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Omics technologies and new approaches in food microbiology

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Abstract

The research in food microbiology has enormously changed. It is known that conventional culture methods are limited for studying food microbiota and that recent approaches, as high-throughput sequencing, omics technologies instead allow to deepen the behaviour of microbial ecology. Indeed, the development of advanced omics methods and bioinformatics has contributed to the investigation of food science topics considered unthinkable few years ago. At the same time, new omics platforms have recently been made available; as a result, these approaches are producing a larger volume of data at a price that is decreasing, and they may become a relevant tool for food microbiology and its application fields. Several omics platforms used to study food microbiota include metagenomics which it is essential to deepen food microbiota. Metatranscriptomics, metaproteomics and metabolomics may be considered enormous complements to metagenomics for these studies. However, no single omics analysis can fully unravel the complexities of food microbial community just providing a partial view of the food ecosystem. Therefore, it is emerging the need to adopt a multi-omics approach based on the integration of different omics methods and able to show more evidence for food biological mechanisms.

This review discuss several approaches, as metagenomics, metatranscriptomics, metaproteomics, and metabolomics and on their impact on food microbiology. Relevant omics studies concerning different food microbiology fields, as food fermentation, food safety, food quality are treated.

At the moment, only a few examples combining different omics approaches have been found in food microbiology study. The current scenario and examples of recently multi-omics works are highlighted, showing the usefulness to adopt this integrated approach in different food microbiology applications. Some limitation are also outlined. In fact, even today, we are aware that the food microbiota complexity and the relatively low number of biological samples can make multi-layer datasets integration a challenging issue.

Biography

Dr. Tiziana Maria Sirangelo is currently studying at Department of Life Sciences, University of Modena and Reggio Emilia, Modena, Italy. She published many articles in reputed journals and attended international conferences.

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