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# Foodomics-Use of Integrated Omics in Nutrition, Food Technology and Biotechnology

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## Introduction

After rather slow beginning, the "omics" methods are gaining in importance for process development and validation in food technology and biotechnology as well as corresponding quality control of starting materials and final products [1]. This methodology is increasingly used for analyses of food composition and quality, food authentication, safety assessment of genetically modified food, identification of food allergens, presence of toxins, analysis of the physiological activity of food proteins and peptides, and the influence of the production process on the chemical, physicochemical and biological properties of food proteins [2], and a specific term "foodomics" was also recently coined. The number of papers dealing with use of omics methods in food processing and nutrition has also rapidly increased, especially on the field of food of animal origin [3]. Advances in whole genome sequencing of plants that are important for human nutrition have also removed the major obstacle for the use of foodomic, especially proteomic methods for food of plant origin [1]. Furthermore, organic food of both plant and animal origin plays an increasingly important role in the food market, therefore foodomic methods are used for the identification and quality assurance of organic food, and discovery of potential fake organic products [4]. Similar to the organic food, the traditional fermented food is again gaining in popularity. In this kind of food of both animal and plant origin such as meat, milk and milk products, wine, beer and other fermented products, changes of the proteome of the substrate (e.g. sausages, fermented milk products and grape juice) and in the starter culture microorganisms (e.g. milk bacteria, bacterial and mixed microflora in fermented meat product, and yeasts in both wine and beer) as well as their interaction play a crucial role in the quality of the final products [4]. Fermentation also means enzymatic digestion of food components, and accumulation of small molecules in the final product. These molecules are frequently responsible for specific flavor of original fermented food and can be used as markers for its originality and identity [5]. On the other hand, in production of both organic and traditional fermented food, thermal and other steps for microbial inactivation and inactivation of toxins and allergens are frequently avoided. It is the reason that this kind of food can get a serious safety risk, especially if contaminated raw materials are used or improperly prepared.

## Foodomics-Towards the Integrated Omics in Food Science

At this moment, foodomics constitute one of the most relevant and fast developing areas in food science. Slowly, but constantly, the formerly fully independent worlds of the experts in food technology and microbiology, nutrition, genomics, proteomics (together with glycomics, phosphoproteomics and other methods dealing with posttranslational modification of proteins) and metabolomics have started to interact. The aim of this cooperation is to ameliorate the food quality and safety, and to prevent food adulteration. The rights of consumers and genuine food processors in terms of food adulteration and fraudulent or deceptive practices in food processing are set out in the European Union regulations regarding food safety and traceability. This system was developed in order to: (i) encourage diverse agricultural production; (ii) protect product names from misuse and imitation; (iii) help consumers by giving them information concerning the specific character of the product [6]. The potential use of foodomics in their development pathway for food production, assessing the safety, originality and quality is shown in figure 1.

As soon as the above mentioned collaboration was intensified, it clearly emerged that the integration of all foodomics disciplines will represent a more suitable tool than each discipline by itself, e.g., proteomics or genomics alone. The result was an intensive collaboration between the experts on different fields of food science and nutrition and omics experts. The use of foodomics enabled, or at least facilitated the answers to the questions that are crucial for food safety, quality, traceability and its protection against adulteration. These points are: (i) geographical origin (ii) handling (iii) quality and originality of the starting material (iv) use of genetically modified food and/or transgenic microbial cultures (v) use of antibiotics, fungicides and herbicides during animal and crop cultivation (vi) microbial contamination during the production process, handling and storage [7].

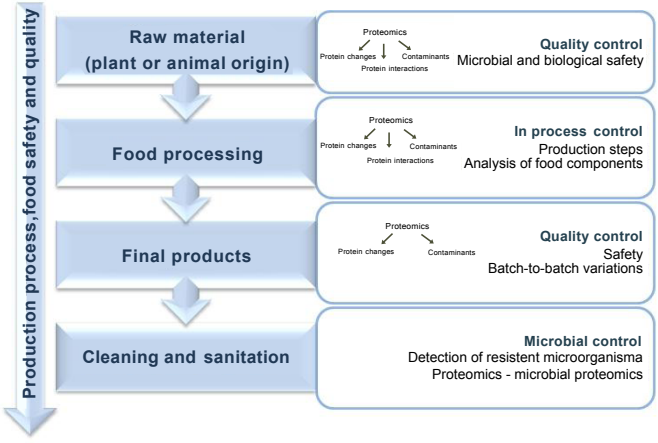


**Figure 1:** Use of foodomics in the development pathway for food production, and assessing food safety, originality and quality [7].

