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Food microbiology and omics approaches

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Since the crucial roles in the success and safety of food industry, microbial functions in food got more and more of researchers' attention, so that the study of the microbial ecology of foods has drastically changed. It is well established that traditional culture methods are very limited for analyzing food microbiota and that High-Throughput Sequencing (HTS) and omics technologies allow a deep understanding of the behaviour of microorganisms in foods. We discuss different sequencing approaches and several HTS investigations of food microbiota, many of them based on amplicon sequencing method. Furthermore, we focus on the four major types of omics approaches, genomics, transcriptomics, proteomics, and metabolomics and on their impact on food microbiology study. Among them, it is now known that the shotgun metagenomic approach (DNA-seq or RNA-seq) is a valuable approach in food microbiology. However, most of the studies based on next generation sequencing just give a partial representation of the food-based ecosystem and it is emerging the need to adopt omics combination approaches (referred to as multi-omics approach), which generate a global view and show more evidence for biological mechanisms. Data generated through a multi-omics approach can improve the knowledge on what happens in food and how the environmental conditions (e.g. in the fermentation process, during the addition of a starter culture) can affect the development of food microbiota and, consequently, may help researchers to obtain insights into the mechanisms that can affect the final characteristics of products. At the moment, only a few examples that combine different omics approaches have been found in food microbiology study. The current scenario and examples of recent works are discussed, showing the usefulness to adopt this integrated approach. Furthermore, instances aimed to elucidate the microorganisms role, integrating WMS (Whole-Metagenome Shotgun) sequencing, metatranscriptomics, metabolomics or metaproteomics are highlighted and certain limitations are outlined.

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