Nigerian Research Journal of Biological Sciences **(ISSN: 2971-7116)**
Volume 5, Issue 2, 2026

Studies on the Fermentation of African Traditional Starchy-Based Foods: A Genomic Approach to the Taxonomy, Diversity, and Roles of Lactic Acid Bacteria

*****Nwachukwu Ifeanyi**,** Nwachukwu Ejikeme and Achi Ome Kalu
Department of Microbiology, College of Natural Sciences,
Michael Okpara University of Agriculture, Umudike, Abia State, Nigeria.
*Corresponding Author: nwachukwu.ifeanyin@mouau.edu.ng

Received 3/10/2026, **Accepted** 19/10/2026, **Published online** 26/10/2026

ABSTRACT

Fermented starchy foods from African staples such as cassava, maize, sorghum and millet are central to local diets, improving digestibility, extending shelf life, enhancing nutritional and organoleptic qualities. These benefits largely stem from microbial fermentation, with lactic acid bacteria (LAB) playing a dominant role. LAB activity during different traditional processes shapes the functional properties of products including fermented cassava granules (gari), corn pap (ogi) and related foods. Historically, scientists characterized LAB communities using culture-dependent phenotypic and biochemical assays. Although useful, these approaches often underestimate microbial diversity, misidentify closely related taxa and miss viable-but-non-culturable organisms. This review synthesizes recent research on fermentation of African traditional starchy foods, emphasizing how genomic and molecular methods are transforming LAB taxonomy, diversity assessment and functional understanding. Key advances discussed include 16S rRNA gene sequencing, whole-genome sequencing and metagenomics. These tools have refined and in some cases revised the taxonomic placement of dominant LAB genera, particularly after the 2020 reclassification of *Lactobacillus*. Genera such as *Lactiplantibacillus*, *Limosilactobacillus*, *Pediococcus*, *Weissella* and *Leuconostoc* are highlighted. The review also evaluates comparative genomic studies revealing strain-level diversity or biogeographic patterns and substrate-specific adaptation among fermentation-associated LAB. In addition, it covers functional genomic insights into carbohydrate utilization, exopolysaccharide production, bacteriocin synthesis and enzyme activities that affect fermentation efficiency and food safety. Finally, the review identifies ongoing gaps in genomic representation of African indigenous LAB compared with global reference databases and proposes opportunities for developing region-specific defined starter cultures. Overall, it argues that genomic approaches can bridge traditional knowledge with modern

biotechnological innovation to support future research and applications in food security and public health.

Keywords: African fermented foods, genomic diversity, lactic acid bacteria, *Lactiplantibacillus*, *Limosilactobacillus*, taxonomy.

INTRODUCTION

Lactic acid bacteria represent a diverse group of Gram-positive, non-spore-forming, catalase-negative microorganisms that play a pivotal role in food fermentation, preservation and enhancement. Primarily converting carbohydrates to lactic acid, LAB contribute to acidification, which inhibits pathogen growth, improves sensory attributes, and boosts nutritional value [1]. Their applications extend to probiotic functions, enzyme production and adaptation to environmental stresses, particularly in resource-limited settings like sub-Saharan Africa, where spontaneous fermentations of staples such as maize, millet and cassava yield nutrient-rich products like corn pap/fermented maize gruel (ogi), spiced millet dough (fura) and fermented cassava paste (fufu) [2]. Recent advancements from 2020 to 2025, driven by omics technologies; metagenomics, transcriptomics and proteomics have elucidated LAB's taxonomy, diversity and functional potentials, underscoring their significance in sustainable food systems [3].

Fermented starchy foods represent a cornerstone of dietary practices in tropical regions, where staples like cassava, maize, sorghum, and rice are transformed through microbial action into nutritious and shelf-stable products. These foods not only address food security by extending shelf life and reducing post-harvest losses but also harbour diverse LAB populations that contribute to human health [4]. In West Africa, cassava-derived products such as fufu and gari are produced via submerged fermentation, where grated cassava is allowed to ferment spontaneously, leading to lactic acid production that lowers pH and detoxifies harmful compounds [5]. Similarly, ogi, undergoes a similar process, often blended with other starches for enhanced nutritional profiles. In East Africa, fermented maize porridge (ugali), from maize or sorghum involves dry fermentation techniques, while Indonesian fermented soybean cake (tempeh), utilizes rice inoculated with fungal and bacterial starters for a sweet, alcoholic product [6].

The significance of these foods lies in their role as natural LAB reservoirs. LAB, including genera like *Lactobacillus*, *Leuconostoc* and *Lactococcus*, dominate the microbiota, outcompeting pathogens through acid production and antimicrobial metabolites. Recent reviews emphasize how

these spontaneous fermentations enhance microbial diversity, with metagenomic studies revealing complex communities adapted to local environments [6]. For instance, in African contexts, fermented cereals and tubers contribute to alleviating malnutrition by improving nutrient density and digestibility, particularly in vulnerable populations. In addition, beneficial microorganisms, such as lactic acid bacteria used in fermentation and as probiotics, contribute to food preservation, nutritional enhancement, and gut health modulation [7]. Probiotics, defined as live microorganisms conferring health benefits when administered in adequate amounts [6, 7], often involve LAB strains like *Lactobacillus* and *Bifidobacterium*, which improve food shelf life and host immunity through mechanisms such as acid production and competitive exclusion [8]. In the context of spontaneously fermented starchy foods such as those derived from sorghum, millet, cassava and maize, common in African, Asian, and Latin American diets, lactic acid bacteria emerge as key players [9]. These microorganisms drive fermentation processes that not only extend shelf life but also improve nutritional profiles and sensory attributes, contributing to food security in resource-constrained settings [10].

Spontaneously fermented starchy foods exemplify the dual nature of microbial ecology in food systems. Microbial contamination can arise along the farm-to-fork continuum, including during harvesting, storage and processing, where pathogens like *Salmonella* spp., *Escherichia coli* and *Listeria monocytogenes* may infiltrate raw materials 11]. Conversely, beneficial microorganisms, particularly LAB such as *Lactobacillus*, *Leuconostoc* and *Pediococcus* species, facilitate controlled fermentation by producing lactic acid, which lowers pH and inhibits spoilage organisms [12]. This process aligns with probiotic principles, where LAB strains confer health benefits, including enhanced gut microbiota and reduced risk of gastrointestinal disorders [13, 14].

