In the food sector, fermentation processes have been the object of great interest in regard to enhancing the yield, the quality, and the safety of the final product. Microbial fermentation has been traditionally used to produce foods denoted by a prolonged shelf life and digestibility. The benefits extended to human health by fermented foods are expressed either directly through the interactions of ingested live microorganisms with the host (probiotic effect) or indirectly as the result of the ingestion of microbial metabolites synthesized during fermentation (biogenic effect). Moreover, several beneficial microbes can inhibit pathogens/spoilers growth and degrade toxins. Several novel microbial-based biotechnological solutions have been recorded and continuous explorations of microbial diversity are being carried out worldwide. In addition, most recently, fermentation has been considered a sustainable approach for maximizing the utilization of bio-resources to address the recent global food crisis. For example, several microbial-based bioconversions have been proposed for the production of enzymes, vitamins, antioxidants, biofuels, feeds, antimicrobial molecules, and other bioactive chemicals, also exploiting agro-industrial wastes [1–6].

The Special Issue “Advances in Microbial Fermentation Processes” covers eleven contributes: eleven original research papers and two reviews. As guest editors, we briefly report an overview of these contributions.

Wang et al. [7] investigated, through quantitative metabolomics and a stoichiometric analysis, the role of the trehalose metabolism in the Penicillium chrysogenum strain. The authors showed the key role of the intact trehalose metabolism in ensuring penicillin production in the P. chrysogenum strain under both steady state and dynamic conditions.

Helmyati and collaborators [8] described an innovation food-based approach to address the stunting problem. They evaluated the ability of a symbiotic milk enriched with iron and zinc and fermented with Lactobacillus plantarum to promote growth in stunted children, obtaining excellent results. The investigation of Yogeswara et al. [9] demonstrated a significant increase in the enzymatic synthesis of GABA using purified recombinant GAD from L. plantarum FNCC 260. In their original paper, Li and coworkers [10] focused on the activity of volatile compounds produced by Bacillus velezensis CT32 on Verticillium dahlia and Fusarium oxysporum responsible for strawberry vascular wilt. This study highlighted the key role of some volatile compounds as a biofumigant for the management of vascular wilt pathogens.

The novel cell-level Fed-Batch (FBC) technology for the high-cell-density cultivation of Saccharomyces cerevisiae was proposed by Malairuang et al. [11] with a clear illustration of the principle of operation, the potential dextrin substrate, and the mechanism of substrate utilization to regulate FBC, FBC kinetics and material balances through a bioreactor design and scale-up. Yepes-García and coworkers [12] provided an important contribution to the knowledge of antibiotic biosynthesis in the Streptomyces genus by studying the relationship between S. clavuligerus ATCC 27064 morphology and CA biosynthesis. An interesting contribution of the influence of different smoking techniques on the development of polycyclic aromatic hydrocarbons (PAH) in traditional dry sausage was presented by...
Mastanjević et al. [13]. These authors showed the crucial role of the smoking method in the formation of PAHs revealing that collagen samples presented significantly lower values than samples created with traditional gut. Malairuang et al. [14] selected a Kluyveromyces marxianus strain for single-step ethanol fermentation, also to establish a practical approach to produce a high-cell-density yeast biomass by an intensive multiple sequential batch simultaneous saccharification and cultivation.

An interesting evaluation of the differences in microbial communities, metabolites, and the aerobic stability between whole-plant corn silages from different areas of Inner Mongolia in North China has been assessed by Wang et al. [15]. Moreover, the same authors investigated the variation of bacterial dynamics during the fermentation process in whole-plant corn silages processed in Heilongjiang, Inner Mongolia and Shanxi of North China [16].

Concerning the review papers, both contributors focused on two interesting topics. Stamatopoulou et al. summarized the state-of-the-art concerning Medium-Chain Fatty Acids (MCFA) by using both pure cultures and mixed microbial communities, highlighting future perspectives to improve MCFA production from complex feedstocks [17]. Pati and collaborators [18] reviewed the aspects related to the quantitative analysis of volatile compounds in wines application by HS-SPME-GC/MS, in particular discussing the optimization approaches in the method development stage and the critical aspects related to quantification methods.

This collection contributed to improve the knowledge on the microbial-based fermentation approaches and on the latest innovative application for promoting and monitoring bacterial action in different biotechnological fields.

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