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Editorial: Fermented foods: characterization of the autochthonous microbiota

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Editorial on the Research Topic

Fermented foods: characterization of the autochthonous microbiota

Fermented foods have been essential in human diets for millennia, valued for their unique flavors, textures, and nutritional benefits. The microbial complexity underlying their production is particularly fascinating. In artisanal fermented foods, the absence of industrial starter cultures allows autochthonous microbiota to play a central role in driving the fermentation process. These microbes can originate from raw materials, the environment, equipment, and even human interaction during production. The result is a dynamic microbial ecosystem that contributes not only to the safety and quality of fermented foods, but also to their distinct organoleptic properties.

Historically, the characterization of these complex microbial communities was limited by traditional microbiological methods. Such approaches provided invaluable insights but often lacked the precision to fully capture the depth and diversity of fermentation microbiota. The advent of OMIC technologies revolutionized our ability to study microbial communities at a metabolic and functional level. These tools have shed new light on the interactions between microorganisms and their substrates, revealing how specific microbial populations influence flavor, aroma, texture, and even safety parameters.

Despite these advances, much of the research has concentrated on large-scale, commercially produced fermented foods, such as wine, beer, and bread. Artisanal products, which often rely solely on their natural microbiota for fermentation, remain

underexplored. This Research Topic sought to address this gap by highlighting studies that focus on the characterization of autochthonous microbiota in artisanal fermented foods.

The papers published in this Research Topic cover a broad range of fermented products from different regions around the world:

“Bacterial composition and physicochemical characteristics of sorghum based on environmental factors in different regions of China” investigates the diverse microbial communities on sorghum used for Jiang-flavored baijiu fermentation (Xie et al.). This study reveals how environmental factors, including soil characteristics and climate, influence the bacterial composition and physicochemical properties of sorghum, ultimately impacting flavor development.

“Effects of sorghum varieties on microbial communities and volatile compounds in the fermentation of light-flavor Baijiu” is another research focusing on the fermentation process of light-flavor baijiu, which compares glutinous and non-glutinous sorghum varieties using PacBio single-molecule real-time (SMRT) sequencing and headspace solid-phase microextraction coupled with gas chromatography mass spectrometry (HS-SPME-GC-MS) (Tang et al.). This paper highlights how variations in microbial diversity correlate with the production of volatile compounds, offering insights into optimizing fermentation practices.

“Metagenomic analysis of core differential microbes between traditional starter and Round-Koji-mechanical starter of Chi-flavor Baijiu” is a metagenomic study comparing traditional and mechanical starters used in Chi-flavor baijiu production, and identifies key microbial taxa that contribute to the flavor and quality differences, providing guidance for improving fermentation processes (Liang et al.).

“Tradition unveiled: a comprehensive review of microbiological studies on Portuguese traditional cheeses, merging conventional and OMICs analyses” is a review gathering findings from conventional and OMIC studies on the microbiota of Portuguese traditional cheeses (Serrano et al.). This document explores the roles of various microbial species in cheese ripening and flavor development, emphasizing the importance of these communities for product safety and quality. Shedding light on the intricate interplay between microorganisms and cheese matrices contributes to unveiling the secrets behind the rich heritage and distinctiveness of these artisanal foods.

“Deciphering the microbial succession and color formation mechanism of “green-covering and red-heart” Guanyin Tuqu” correlates the temporal profiles of microbial community succession with the main environmental variables (temperature, moisture, and acidity) and spatial position (center and surface) in “Green-covering and red-heart” Guanyin Tuqu throughout fermentation, elucidating the physiological characteristics of core microorganisms responsible for the unique color formation in this special fermentation starter (Zhu et al.).

“Formic acid enhances whole-plant mulberry silage fermentation by boosting lactic acid production and inhibiting harmful bacteria” investigates the impact of four additives and combinations thereof on fermentation quality and bacterial communities associated with whole-plant mulberry silage,

showing that formic acid significantly enhances lactic acid production while suppressing undesirable bacterial growth and improving overall silage quality (Hao et al.).

“Metagenomics profiling of the microbial community and functional differences in solid-state fermentation vinegar starter (seed *Pei*) from different Chinese regions”, a research focusing on the seed *Pei* used in vinegar fermentation, employs metagenomic analysis to reveal the microbial composition and functional differences among starters from different regions, providing a new perspective on formulating vinegar fermentation starters and developing commercial fermentation agents for vinegar production (Han et al.).

“Rapid identification of lactic acid bacteria at species/subspecies level via ensemble learning of Ramanomes” introduces a novel approach for the rapid identification of lactic acid bacteria using single-cell Raman spectroscopy combined with machine learning techniques (Ren et al.). This method promises to enhance the efficiency and accuracy of lactic acid bacteria identification in fermented foods.

In “Isolation and *in vitro* screening of the probiotic potential of microorganisms from fermented food products” microorganisms from traditional fermented foods, of both animal and plant origin, are isolated and evaluated for their probiotic potential based on a set of *in vitro* assays, identifying promising candidates for future functional food applications (Ntiantiasi and Lianou).

Overall, the diversity of studies published in this Research Topic reflects the global importance of artisanal fermented foods and the ongoing scientific efforts to decode the intricate microbial processes behind them. These studies not only contribute to our scientific knowledge, but may also have practical implications for improving food quality, safety, and the preservation of artisanal products.

We are confident that this Research Topic will serve as a valuable resource for researchers, food technologists, and industry professionals interested in fermented foods. The papers herein provide a comprehensive overview of the role the autochthonous microbiota plays in shaping fermented foods, emphasizing the relevance of understanding these microbial communities to enhance food quality and safety.

Thanks to all the contributors and their excellent work, this Research Topic should inspire further research in this fascinating area of food science and technology.

Author contributions

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Conflict of interest

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