However, emerging threats, such as climate change-induced shifts in pathogen prevalence and antimicrobial resistance, exacerbate risks in spontaneous fermentations, which lack standardized starter and rely on indigenous microbiota [11]. For instance, rising temperatures may favour cultures thermotolerant pathogens, while irregular rainfall could increase mycotoxin contamination of starchy substrates like cassava. In spontaneously fermented starchy foods, microbial hazards primarily stem from raw material contamination and suboptimal processing conditions. Foundational studies, such as those on *Salmonella* persistence in fermented cereals, highlighted how inadequate acidification allows pathogen survival [15].

This review therefore examines recent research on the fermentation of African traditional starchy foods, how genomic and molecular approaches are reshaping our understanding of lactic acid bacteria role in African traditional starchy fermented foods. It aims to identify gaps in the taxonomy, diversity and genomic representation of indigenous African LAB relative to global reference databases and highlight opportunities for developing region-specific defined starter cultures.

SPONTANEOUS FERMENTATION OF STARCHY-BASED FOODS IN NIGERIA AND AFRICA

LAB diversity in fermented foods is vast, influenced by substrate, geography and fermentation conditions. Globally, LAB dominate dairy, vegetable, cereal and meat fermentations, with over 200 species identified via high throughput sequence (HTS) [16]. In dairy, *Streptococcus thermophilus* and *Lactobacillus delbrueckii subsp. bulgaricus* prevail, producing exopolysaccharide (EPS) for texture and bacteriocins for safety [17]. Cereal fermentations like sourdough feature *Fructilactobacillus sanfranciscensis* and *Lactiplantibacillus plantarum*, enhancing mineral bioavailability through phytase activity [17].

In Africa, fermented foods address food insecurity, with LAB diversity reflecting indigenous practices. Nigerian products like ogi (maize-based) harbour *Lactiplantibacillus plantarum*, *Leuconostoc mesenteroides* and *Limosilactobacillus fermentum*, which detoxify cyanogens and biofortify vitamins [18]. Gari and fufu from cassava show similar taxa, reducing anti-nutrients like phytates by 50-70% [19]. Eastern African foods, such as Ethiopian sourdough flatbread (injera) and Kenyan fermented soured milk (mursik), involve *Lactiplantibacillus plantarum* and *Streptococcus infantarius*, improving digestibility and immunity [20]. Microbial succession in these spontaneous fermentations starts with *Enterococcus* and *Leuconostoc*, shifting to acid-tolerant *Lactobacillus* spp., as revealed by metagenomics [21]. Diversity contributes to functional attributes; in African cereal beverages like West African traditional beer (pito) and Nigeria traditional beer (burukutu), LAB produce B vitamins, (as shown in Table 1), alleviating "hidden hunger" and boosting immunity [22]. Vitamin synthesis however is strongly strain-specific and many LAB especially dairy strains are actually auxotrophic for several B vitamins. It should be noted also that LAB species do not synthesize some vitamins like A, C, D and E because these vitamins depend on biosynthetic machinery that LAB lack [23, 24].

Challenges include pathogen contamination, but LAB's antimicrobial metabolites mitigate risks [19]. Globally, comparative genomics shows food-gut axis linkages, with LAB from African fermentations mirroring gut strains for probiotic transfer [24]. LAB's probiotic potentials include gut modulation, pathogen inhibition and health promotion. Strains like *Lactiplantibacillus plantarum* and *Lacticaseibacillus rhamnosus* survive gastro-intestinal (GI) stresses, adhere to epithelial cells and produce bacteriocins against *E. coli* and *Salmonella* [26]. In vitro tests show adhesion via auto-aggregation and hydrophobicity, with clinical trials confirming benefits for irritable bowel syndrome (IBS) [17].

Table 1: Common vitamins synthesized by LAB species and their applications

Vitamin	Common Name	Primary Probiotic Producers	Key Biological Function
Vitamin B1	Thiamine	*Lactobacillus fermenti*, *Bifidobacterium bifidum*	Energy metabolism and nerve function
Vitamin B2	Riboflavin	*Lactobacillus rhamnosus, Leuconostoc mesenteroides*	Cellular respiration and antioxidant protection
Vitamin B3	Niacin	*Lactobacillus plantarum*	DNA repair and cellular signaling
Vitamin B5	Pantothenic acid	*Bifidobacterium infantis*, *Bifidobacterium breve*	Synthesis of coenzyme A and fatty acids
Vitamin B6	Pyridoxine	*Lactobacillus acidophilus*, *Bifidobacterium longum*	Amino acid metabolism and neurotransmitter synthesis
Vitamin B8	Biotin	*Bifidobacterium animalis*, *Lactobacillus helveticus*	Carbon dioxide transfer and fat/carbohydrate metabolism
Vitamin B9	Folate	*Bifidobacterium adolescentis*, *Streptococcus thermophiles*	DNA synthesis and red blood cell formation
Vitamin B12	Cobalamin	*Lactobacillus reuteri*, *Propionibacterium freudenreichii*	Red blood cell maturation and neurological health
Vitamin K2	Menaquinone	*Lactococcus lactis*, *Bacillus subtilis*	Blood coagulation and bone calcium regulation

In Africa, LAB from fermented camel milk exhibit probiotic traits, including bile tolerance and antimicrobial activity, supporting malnutrition alleviation [2]. Nigerian yogurt isolates produce exopolysaccharide (EPS) for gut health, with strains like *Streptococcus thermophilus* enhancing texture and probiotics [22]. Global studies highlight antioxidant effects, with LAB reducing cholesterol via bile salt hydrolase (BSH) and modulating microbiota [27]. Engineered strains

amplify these potentials for personalized nutrition [16]. African fermented foods exhibit regional biases: West Africa emphasizes *Lactiplantibacillus* in cereals, East Africa *Weissella* in teff-based products [2]. In Nigeria, ogi, gari, and fufu host diverse LAB, contributing to malnutrition alleviation via biofortification. Metagenomics in palm wine and coffee highlights LAB-yeast synergies. Commercialization erodes diversity by 25%, necessitating biobanks [3].

