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Editorial: Traditional ethnic fermented foods and their naturally associated microbial resources: sustainable source for promoting human health, food safety, and security

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Editorial on the Research Topic

Traditional ethnic fermented foods and their naturally associated microbial resources: sustainable source for promoting human health, food safety, and security

Traditional ethnic fermented foods (EFFs) are gaining global popularity due to their numerous health benefits and safe consumption. EFFs vary based on substrate or ingredients and fermentation processes, with over 5,000 varieties worldwide (Suzzi and Corsetti, 2020). Minor changes to fermentation or ingredients can lead to significant changes in the final product. Thus, EFFs have been transformed to create new products with distinct taste, flavor, and quality since time immemorial. Nonetheless, EFFs are often produced in uncontrolled natural conditions, providing contamination risk by pathogenic microorganisms (Suzzi and Corsetti, 2020; Johler and Guldimann, 2021). Therefore, traditional EFFs require thorough microbial, nutritional and quality analysis to ensure consumer safety. While some autochthonous species can eliminate unwanted microbes during fermentation, the mechanisms of microbial interactions within EFFs are not well-understood, limiting the development of healthier fermented foods. Thus, it is crucial to have a deeper understanding of fermentation processes and the functional roles of EFF-associated microbes within raw materials for future bioprospecting and improved food fermentations.

Traditional palm-wine fermentation resides various autochthonous microbes, affecting the quality of beverage. Djeni et al. used high throughput sequencing and mass spectrometry to study microbiota dynamics and metabolite profiles during palm-wine fermentation in the West African country of Côte d'Ivoire. Intriguing dynamic interaction was found between *Saccharomyces cerevisiae* and *Hanseniaspora* spp. during palm-wine tapping. Fructophilic lactic acid bacteria declined at later tapping stages, while acetic acid bacteria became dominant in the final stage. *Lactobacillus* remained dominant throughout tapping. Additionally, early tapping stages contained more essential amino acids. Conclusively, comprehending microbial succession and biochemical changes during palm-wine tapping aids designing optimal starter cultures and manipulating the process for quality palm-wine production.

The enhanced survivability in the gastrointestinal (GI) tract can promote successful establishment of probiotic species in the host organism (Szulifman and Shemesh, 2021). *Kluyveromyces marxianus* represents the predominant probiotic yeast population of kefir. Youn et al. demonstrated that kefir-isolated *K. marxianus* strains possess superior survivability in simulated GI environments attributed to phenol tolerance, higher hydrophobicity, biofilm-forming and auto-aggregation abilities. Furthermore, *K. marxianus* metabolized wide-range of substances, enhancing its establishment in the host GI tract. Decomposing complex substrates into intermediate fermentation products like fumarate, succinate, and lactate in the host GI tract can help probiotics such as *K. marxianus* obtain energy (Rowland et al., 2018).

In another study, Tan et al. explored promising probiotic isolates derived from Singapore-sourced kefir grains, which showed enhanced survivability in acid and bile environments. The isolates also demonstrated antimicrobial activity against enteric pathogens in several model systems. Overall, these kefir isolates represent potential probiotic candidates, which can reduce the burden of enteric pathogen associated diseases and benefit human health. Future studies are needed to confirm the safety and efficacy of kefir-derived probiotics.

Enhanced survivability of beneficial microbiota has been an important requirement for many fermented foods or feed ingredients (Ogiy et al., 2016; Yahav et al., 2018). Bora et al. investigated the bacterial diversity and metabolome of fermented mustard-seed food products. The study used LC-MS-based metabolomics and high throughput sequencing to reveal the dominance of endospore-forming and proteolytic *Bacillus* in Kahudi and *Lysinibacillus* in Kharoli. Furthermore, the abundance of different bioactive metabolites within the fermented foods could account for the thriving of beneficial microbiota in the stringent fermentation environments of such EFFs.

Additional study by Ma et al. characterized the wheat fermentation process of *Saccharopolyspora rosea*. Functional genomic analyses of a promising strain A22 with high amylase and glucoamylase activities enabled the identification of tolerance mechanism of the yeast during wheat qu and huangjiu fermentation. The findings have implications for the application of *S. rosea* A22 in huangjiu fermentations.

The meta-omics approaches are often used to understand the effects of microbiota on the quality, safety and organoleptic properties of EFFs, especially to study microbiota-derived enzymes and metabolites (Zhang et al., 2019; Herold et al., 2020; Galata et al., 2021). Wang et al. applied metaproteomics and whole metagenome sequencing to investigate the microbiota-derived extracellular enzymes during traditional fermentation of the Chinese fish sauce, Yu-lu. Metaproteomic analysis identified 571 proteins and 36 types of microbial enzymes involved in amino acid metabolism during the fermentation, providing significant insight into the metaproteome associated with the formation of taste metabolites of the fish sauce. Furthermore, metaproteome-metagenome mapping identified four major bacterial genera, belonging to Firmicutes and Proteobacteria phyla, as the primary microbial sources of the fish sauce proteins. The findings of Wang et al. provided insight into the metabolic functions of microbiota during fish sauce fermentation,

which further potentiate applications in the process regulation and quality monitoring in the fish sauce industry.

Another challenging facet of the shifting fermented food research paradigm is the development of functional fermented food products. In an effort to deduce a mechanism for manipulating the physiological traits of bacteria in fermented food products, Raz et al. studied the interaction of milk fat globules (MFG) with the model dairy bacterium, *Bacillus subtilis*. Small MFG induced bacterial growth while large MFG restricted it and induced biofilm formation. Raz et al. highlighted that the MFG size determined its polar lipid composition, and the growth promoting property of the small MFG could be due to the ability of the bacterium to utilize lipid content of the milk fat more efficiently as compared to the large MFG. The authors identified the growth modulating role of the polar lipids in the MFGs, highlighting that a specific phospholipid, phosphatidylethanolamine (PE), activates increased cell proliferation by the large MFG while suppressing biofilm formation.

The regulations and standards for fermented foods often vary between countries and organizations, and there is a need for updated global frameworks due to advancements in technology and market globalization. Mukherjee et al. reviewed these regulatory frameworks, and discussed the potential benefits and drawbacks of establishing a universal regulatory framework for fermented foods to ensure consumer safety and security.

Overall, this editorial covered various aspects of EFFs, including traditional fermentation processes, microbial communities, and their properties, functions and applications. This compilation of manuscripts has expanded our current knowledge of developing EFFs as sustainable food sources for promoting health, safety, and security. Nevertheless, challenges in the shifting paradigm of fermented food research still need further investigations.

Author contributions

DN, RW, and MS were the topic editors for traditional ethnic fermented foods and their naturally associated microbial resources, sustainable source for promoting human health, food safety, and security. All authors contributed equally to the article and approved the submitted version for publication.

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Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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