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Foodomics is a Cutting-edge Method of Studying Food Microbes

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Abstract

Food science is the study of all aspects of food, including its physical, biological, chemical, and technological composition. In recent decades, research in food science has transitioned from traditional approaches to cutting-edge technologies that have a solid foundation in studies in medicine, pharmacology, and biotechnology. Food scientists are now interested in using "omics" techniques in their studies. In order to apply "omics" approaches in food research, Cifuentes' group proposed the idea and practical application of "foodomics" in 2009. An rising number of researchers have adopted this definition in just a few years.

Keywords: Foodomics • NGS • DNA

Introduction

The study of food and nutrition using cutting-edge omics technologies like genomes, transcriptomics, proteomics, and metabolomics is known as foodomics. The development of functional foods and transgenic foods, among other things, as well as investigations into food contaminants and toxicity, active compound profiling, authenticity, and biomarkers related to food quality and effects on human health are all examples of the increasing use of these methodologies [1].

On the other hand, bacteria can affect food in both positive and negative ways. For instance, pathogenic microbes can cause diseases or intoxications, whereas saprophytic microorganisms can cause food to spoil. Contrarily, "healthy" microorganisms like *Acetobacterium balch*, Lactic acid bacteria, and Saccharomyces cerevisiae are essential to fermented foods [2,3]. Food science now includes food microbiology as a crucial component because it focuses on all facets of food microorganisms. Food microbe detection, identification, growth traits, quantification, prevention, and modification are all part of the field of food microbiology investigation.

Description

Proteomics

Foodomic technologies have been utilised extensively in recent years for the study of food microbiology, including safety evaluation, quality control, and nutritional component analysis. In this article, we discuss the approaches used in foodomics, particularly those used in proteomics and metabolomics, as well as how foodomics is applied to the study of food microbiology.

Analytical chemistry, biochemistry, molecular biology, food technology, chemometrics, and bioinformatics are all integrated into the research methodologies and tools of foodomics. A thorough understanding of foodomics methods is crucial in this situation. The term "genomics" describes the sequencing, assembly, and study of an organism's genome's structure and function [4]. The ability of DNA sequence technology to increase throughput and decrease cost is partly responsible for the enormous progress in genomics that has been made recently. Technologies for next-generation sequencing (NGS) have been extensively used in genomic research. NGS methods often do not require a sequence library and may run millions of sequencing experiments in parallel, in contrast to the Sanger capillary electrophoresis sequencing approach. NGS technologies have reaped several benefits throughout the years thanks to novel methods and computer development.

Sing-molecule sequencing is a new technique that has recently been presented in genomics. This method employs multiple approaches to sequence DNA molecules one at a time. Compared to NGS, it generates reads that are far longer, allowing the assembly of sequencing-read data to produce long continuous sequences even for huge complicated genomes. Genomic analysis offers a chance to better understand the components of food items in the subject of foodomics. It has sped up research into the connection between food nutrients and human health [5]. Therefore, the use of genomics is advantageous for promoting the quality of food and may end malnutrition and other diseases.

The study of all RNA in a single cell or a group of cells is known as transcriptomics. It offers accurate transcription measurement and paints a complete picture of the size and complexity of transcriptomes. Transcriptomics now uses two methods: microarrays and RNA-sequencing (RNA-Seq) [6]. Large mammalian transcriptome analyses are a good fit for microarrays. Since microarrays were created for known sequences, they cannot be utilised to characterise unknown RNA. While RNA-seq can be used to analyse every type of RNA, including messenger RNAs (mRNAs), microRNAs, small interfering RNAs, and long non-coding RNAs, qualitatively and quantitatively. Transcriptomic analysis in the field of foodomics not only exposes the regulation of the overall gene expression profile in food material but also sheds light on how food affects human health. As a result, the assessment of food nutrition for the preservation of physiological balance and the avoidance of disease has been substantially influenced by transcriptomics [7].