DIVERSITY AND ECOLOGICAL ROLE OF LACTIC ACID BACTERIA IN TRADITIONAL FERMENTATIONS

The taxonomy of LAB has undergone significant refinement in recent years, facilitated by omics integration. LAB belong to the phylum Firmicutes, class Bacilli, and order Lactobacillales, encompassing genera such as *Lactobacillus*, *Lactococcus*, *Leuconostoc*, *Pediococcus*, *Streptococcus* and *Enterococcus* [25]. The introduction of "lactobacillomics" an interdisciplinary field merging genomics, transcriptomics, proteomics and metabolomics has revolutionized LAB research by elucidating genetic, metabolic and functional traits [26]. For instance, whole-genome sequencing (WGS) and 16S rRNA amplicon sequencing have identified strain-level variations, revealing genes for bacteriocin production, vitamin synthesis and stress response [28].

The LAB communities in traditional fermented starchy foods are characterized by high diversity and regional specificity. Metagenomic analyses reveal that *L. plantarum* dominates at 30–55%, followed by *L. fermentum* (15–25%) and *Leuconostoc* spp. (5–15%) [29]. Alpha-diversity, measured by Shannon indices, peaks in mixed-substrate fermentations like ogi-cassava blends, reaching 2.5 – 4.0, reflecting robust microbial ecosystems [29]. Regional clustering is pronounced; West African cassava fermentations enrich *Enterococcus faecium*, East African sorghum-based ugali favours *L. delbrueckii*, and Asian fermented glutinous rice (tape), supports *L. lactis* [28, 29]. Succession dynamics underscore the ecological roles of LAB. Heterofermenters like *Leuconostoc* initiate fermentation by generating carbon dioxide, which lowers oxygen levels, paving the way for homofermenters like *Lactobacillus* to dominate acidification [31]. This shift drops pH from 6.5 to 4.0, enhancing preservation. Recent studies using amplicon sequencing confirm these patterns across African and Asian products, highlighting how substrate composition influences microbial assembly [31]. Globally, taxonomic reclassification has scattered *Lactobacillus* species into 25 genera, including *Lactiplantibacillus*, *Limosilactobacillus* and

Ligilactobacillus, based on phylogenetic and ecological data [32]. Omics have linked these taxa to food niches; for example, metagenomics in fermented meats shows dominance by *Lactilactobacillus sakei* and *Lactiplantibacillus plantarum*, with genes for carbohydrate metabolism and antimicrobial production [28, 33]. In African contexts, shotgun metagenomics of fermented cereals like ogi and gari highlights *Lactiplantibacillus plantarum* and *Limosilactobacillus fermentum* as core taxa, contributing to functional pathways for toxin degradation and nutrient enhancement [28, 34].

Multi-omics approaches have uncovered ecological interactions; transcriptomics reveals upregulated genes for EPS synthesis in *Leuconostoc mesenteroides* under osmotic stress, while proteomics identifies proteins for acid tolerance in *Lactiplantibacillus plantarum* [29, 34]. In developing regions, these tools enable strain mining for biofortification, for example, metatranscriptomics in Nigerian fufu fermentation identifies folate-producing pathways in *Lactiplantibacillus plantarum*, addressing micronutrient deficiencies [18, 35]. Overall, omics integration has not only refined taxonomy but also paved the way for engineered LAB strains, enhancing their utility in food microbiology [16].

Key LAB genera in fermented foods include *Lactiplantibacillus*, *Limosilactobacillus*, *Leuconostoc*, *Pediococcus* and *Weissella*, each with distinct roles. *Lactiplantibacillus plantarum* is versatile, thriving in low-pH, high-salt environments and dominating cereal fermentations in West Africa [2, 36]. In Nigerian ogi, it succeeds heterofermenters like *Leuconostoc mesenteroides* as pH drops to 3.8 [30, 37]. *Limosilactobacillus fermentum* excels in dairy, producing short chain fatty acids (SCFAs) such as acetate, propionate, butyrate and vitamins [22, 38]. *Leuconostoc* species, heterofermentative, contribute CO_2 and ethanol, enhancing texture in vegetable fermentations. *Pediococcus pentosaceus* aid in homofermentation, common in African cereals. In brine-type foods like sauerkraut, *Lactiplantibacillus* and *Leuconostoc* co-dominate, while sugar-based like Turkish fermented milk drink (kefir) feature *Acetobacter* alongside LAB [39]. Meta-analyses confirm *Lactobacillus*-related genera at 70% dominance, with regional biases: West Africa favours *Lactiplantibacillus*, East Africa *Weissella* [2, 40]. Novel species identified via metagenomics include 10 metagenome-assembled genomes (MAGs) from fermented foods, such as *Acetobacter* and *Gluconobacter* variants. In Nigerian products, diversity spans

Lactiplantibacillus pentosus in Nigeria millet beverage (kunu-zaki) and *Lactococcus lactis* in Northern Nigeria soft cheese (wara) [39].

Metabolic profiles divide LAB into homofermenters (>90% lactic acid via Embden-Meyerhof-Parnas pathway) and heterofermenters (lactic acid, CO_2, ethanol via phosphoketolase pathway) [5, 40]. Homofermenters like *Lactiplantibacillus plantarum* and *Pediococcus* ensure rapid acidification, crucial for preservation. Heterofermenters like *Leuconostoc* and *Weissella* add flavour complexity through secondary metabolites [42]. In African fermentations, succession reflects this: heterofermenters initiate in ogi, yielding to homofermenters as acidity increases [30, 42]. In coffee and palm wine, LAB produce organic acids, lowering pH and enhancing safety. Biofortification potential is notable, with LAB synthesizing B-vitamins; e.g., *Enterococcus malodoratus* produces gamma-aminobutyric acid (GABA). In rice biofortification, LAB improve mineral solubility [31]. Anthropogenic pressures, including starter culture use, reduce diversity by 25% [3, 43]. Preservation via biobanks is essential to maintain genetic resources for sustainable food systems. In developing regions like Africa, this supports the 'United Nations' sustainable development goals (SDG) against malnutrition.

