. A., Groot, J. & Beek, T. A. (2006). A Liquid Chromatography- Mass Spectrometry- Based Metabolome Database for Tomato. Plant Physiol, 141:1205-1218.

Natarajan, S. S, Xu, C., Cregan, P., Caperna, T. J., Garrett, M. W. & Devanand, L., (2009). Utility Of Proteomics Techniques for Assessing Protein Expression. Regulate Toxicol Pharmacol; 54: 32–6.

Nedjip, G., & Karaogul, E. (2021). ADSORPTIVE BUBBLE SEPARATION METHODS (ABSM): FOAM FRACTION. INTERNATIONAL JOURNAL OF CURRENT NATURALSCIENCE AND ADVANCED PHYTOCHEMISTRY, 1(1), 27-43.

Nenni, M., Çelebier, M. & Süslü, İ. (2020). Proteomic Studies Overview, an Overview of Protemic Studies, Hacettepe University Journal of the Faculty of Pharmacy 40(1): 48-58.

O'Donnella, R., Holland, J. W., Deeth, H. B. C. & Alewood, P. (2004). Milk Proteomics. Int Dairy J, 14: 1013-1023.

O'Farrell, P. H. (1975). High Resolution Two-Dimensional Electrophoresis of Proteins. Journal of Biological Chemistry, 250(10): 4007-4021.

O'Flaherty S. & Klaenhammer, T.R. (2011). The Impact of Omic Technologies on The Study of Food Microbes. Annu Rev Food Sci Technol, 2: 353-371.

Omana, D. A., Liang, Y., Kav, N. V. & Wu, J. (2011). Proteomic Analysis of Egg White Proteins During Storage. Proteomics, 11: 144-153.

Ong, S. E., & Pandey, A. (2001). An Evaluation of The Use of Two-Dimensional Gel Electrophoresis in Proteomics. Biomolecular Engineering, 18(5): 195-205.

Ordovas, J. M. & Corella, D. (2004). Nutritional Genomics. Annu Rev Genomics Hum Gene, 5: 71-118.

Özcengiz, G. (2007). Proteomics: The Most Powerful Technology of The Post-Genomic Era. METU Newsletter. 15: 13-9.

Pedreschi, R., Hertog, M., Lilley, K. S., & Nicola, B. (2010). Proteomics for The Food Industry: Opportunities and Challenges. Crit Rev Food Sci Nutr, 50: 680-692.

Peng., J., & Gygi, S. P., 2001. Proteomics: The Move to Mixtures. Journal of Mass Spectrometry, 36(10): 1083-1091.

Piras, C., Roncada, P., Rodrigues, P. M., Bonizzi, L. & Soggiu, A. (2016). Proteomics in Food: Quality, Safety, Microbes, and Allergens. Proteomics, 16(5): 799-815.

Planque, M., Arnould, T., Dieu, M., Delahaut, P., Renard, P. & Gillard, N. (2016). Advances in Ultra-High Performance Liquid Chromatography Coupled to Tandem Mass 120 Spectrometry for Sensitive Detection of Several Food Allergens in Complex and Processed Foodstuffs. J.Chromatogr. A., 1464: 115–123.

Prasad, C., Dalton, L., Cde, R., Levy, H. (1998). Role Of Diet Therapy in Management of Hereditary Metabolic Diseases. Nutr Research, 18: 391-402.

Qui, N., Ma, M., Zhao, L., Liu, W., Li, Y. & Mine, Y. (2012). Comparative Proteomic Analysis of Egg White Proteins Under Various Storage Temperatures. Journal of Agricultural and Food Chemistry, 60: 7746–7753.

Rabilloud, T. (2002). Two-Dimensional Gel Electrophoresis in Proteomics: Old, Old Fashioned, But It Still Climbs Up The Mountains. PROTEOMICS: International Edition, 2(1): 3-10.

Rabilloud, T., Chevallet, M., Luche, S. & Lelong, C. (2010). Two-Dimensional Gel Electrophoresis in Proteomics: Past, Present and Future. Journal of Proteomics, 73(11): 2064-2077.

Raikos, V., Hansen, R., Campbell, L. & Euston, S. R. (2006). Separation and Identification of Hen Egg Protein Isoforms Using Sds–Page and 2d Gel Electrophoresis with Maldi-Tof Mass Spectrometry. Food Chemistry, 99(4): 702-710.

Rapoport S. I., Ramadan E. & Basselin M. (2011). Docosahexaenoic Acid (DHA) Incorporation into The Brain from Plasma, As An In Vivo Biomarker of Brain DHA Metabolism and Neurotransmission. Prostaglandins Other Lipid Media, 96: 109-113.

Resetar, D., Pavelic, S. K. & Josic, D. (2015). Foodomics for Investigations of Food Toxins. Current Opinion in Food Science, 4: 86-91.

Roncada, P., Piras, C., Soggiu, A., Turk, R., Urbani, A. & Bonizzi, L. (2012). Farm Animal Milk Proteomics. J Prot,. 75(14): 4259-74.