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## High-throughput Methods

Both the sampling and the high-throughput sample preparation are the first critical point in foodomic analyses. They are critical for both exact and very fast analytical work. Optimization of sample preparation, extraction and parallel chromatographic separation of extracts before further analysis by use of robotics is the first step on the way for fast and exact omics food analyses. The use of miniaturized columns packed with bulk supports or containing monoliths for parallel separation of 96 samples was already introduced [8]. Different chromatographic supports can be used for stepwise separation of complex biological mixtures before further proteomic and metabolomic analyses.

Already three years ago, we emphasized that most proteomic analyses of food components are based on protein separation by gel electrophoresis [7]. In proteomic analysis of food, the 2D electrophoresis is still the most used method for protein separation before their identification by LC-MS/MS [1]. Although this method provides very high resolution and effective separation of very similar components, it is time-consuming and the use of robotics for high-throughput sampling is difficult. The use of gel-free proteomics enables the sample preparation and high-throughput analysis of samples, as well as integration of other parallel omics methods, e.g., determination of metabolites in the same analytical run. For quantitative analyses, gel-free, label-free methods with application of the corresponding software will be introduced. New software can be used for direct comparison of samples at both protein (proteomics), peptide and other low molecular weight components (peptidomic, metabolomic) level in order to determine differently expressed components on the further way of determination of possible candidates and validation of (bio) marker candidates [7].

## Development of Methods for Determination of Food Quality and Originality

In order to determine the discrimination of fresh versus frozen meat (http://www.spiegel.de/spiegel/print/d-81562346.html, Der Spiegel online), several foodomic methods can be used such as DNA based techniques, spectroscopy (including the NMR), sensory methods and bio imaging. Omics methods are also gaining importance for determination of the used antibiotics in meat production, use of growth promoter abuse by metabolomic or proteomic methods [1,7], adulteration of raw materials in production of high-value food [9,10], and in order to determine the speed of the spoilage of raw material [11]. It was already demonstrated that previous, very effective methods for food analysis and detection of adulterations can be further optimized by introduction of new, rapid and more sensitive methods at the higher level of the present state-of-the art [9,12]. Important contribution will be the application of so-called "activomics". It is the method that is following the change of enzyme activities in target samples (e.g., different proteases or kinases) by use of MALDI-TOF mass spectrometry. In combination with other methods, activomics can explore the changes in the food during storage (e.g., freezing, or freezing/thawing) as well as during the production process, or changes caused by microbial contamination.

Russo et al. [12] demonstrated that the adulteration by replacement of buffalo by bovine milk can be detected by analyses of post-translation modifications, in this case, casein phosphopeptides. Introduction of this methodology will be also be very useful for (phospho) proteomic and genomic meat analysis [13].

With few exceptions, glycomic and phosphoproteomic analyses in foodomics are now limited to milk [7]. Analyses of changes of post-translational modifications, primarly glycosylation and phosporylation will be applied in order to determine the quality and originality of the starting materials following the changes during food fermentation, as well as typical pattern related to food adulterations. Additional information will be gained by parallel investigation of phospholipids' changes [14].

Imaging mass spectrometry is further method for determination of the distribution of small molecules and small and middle sized proteins in complex biological samples. This method was mostly used in medicine for discovery of disease biomarkers [15] which can be adapted for use in food analysis.

The field of foodomic disciplines is a rapidly evolving scenario filled with the technological innovations (high-throughput sample preparation, optimized LC and MS instruments), bioinformatics tools (e.g., in direction of the label-free quantitative MS analysis) and other practical issues in this field. The coordination of the collaboration of all participating groups will finally result in an integration of all applied omic disciplines converging to the field of foodomics and it will represent more suitable tool than each discipline alone in providing the answers that are addressed above.

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