The taxonomy and diversity of LAB have been profoundly reshaped by genomic insights since 2020, revealing a rich tapestry of genera adapted to fermented food niches. In African contexts, LAB like *Lactiplantibacillus plantarum* and *Limosilactobacillus fermentum* drive fermentations, offering nutritional and health benefits [38]. Omics approaches illuminate functional potentials, but diversity loss poses challenges. Future research should prioritize bioprospecting and conservation to harness LAB for global food security and health. Traditional fermented starchy foods have long been integral to the diets of populations in tropical regions, serving not only as staple sources of nutrition but also as vital reservoirs of lactic acid bacteria. These foods, including fufu, gari, ogi, ugali and tape, exemplify spontaneous fermentation processes that enhance food security, microbial diversity and overall health outcomes [44].

Fermentation in these contexts typically occurs over 24–72 hours at ambient temperatures ranging from 25–40 °C, leading to significant biochemical transformations that reduce anti-nutritional factors and improve digestibility [43]. For instance, in cassava-based products like fufu and gari, fermentation can detoxify cyanogenic compounds by up to 90%, primarily through the action of LAB-produced enzymes such as amylases and proteases [4, 45]. This process not only

mitigates health risks associated with cyanogens but also boosts the bioavailability of essential nutrients, contributing to improved food security in regions prone to malnutrition.

The microbial ecology of these fermented starchy foods is dominated by LAB, which play a pivotal role in acidification, flavour development and preservation. Studies highlight that LAB communities in these foods exhibit high alpha-diversity, with Shannon indices ranging from 2.5 to 4.0, particularly in blended substrates like ogi combined with cassava [44]. Dominant species include *Lactobacillus plantarum* (accounting for 30–55% of the community), *Lactobacillus fermentum* (15–25%) and *Leuconostoc* species (5–15%) [44]. Regional variations in LAB composition are evident: West African products like fufu and gari often favour *Enterococcus faecium*, while East African ugali is enriched with *Lactobacillus delbrueckii*, and Asian tape features *Lactococcus lactis* [40, 42]. These patterns reflect adaptations to local substrates, environmental conditions and cultural practices. Succession dynamics during fermentation further illustrate the functional roles of LAB; heterofermentative species initiate the process by producing CO_2 and organic acids, creating an anaerobic environment that favours homofermentative LAB, which drive pH reduction from 6.5 to 4.0, inhibiting spoilage organisms [30]. The functional attributes of LAB isolated from these foods extend beyond fermentation to probiotic potential, offering health benefits such as pathogen inhibition and enhanced nutrient absorption. For example, *L. plantarum* strains from cassava fermentations produce bacteriocins like plantaricin, which effectively inhibit pathogens such as *Escherichia coli* [35]. Additionally, LAB phytases increase mineral bioavailability, with iron absorption enhanced by up to 30%, and protein content rising by 5–8% through proteolytic activity [17, 43]. These traits are particularly relevant in addressing malnutrition, affecting approximately 149 million children in tropical regions [46].

However, challenges such as microbial variability, mycotoxin contamination and inconsistent fermentation outcomes persist. The adoption of defined starter cultures, such as combinations of *L. plantarum* and *L. fermentum*, has been shown to reduce fermentation time by 50% and improve product consistency [47]. Metagenomic analyses have revealed novel LAB strains with potential applications in biofortification and therapeutic interventions, underscoring the value of these traditional foods as microbial heritage resources [46, 48].

Phenotypic traits, including acid and salt tolerance, agree with LAB classification and adaptation. Genotypically, pan-genomes reveal accessory genes for niche specialization, e.g. EPS biosynthesis

in dairy LAB for texture [32]. In African foods, genotypic diversity is high, with uncultured lineages comprising 20–30% [4]. Metagenomics in Nigerian fermented milk (nunu) highlighted probiotic LAB with health-associated genes.

PROBIOTIC CRITERIA AND FUNCTIONAL PROPERTIES OF LAB

LAB biosynthesize enzymes critical for fermentation and health. Key enzymes include lactate dehydrogenase (LDH) for lactic acid production, phytase for phytate degradation and proteases/lipases for flavour precursors [17, 28]. In yogurt, LAB produce β-galactosidase for lactose hydrolysis, aiding digestion [17]. Glutamate decarboxylase (GAD) in *Levilactobacillus brevis* synthesizes GABA for antihypertensive effects [23, 28] (Table 2).

African strains from ogi produce phytase, enhancing mineral absorption [33]. Omics reveal biosynthetic pathways; genomics identifies rib operons for riboflavin in *Lactococcus lactis* [18, 46]. Optimization via fed-batch fermentation boosts enzyme yields, supporting functional foods [34]. LAB from fermented starchy foods exhibit probiotic traits that extend their utility beyond food production. *L. plantarum* isolates demonstrate strong inhibitory activity against pathogens like *E. coli* via bacteriocins such as plantaricin. These antimicrobials disrupt cell membranes, providing natural bio-preservation [36]. Furthermore, LAB enhance nutrient bioavailability; phytases degrade phytic acid, increasing mineral uptake, while proteases improve protein digestibility [35].

In the context of health, these LAB strains show promise in alleviating malnutrition. Fermented foods like gari and ogi serve as vehicles for probiotic delivery, modulating gut microbiota and improving immune function. Studies indicate their role in reducing diarrheal diseases in children by competing with enteropathogens and producing short-chain fatty acids that strengthen gut barriers [47]. Additionally, metagenomics has identified novel strains with enhanced vitamin synthesis capabilities, positioning these foods as tools for biofortification in resource-limited settings.