Rubert, J., Zachariasova, M. & Hajslova, J. (2015). Advances In High – Resolution Mass Spectrometry Based on Metabolomics Studies for Food – A Review: Food Additivies & Contaminants: Part A, 32 (10): 1685 – 708.

Rubio-Aliaga I, Köchhar S. & Silva-Zolezzi, I. (2012). Biomarkers of Nutrient Bioactivity and Efficacy: A Route Toward Personalized Nutrition. J Clin Gastroenterol. 46: 545-554.

Sakin, Y. S. & Tanoğlu, A. (2016). "Prebiotics and Their Effects on Human Health", Prebiotics Prebiotics Review, 5: 210–233.

Seng, P., Drancourt, M., Gouriet, F., La Scola, B., Fournier, P. E., Rolain, J. M., D. & Raoult, D. (2009). Ongoing Revolution in Bacteriology: Routine Identification of Bacteria By Matrix-Assisted Laser Desorption Ionization Time-Of-Flight Mass Spectrometry. Clin. Infect. Dis. 49: 543–551.

Serrazanetti, D. I., Guerzoni, M. E., Corsetti, A. & Vogel, R. (2009). Metabolic Impact and Potential Exploitation of The Stress Reactions in Lactobacilli. Food Microbiol, 26: 700-711.

Sevimli, M. & Özçelik, N. (2013). Protein Expression Changes in Breast Cancer and Their Importance. Dicle Medical Journal, 40(1) :161-168.

Shubo, L., Yufeng, T., Pingyingzi, J., Ying, L., Xiaoling, L. & Hongshun, Y. (2021). Recent Advances in The Application of Metabolomics for Food Safety Control and Food Quality Analyses. Critical Reviews in Food Science and Nutrition, 61(9): 1448-1469.

Singh, N., Barthwal, R., Negi, A., Aggarwal, S., Kathuria, D., Kumar, V. & Paul, M. (2024). Foodomics: futuristic omic strategies to assess the impact of food nutrients on human health and gut microbiome. International Journal of Food Science and Technology, Early View, Online Version, March 2024. https://doi.org/10.1111/ijfs.17041

Smith R. (2009). Two-Dimensional Electrophoresis: An Overview. In: Two-Dimensional Electrophoresis Protocols, Sheehan D, Tyther R (editors), Humana Press, New York, 3-9.

Taşdemir, A. (2017). "Probiotics, Prebiotics, Synbiotics", Health Academy Kastamonu, 2(1): 71–88.

Wenk, M. R. (2005). The Emerging Field of Lipidomics. Nat Rev Drug Discov, 4: 594-610.

Wimmers, K., Murani, E., & Ponsuksili, S. (2010). Functional Genomics and Genetical Genomics Approaches Towards Elucidating Networks of Genes Affecting Meat Performance in Pigs. Brief Funct Genomics, 9: 251-8.

Wishart, D. S. (2008). Metabolomics: Applications to Food Science and Nutrition Research. Trend Food Sci Tech, 19: 482-493.

Wittmann, L. B., Graack, H. R., & Pohl, T. (2006). Two-dimensional Gel Electrophoresis as Tool for Proteomics Studies in Combination with Protein Identification By Mass Spectrometry. Proteomics, 6(17): 4688-4703.

Wu, R., Wang, W., Yu, D., Zhang, W., Li, Y., Sun, Z., Wu, J., Meng, H. & Zhang, H. (2009). Proteomics Analysis of Lactobacillus Casei Zhang, A New Probiotic Bacterium Isolated From Traditional Home-Made Koumiss in Inner Mongolia of China. Mol Cell Proteomics, 8: 2321-2338.

Xu, Y. J., Wang, C., Eugene, W. & Nam, C. (2014). Recent Developments and Applications of Metabolomics in Microbiological Investigations. Trac Trends in Analytical Chemistry, 56: 37-48.

Yaman, Ö. (2015). An Overview of Metabolomics Studies in Medicine. Journal of Bahri Dagdas Animal Research, 3(1): 33-46.

Yilmaz, İ. & Özpınar, H. (2019). Metabolomic Applications in The Fields of Nutrition and Food: An Overall Assessment, IGUSABDER, 8: 827-839.

Yuan, J., Zhu, L., Liu, X., Li, T., Zhang, Y., Ying, T., Wang, B., Wang, J., Dong, H., Feng, E., Li, Q., Wang, J., Wang, H., Wei, K., Zhang, X., Huang, C., Huang, P., Huang, L., Zeng, M. & Wang, H. (2006). A Proteome Reference Map and Proteomics Analysis of Bifidobacterium Longum Ncc2705. Mol Cell Proteomics, 5: 1105-1118.

Zapata, I., Zerby, H. N., & Wick, M. (2009). Functional Proteomic Analysis Predicts Beef Tenderness and The Tenderness Differential. J Agric Food Chem, 57: 4956-4963.

Zhang X., Yeeleng Y., Dong W., Chen G., & Chen F. (2008). Novel Omics Based Technology in Nutrition Research. Biotechnol Adv, 26: 169-176.