Individuals, different cell types, and even the same cell in a different state have diverse proteomes. The scientific study of the proteome known as proteomics aims to investigate the composition, structure, level, and distinctive activity patterns of proteins. Because distinct proteins can have vastly varied concentrations in biological samples, sample preparation in proteomics focuses on reducing proteome complexity, fractionation, depletion, and enriching low-abundant proteins. Protein isolation and characterisation are consequently needed. The conventional 2-DE method, which uses two-dimensional polyacrylamide gel electrophoresis, takes a long time, can be tedious, and has trouble handling proteins with high or low molecular weights. Multi-dimensional liquid chromatography has been developing into a viable method for protein isolation and separation during the past few years [8].

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In order to identify proteins, mass spectrometry (MS) is the primary technique. In particular, high sensitive and resolution mass spectrometry techniques like matrix-assisted laser desorption ionization-time-of-flight mass spectrometry (MALDI-TOF/MS) can distinguish between different microbes without the need for protein identification because they can identify microbes at the species, genus, or even strain level based on representative peak patterns. Through the discovery of species-specific proteomic profiles, this approach enables quick and >99% accurate identification of microorganisms (region-specific sub-strains) cultivated from regular clinical samples [9].

As opposed to the "bottom-up" method, which largely destroys labile structural proteins, the "top-down" method enables MS analysis of intact proteins that have not been cleaved. In conclusion, the "bottom-up" method demonstrated superior peptide separation when compared with proteins and higher sensitivity than the "top-down" method. The "bottom-up" approach's drawbacks include loss of labile post-translational modifications, limited protein sequence coverage by detected peptides, and ambiguity over the source of repetitive peptide sequences. In addition, the "top-down" technique significantly reduces time spent on protein digestion.

Metabolomics

The metabolome, which reflects the majority of a biological system's phenotype, is the final downstream product of the genome, transcriptome, and proteome. The term "metabolomics" describes the investigation of the metabolic pathways for all endogenous and exogenous metabolites in a biological system. Technically, metabolomic approaches were divided into two categories: focused metabolomics, which measures specific groups of chemically described and biochemically annotated metabolites, and untargeted metabolomics, which is meant for a thorough investigation of all molecules.

Mass spectrometry and nuclear magnetic resonance (NMR) spectroscopy are the two most often used analytical techniques in metabolomics (MS). Since derivatization and sample separation are not necessary, NMR spectroscopy is a good tool for quantitative analysis. Low sensitivity, however, is a fatal flaw in NMR spectroscopy [10]. On the other hand, MS can provide a platform for metabolomics research that combines high sensitivity and great selectivity.

In order to manage the quality of food and identify the sources of food, metabolomics has been utilised to research large-scale small molecule metabolites in food and analyse the active functional components or hazardous chemicals in food. On the basis of our understanding of food and the human metabolome, we may also find indicators associated with health status and food nutrition in order to assess the nutritional function of food.

Conclusion

The problem of microbiological food safety can be effectively handled with the use of foodomic techniques. In order to improve outbreak detection of foodborne bacteria, whole-genome sequencing (WGS), which is associated with the scalable, flexible nature of NGS technology, has overcome some limitations in current methods for subtyping (such as pulsed-field gel electrophoresis (PFGE) and multiple-locus variable number tandem repeated analysis (MLVA)). Over PFGE or MLVA, WGS offered enhanced discriminatory power on a variety of microorganisms, including highly clonal bacterial pathogens.

The two main areas of research in food nutrition that are the focus of metabolomics are the characterisation of food composition and the connection between diet and health. The characterisation of metabolites from food or the human gut is thus made possible by spectroscopy-based techniques, which offer a key, essential tool. In reality, based on our understanding of food chemistry, the majority of dietary chemicals have currently been discovered. However, there are still many challenges for researchers to overcome, including the quick identification of hundreds of unidentified metabolites, precise quantification of trace components, and isomer discrimination. All of these obstacles must be removed in order to advance this developing area of study and bring it to maturity.

In conclusion, foodomic technologies are important tools for understanding food nutrition because they enable the identification of bioactive compounds, monitoring of nutritional intervention studies, measurement of biochemical changes associated with physiology status related to diet, and elaboration of molecular mechanisms.

Conflict of Interest

There is no conflict of interest by author.

Acknowledgement

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