In spite of their benefits, traditional fermentations face challenges including variability in microbial composition, potential mycotoxin accumulation and hygiene issues. Spontaneous processes can lead to inconsistent quality, with risks of contamination by aflatoxin-producing fungi in starchy substrates [48]. To address this, defined starter cultures have been developed, combining

L. plantarum and *L. fermentum* to standardize fermentation, reducing time by 50% and minimizing contaminants [34]. Innovations in starter technology, including freeze-dried cultures, have shown efficacy in recreating traditional profiles while enhancing safety. Directed evolution of microbial communities further promises resilient starters that adapt to climate variations in tropical regions. These advancements, supported by multi-omics approaches, enable precise manipulation of LAB for optimized functional foods [49].

PROBIOTIC PROPERTIES AND ENZYME PRODUCTION BY LAB

Lactic acid bacteria exemplify beneficial microorganisms that contribute to these goals through fermentation processes and probiotic applications. These bacteria, including genera such as *Lactobacillus*, *Lactococcus*, and *Pediococcus*, are integral to traditional and industrial food production, where they enhance sensory attributes, extend shelf life, and inhibit pathogens [50]. LAB fulfill these advantages by producing antimicrobial compounds during fermentation, such as lactic acid, bacteriocins and hydrogen peroxide, which lower pH and create unfavorable conditions for spoilage organisms [36]. Probiotics often involve LAB strains that modulate gut microbiota, bolster immune function, and prevent infections [35]. Emerging threats, such as climate change-induced shifts in pathogen prevalence e.g. increased *Salmonella* outbreaks due to warmer temperatures; further highlight the need for resilient LAB in sustainable food systems. In developing countries, where food safety infrastructure is limited, LAB-driven fermentation offers a low-cost strategy for preservation, contrasting with advanced regulatory frameworks in developed nations that emphasize hazard analysis and critical control points (HACCP) principles.

In fermented foods, LAB contribute to nutritional enhancement by synthesizing vitamins, exopolysaccharides and bioactive peptides, which also impart techno-functional properties like improved texture and flavour [13, 37]. Probiotic properties of LAB include acid and bile tolerance, adhesion to intestinal mucosa, and immunomodulatory effects [37].

Strains like *Lactobacillus rhamnosus* GG demonstrate survival in gastric acid and bile, adherence to enterocytes and modulation of immune responses by reducing inflammation markers [38]. These properties are strain-specific, with *Lactobacillus* species often exhibiting antimicrobial, anti-inflammatory and antioxidant activities [39, 40]. In ethnic fermented dairy products, LAB from diverse sources show probiotic potential through mechanisms like biofilm protection and

metabolite production [10]. Recent reviews emphasize LAB's role in improving insulin resistance, reducing anxiety and enhancing gut health, particularly in pregnancy and allergy management [40].

LAB are prolific producers of enzymes with industrial applications, including amylases, proteases, lipases and phytases, which are utilized in food processing for starch hydrolysis, protein degradation, and nutrient bioavailability [17,35]. The primary categories of enzymes produced by probiotic LAB species are outlined in Table 2 below.

Table 2: Different categories of enzymes produced by probiotic LAB and their application

1. Carbohydrate-Degrading Enzymes (Carbohydrases)

Enzyme	Primary Probiotic Source	Functional Role / Substrate	Source
β-Galactosidase (Lactase)	*Lactobacillus acidophilus*, *Streptococcus thermophilus*, *Bifidobacterium longum*	Hydrolyzes lactose into glucose and galactose; alleviates lactose intolerance symptoms.	[18]
Amylase	*Lactiplantibacillus plantarum*, *Bacillus paranthracis*, *L. fermentum*	Breaks down starch and complex polysaccharides into short oligosaccharides.	[17]
Cellulase	*Limonilactobacillus fermentum*, *Bacillus paranthracis*	Degrades cellulose from plant material into digestible glucose components.	[35]
Fructanase / Glycosidases	*Bifidobacterium* species, *L. plantarum*	Hydrolyzes plant-derived oligosaccharides and prebiotic fibers (e.g., inulin).	[17]
Sucrase (Invertase)	*Lacticaseibacillus casei*, *L. acidophilus*	Converts sucrose (table sugar) into glucose and fructose molecules.	[42]

2. Protein and Lipid-Digesting Enzymes

Enzyme	Primary Probiotic Source	Functional Role / Substrate	Source
Proteases (Proteinases)	*Lactococcus* species, *Lactobacillus delbrueckii*, *Bacillus subtilis*	Breaks down long-chain proteins (like casein in dairy) into bioavailable peptides.	[40]
Peptidases (e.g., Aminopeptidases)	*Lacticaseibacillus casei*, *Bifidobacterium* species	Breaks down short-chain peptides into individual essential amino acids.	[17, 35]
Lipases / Esterases	*L. plantarum*, *L. acidophilus*	Hydrolyzes lipids and dietary triacylglycerols into free fatty acids and glycerol.	[27]
Keratinase	*Bacillus* probiotic strains	Specialized proteinase that degrades tough keratin proteins (often optimized for animal feed).	[31]

3. Metabolic and Anti-Nutritional Counteracting Enzymes

Enzyme	Primary Probiotic Source	Functional Role / Substrate	Source
Bile Salt Hydrolase (BSH)	*L. plantarum*, *Bifidobacterium animalis*	Deconjugates bile salts; clinically linked to lower systemic cholesterol absorption.	[34]
Phytase	*Lactobacillus paracasei*, *L. plantarum*	Breaks down phytic acid (an anti-nutrient in grains/nuts) to release bound minerals like iron and zinc.	[46]
Linoleate Isomerase	*Lactic acid bacteria (LAB)*	Bioconverts standard linoleic acid into Conjugated Linoleic Acid (CLA), which exerts anti-inflammatory traits.	[25]

These enzymes are generally recognized as safe (GRAS) and contribute to biorefining processes, such as in green crops where LAB facilitate lactic acid and bioethanol production [25]. Advances in biotechnology have focused on polylactic acid precursors from LAB fermentation, highlighting optically pure lactic acids for sustainable materials. Enzyme systems in LAB are classified based on their roles in metabolism, with proteolytic enzymes essential for amino acid liberation during

fermentation. Heteropolysaccharides from LAB enhance viscosity in dairy products, while genetic engineering improves enzyme yields.

Stress responses in LAB are critical for maintaining probiotic properties and enzyme production. LAB employ mechanisms like proton pumps, macromolecule protection and global regulators (e.g. HrcA, CtsR) to withstand acid, osmotic, oxidative and thermal stresses [41, 50]. Proteomic profiling shows alterations in metabolism and cell envelope integrity under stress, with cross-protection enhancing robustness. Gaps include limited insights into multi-stress interactions in industrial settings, affecting enzyme stability and probiotic survival during processing and gut transit. Spontaneous fermentation of starchy substrates in tropical regions typically spans 24–72 hours at 25–40 °C, conditions that favour LAB proliferation [51]. During this period, LAB metabolize carbohydrates into lactic acid, reducing pH and creating an inhospitable environment for spoilage microbes. A key benefit is the degradation of anti-nutritional factors; in cassava products, cyanogens are hydrolyzed by up to 90%, mitigating toxicity risks associated with raw consumption [52]. Enzymes such as amylases and proteases produced by LAB further enhance digestibility by breaking down starches and proteins into simpler forms, increasing caloric availability and nutritional value.

In fermented maize and cassava blends like ogi, LAB activity boosts B-vitamin content and mineral bioavailability through phytate degradation [17, 53]. Phytases, extracellular enzymes from *L. plantarum* and related species, chelate minerals like iron and zinc, making them more accessible for absorption. Studies indicate a 30% increase in iron bioavailability in fermented cassava products, a critical factor in combating anemia in tropical children [54]. Moreover, protein levels rise by 5–8% due to microbial synthesis and proteolysis, transforming these foods into functional staples for protein-energy malnutrition [55, 56].

CONCLUSION

African traditional starchy fermented foods, including ogi, kenkey, gari, fufu, injera and others, remain crucial to food security, nutrition and cultural identity across the continent. Lactic acid bacteria, notably *Lactiplantibacillus*, *Limosilactobacillus*, *Weissella*, *Leuconostoc* and *Pediococcus*, drive these fermentations by acidifying the substrate, inhibiting spoilage organisms and pathogens and improve flavour and texture. Their metabolic versatility explains why

spontaneous fermentation, despite its variability, has sustained communities for generations. Many strains also hydrolyze starch, reduce anti-nutritional factors such as phytates, detoxify poisonous compounds and show probiotic potential.

Genomic approaches have transformed understanding of these systems. Amplicon sequencing, shotgun metagenomics and whole-genome sequencing reveal microbial diversity and succession that culture-dependent methods miss. This taxonomic resolution is essential for distinguishing beneficial, technologically useful strains from potential opportunists. Comparative genomics further links taxonomy to metabolic capacity, adaptation and safety traits such as antibiotic resistance genes and exposes genes underlying acid tolerance, bacteriocin synthesis and carbohydrate utilization.

Nevertheless, significant gaps remain. African fermented food microbes are underrepresented in public genome databases, fermentation practices are poorly standardized and most studies are descriptive rather than functional. Future research should combine metatranscriptomics and metabolomics with phenotypic validation, build regional reference genome collections and assess strain safety. Developing well-characterized indigenous starter cultures, supported by affordable sequencing capacity within Africa, will improve product safety, consistency and nutritional value while preserving culinary heritage and strengthening local food systems. Translating genomic insights into practical, community-level applications is therefore the field's next major challenge.

REFERENCES

1. Zheng, J., Wittouck, S., Salvetti, E., Franz, C. M. A. P., Harris, H. M. B., Mattarelli, P., O'Toole, P. W., Pot, B., Vandamme, P., Walter, J., Watanabe, K., Wuyts, S., Felis, G. E., Gänzle, M. G. & Lebeer, S. (2020). A taxonomic note on the genus *Lactobacillus*: Description of 23 novel genera, emended description of the genus *Lactobacillus* Beijerinck 1901, and union of Lactobacillaceae and Leuconostocaceae. *International Journal of Systematic and Evolutionary Microbiology*, *70*(4), 2782–2858.
2. Owusu-Kwarteng, J., Akabanda, F., Johansen, P., Jespersen, L. & Nielsen, D. S. (2023). African cereal fermentations: A review on microbial diversity and technological applications. *Foods, 12(5),* Article 1024.

3. Mokoena, M. P., Mutanda, T. & Olaniran, A. O. (2021). Perspectives on the probiotic potential of lactic acid bacteria from African traditional fermented foods and beverages. *Food and Nutrition Research, 65*, Article 2964.
4. Walsh, A. M., Macori, G., Kilcawley, K. N. & Cotter, P. D. (2023). Meta-analysis of cheese microbiomes highlights contributions to multiple aspects of quality. *Nature Food, 4(6),* 500–510.
5. Sun, Z., Harris, H. M. B., McCann, A., Guo, C., Argimón, S., Zhang, W., Yang, X., Jeffery, I. B., Cooney, J. C., Kagawa, T. F., Liu, W., Song, Y., Salvetti, E., Wrobel, A., Rasinkangas, P., Parkhill, J., Rea, M. C., O'Sullivan, O., Ritari, J., Douillard, F. P., Ross, R. P., Yang, R., Briner, A. E., Felis, G. E., de Vos, W. M., Barrangou, R., Klaenhammer, T. R., Caufield, P. W., Cui, Y., Zhang, X. & O'Toole, P. W. (2024). Expanding the biotechnology potential of lactobacilli through comparative genomics of 213 strains and associated genera. *Nature Communications, 15(1),* 1–15.
6. Hill, C., Guarner, F., Reid, G., Gibson, G. R., Merenstein, D. J., Pot, B., Morelli, L., Canani, R. B., Flint, H. J., Salminen, S., Calder, P. C. & Sanders, M. E. (2014). Expert consensus document: *The International Scientific Association for Probiotics and Prebiotics consensus statement on the scope and appropriate use of the term probiotic. Nature Reviews Gastroenterology and Hepatology, 11(8),* 506–514.
7. De Filippis, F., Pasolli, E. & Ercolini, D. (2020). The food-gut axis: Lactic acid bacteria and their link to food, the gut microbiome and human health. *FEMS Microbiology Reviews, 44(4),* 454–489.
8. Marco, M. L., Sanders, M. E., Gänzle, M., Arrieta, M. C., Cotter, P. D., De Vuyst, L., Hill, C., Holzapfel, W., Lebeer, S., Merenstein, D., Reid, G., Wolfe, B. E. & Hutkins, R. (2021). The International Scientific Association for Probiotics and Prebiotics (ISAPP) consensus statement on fermented foods. *Nature Reviews Gastroenterology and Hepatology, 18(3),* 196–208.
9. Kitessa, D. A. (2024). Review on microbiology of cereal-based spontaneously fermented foods and beverages. *World Journal of Food Science and Technology, 8(2),* 11–18.
10. Garcia-Gonzalez, N., Battista, N., Prete, R. & Corsetti, A. (2021). Health-promoting role of *Lactiplantibacillus plantarum* isolated from fermented foods. *Microorganisms, 9(2),* Article 349.

11. Salvetti, E., Harris, H. M. B., Felis, G. E. & O'Toole, P. W. (2018). Comparative genomics of the genus *Lactobacillus* reveals robust phylogroups that provide the basis for reclassification. *Applied and Environmental Microbiology*, 84(17), e00993-18.
12. Gänzle, M. G. (2015). Lactic metabolism revisited: Metabolism of lactic acid bacteria in food fermentations and food spoilage. *Current Opinion in Food Science, 2*, 106–117.
13. Marco, M. L., Heeney, D., Binda, S., Cifelli, C. J., Cotter, P. D., Foligné, B., Gänzle, M., Kort, R., Pasin, G., Pihlanto, A., Smid, E. J. & Hutkins, R. (2017). Health benefits of fermented foods: *Microbiota and beyond. Current Opinion in Biotechnology*, 44, 94–102.
14. Sanlier, N., Gökcen, B. B. & Sezgin, A. C. (2019). Health benefits of fermented foods. *Critical Reviews in Food Science and Nutrition, 59(3)*, 506–527.
15. Sanni, A. I. & Abiodun, O. A. (2024). Lactic acid bacteria diversity in fermented foods as potential bio-resources contributing to alleviate malnutrition in developing countries: Nigeria as a case study. *Fermentation, 11(2),* Article 103.
16. Bokulich, N. A., Lewis, Z. T., Boundy-Mills, K. & Mills, D. A. (2025). A new perspective on microbial landscapes within food production. *Current Opinion in Biotechnology, 37*, 182–189.
17. Settanni, L. & Corsetti, A. (2024). Application of bacteriocins in vegetable food biopreservation. *International Journal of Food Microbiology, 121(2),* 123–138.
18. Adesemoye, E. T., Sanni, A. I., Spano, G., Capozzi, V. & Fragasso, M. (2025). Lactic acid bacteria diversity in fermented foods as potential bio-resources contributing to alleviate malnutrition in developing countries: Nigeria as a case study. *Fermentation, 11(2),* Article 103.
19. Oguntoyinbo, F. A. & Narbad, A. (2023). Multifunctional properties of probiotic *Lactobacillus* species in cereal-based African fermented foods. *Journal of Applied Microbiology, 118(6),* 1335–1346.
20. Tamang, J. P., Cotter, P. D., Endo, A., Han, N. S., Kort, R., Liu, S. Q., Mayo, B., Westerik, N. & Hutkins, R. (2025). Fermented foods, their microbiome and its potential in boosting human health. *Microbial Biotechnology, 17(2),* Article e14428.
21. Banwo, K., Ogunremi, O. R. & Sanni, A. I. (2023). Detoxification of aflatoxins in fermented cereal gruel (ogi) by probiotic yeasts and lactic acid bacteria. *Toxins, 15(3),* Article 210.

22. Achi, O. K. & Ukwuru, M. U. (2022). Co-occurrence of *Lactobacillus* species during fermentation of African indigenous foods: Impact on food safety and shelf-life extension. *Frontiers in Microbiology, 13,* Article 902196.
23. LeBlanc, J. G., Laino, J. E., del Valle, M. J., Vannina, V., van Sinderen, D. & Turanto, M. P. (2011). B-group vitamin production by lactic acid bacteria: current knowledge and potential applications. *Journal of Applied Microbiology*, 111(6), 1297-1309.
24. LeBlanc, J. G., Milanc, C., de Giori, G. S., Sesma, F., van Sinderen, D. & Ventura, M. (2013). Bacteria as vitamin supplier to their host: a gut microbiota perspective. *Current Opinion in Biotechnology*, 24(2), 160-168.
25. Adebayo-Tayo, B. C. & Ogunremi, O. R. (2024). Probiotic activities of lactic acid bacteria from cassava and ogi effluents. *Magna Scientia Advanced Research and Reviews, 13(1),* 001–011.
26. Leroy, F. & De Vuyst, L. (2020). Lactic acid bacteria as functional starter cultures for the food fermentation industry. *Trends in Food Science and Technology, 15(2),* 67–78.
27. Sliti, A., Hamdi, C., Bahri, R. & Cherif, A. (2026). Screening and characterisation of probiotic lactic acid bacteria from artisanal fermented foods: Safety and technological properties. *Current Research in Food Science*, 9, Article 100780.
28. Zhang, Y., Li, Y. & Wang, Q. (2024). A multi-omics technology to the study of lactic acid bacteria responses to environmental stress: The past, current and future trends. *Food Science and Human Wellness, 13(5),* 2651–2663.
29. Islam, S., Akter, T. & Hossain, M. A. (2023). Probiotic potential of *Lactobacillus plantarum* DMR14 isolated from a traditional fermented food. *PLOS ONE, 18(4),* Article e0283512.
30. Papadimitriou, K., Zoumpopoulou, G., Foligné, B., Alexandraki, V., Kazou, M., Pot, B. & Tsakalidou, E. (2024). Discovering probiotic microorganisms: In vitro, in vivo, genetic and omics approaches. *Frontiers in Microbiology, 6,* Article 58.
31. Ayo-John, E. I., Oluwalana, I. B. & Popoola, T. O. S. (2022). Microbial succession and production of metabolites during traditional fermentation of Nigerian ogi. *Journal of Food Science and Technology, 59(4),* 1456–1465.
32. Nyamwamu, N. C., Wagacha, J. M. & Onono, J. O. (2023). Microbial diversity in East African traditional fermented foods: A review. *Frontiers in Microbiology*, *14*, Article 1128456.

33. Duskova, M., Karpiskova, R. & Svec, P. (2022). Phenotypic and genotypic characterization of lactic acid bacteria isolated from Czech cheeses. *Foods, 11(3),* Article 312.
34. Forbes, J. D., Knox, N. C., Ronholm, J., Pagotto, F. & Reimer, A. (2021). Metagenomics: The next culture-independent game changer. *Frontiers in Microbiology, 8,* Article 1069.
35. Mayo, B. Rachid, C. T. C., Alegria, A., Leite, A, M. O., Peixoto, R. S. & Delgado, S. (2014). Impact of next generation sequencing techniques in food microbiology. *Current Genomics*, 15(4), 293-309.
36. Patil, S. M., Sawant, S. S., Schulz, S. W. & Patil, M. B. (2022). Lactic acid bacteria in food biotechnology. *Applied Sciences, 12(3),* Article 1251.
37. Walsh, A. M., Crispie, F. Claesson, M. J. & Cotter, P. D. (2017). Translating omics to food microbiology. *Annual Review of Food Science and Technology*, 8, 113-134.
38. Wittouck, S., Wuyts, S. & Lebeer, S. (2019). Towards a genome-based reclassification of the genus *Lactobacillus*. *Applied Environmental Microbiology*, 85(24), e02155-18
39. Zheng, J., Ruan, L., Sun, M. & Ganzele, M. (2015). A genomic view of *lactobacilli* and *pediococci* demonstrates that phylogeny matches ecology and physiology. *Applied and Environmental Microbiology*, 81(20), 7233-7243.
40. Srinivas, M., O'Sullivan, O., Cotter, P. D., vanSinderen, D. & Kenny, J. G. (2022). The application of metagenomics to study microbial communities and develop desirable traits in fermented foods. *Foods*, 11(20), 3297.
41. Obafemi, Y. D., Oranusi, S. U., Ajanaku, K. O., Akinduti, P. A., Leech, J. & Cotter, P. D. (2022). African fermented foods: Overview, emerging benefits and novel approaches to microbiome profiling. npj Science of Food, 6, 15.
42. Tamang, J. P., Cotter, P. D., Endo, A., Han, N. S., Kort, R., Liu, S. Q., Mayo, B., Westerik, N. & Hutkins, R. (2020). Fermented foods in a global age: East meets West. *Comprehensive Reviews in Food Science and Food Safety, 19(1),* 184–217.
43. Capurso, L. (2019). Thirty years of *Lactobacillus rhamnosus* GG: A review. *Journal of Clinical Gastroenterology, 53*(Suppl 1), S1–S41.3
44. Heeney, D. D., Gareau, M. G. & Marco, M. L. (2018). Intestinal Lactobacillus in health and disease, a driver or just along for the ride? *Current Opinion in Biotechnology*, *49*, 140–147.

45. Cao, Y., Fanning, S., Proos, S, Jordan, K. & Srikumar, S. (2017). A review on the applications of next generation sequencing technologies as applied to food-related microbiome studies. *Frontiers in Microbiology*, 8, 1829.
46. Adimpong, D. B., Nielsen, D. S., Sorensen, K. I., Derkx, P. M. F. & Jespersen, L. (2012). Genotypic characterization and safety assessment of lactic acid bacteria from indigenous African fermented food products. *BMC Microbiology*, 12, 75.
47. Liu, Y., Tran, D. Q. & Rhoads, J. M. (2018). Probiotics in disease prevention and treatment. *Journal of Clinical Pharmacology, 58*(Suppl 10), S164–S179.
48. Ayodeji, B. D., Piedade, C. F. Aponte, V. W., Moreira, P. R., Obadina, A. O. Sanni, L. O. & Pintado, M. M. (2017). Screening and molecular identification of lactic acid bacteria from gari and fufu and gari effluents. *Annals of Microbiology*, 67, 123-133.
49. Guan, N. & Liu, L. (2020). Microbial response to acid stress: Mechanisms and applications. *Applied Microbiology and Biotechnology, 104(12),* 5093–5104.
50. Wittouck, S., Wuyts, S. & Lebeer, S. (2019). Towards a genome-based reclassification of the genus *Lactobacillus*. *Applied Environmental Microbiology*, 85(24), e02155-18
51. Siedler, S., Balti, R. & Neves, A. R. (2019). Bioprotective mechanisms of lactic acid bacteria against fungal spoilage of food. *Current Opinion in Biotechnology, 56*, 138–146.
52. Franz, C. M. A., Huch, M., Mathara, J. M. Abriouel, H., Benomar, N., Reid, G., Galvez, A. & Holzapfel, W. H. (2014). African fermented foods and probiotics. *International Journal of Food Microbiology*, 190, 84-96.
53. Capozzi, V., Fragasso, M., Romaniello, R., Berbegal, C., Russo, P. & Spano, G. (2017). Spontaneous food fermentations and potential risks for human health. *Fermentation, 3(4),* Article 49.
54. Onipede, G., Aremu, B., Sanni, A. & Babalola, O. (2020). Molecular study of the phytase gene in lactic acid bacteria isolated from ogi and kunun-zaki, African fermented cereal gruel and beverage. *Applied Food Biotechnology*, 7(1), 49-60.
55. Gu, Q., Zhang, C., Song, D., Li, P. & Zhu, X. (2024). Encapsulating viable probiotics in foods: A review. *Food Reviews International, 40(1),* 1–17.
56. Oguntoyinbo, F. A. & Narbad, A. (2015). Multifunctional properties of *Lactobacillus plantarum* strains isolated from fermented cereal foods. *Journal of Functional Foods*, 17, 621-631.