Transactions on Materials, Biotechnology and Life Sciences
ISSN: 2960-1932, eISSN: 2960-2319 | Volume 9
FENBC 2026

Comparative Impact of Bacterial and Yeast Probiotic Strains in Functional Foods: Mechanisms, Efficacy and Applications

Xiaoning Zhang [1, *]

[1] College of Science, Technology, Engineering, Mathematics & Management (CSTEMM), University of Wisconsin-Stout, Menomonie, 54751 United States

* Corresponding Author Email: zhangx0434@my.uwstout.edu

Abstract. This review systematically examines four principal probiotic groups in the context of functional food applications: *Lactobacillus*, represented by *L. rhamnosus* GG (LGG), which enhances epithelial barrier integrity via SpaCBA pili-mediated adhesion and secreted proteins Msp1/p75 and Msp2/p40 that activate EGFR-Akt signaling to attenuate cytokine-induced apoptosis; *Bifidobacterium*, which mediates ecosystem-level colonic regulation through acetate-driven cross-feeding with butyrate-producing taxa and strain-specific immunomodulation including NF-κB suppression and IL-10 induction; *Streptococcus thermophilus*, whose high β-galactosidase activity directly hydrolyzes lactose during intestinal transit, with clinical evidence confirming viability-dependent reduction in breath-hydrogen excretion and elevation of plasma butyrate; and *Saccharomyces boulardii*, a eukaryotic probiotic resilient to many antibiotics that mediates rapid, transient anti-diarrheal effects through serine protease-mediated toxin degradation, mucosal IgA stimulation, and MAP kinase-dependent suppression of pro-inflammatory mediators, with clinical trials confirming significant reductions in antibiotic-associated diarrhea incidence across adult and pediatric populations. Translational trends toward postbiotics and personalized nutrition are highlighted, alongside persistent challenges including heterogeneity in strain annotation and dosing, variability in host responses, and the paucity of long-term safety data. Three priority directions are identified: systematic clinical validation of strain-specific effects and dose–response relationships; development of standardized pipelines for personalized probiotic recommendations integrating microbiome diagnostics with rigorous clinical evidence; and cautious exploration of engineered probiotic chassis and metabolite-based products with explicit assessment of technical feasibility, regulatory pathways and safety.

Keywords: Bacterial; Yeast Probiotic Strains; Functional Foods.

1. Introduction

The FAO/WHO defines probiotics as live microorganisms that, when administered in adequate amounts, confer a health benefit on the host. Probiotics have many health benefits, some notable improvements such as in gastrointestinal health, in modulation of the immune system, and in the strengthening of intestinal barrier function. One important thing is that there has been evidence proving that different probiotic strains have distinct health benefits. Strain specificity in probiotics has been confirmed in systematic reviews, which have shown that the efficacy is strain dependent and not just the general category of probiotics [1]. This strain-specificity has promoted research to focus on characterization of well-defined strains with explicit identifiers and proven functional properties.

The practice of probiotics can be traced back to long ago. In 1907 Elie Metchnikoff observed that Bulgarian rural people who regularly consumed fermented dairy seems to have longer lifespan, and this promotes his hypothesis which is replacing harmful microbes in the gut with beneficial lactic acid bacteria could promote health and delay ageing [2]. Henri Tissier isolated *Bifidobacterium* from the feces of breastfed infants around the same time and discovered that it was able to inhibit harmful microorganisms causing diarrhea. Subsequently, Henri Boulard also isolated *Saccharomyces boulardii* in 1923 after studying traditional diarrhea medicine and lychee and mangosteen-peel based remedies. Later, in the 1930s, Minoru Shirota developed fermented milk products containing

Lactobacillus casei Shirota and commercialized as Yakult. These milestones have formed the conceptual and applicative framework within which modern probiotic research operates.

This review aims to systematically summarize the recent research studies on *Lactobacillus*, *Bifidobacterium*, *Streptococcus*, and yeast probiotics mainly *Saccharomyces boulardii*, focusing on human research studies published in recent years. By integrating these findings with today's trends, especially in food fermentation and functional food innovation, this paper presents fresh ideas on shifting landscape of probiotics in human health and future directions of research and application.

2. *Lactobacillus* Species

Probiotic effects are strain-specific and depend on the genetic content of each strain, especially its capacity for gastric survival, epithelial adhesion, and production of bioactive metabolites. Therefore, there has been increasing interest in well-characterized strains with explicit strain designations and proven functional properties.

Members of lactic acid bacteria (LAB) group—particularly the genus *Lactobacillus*—are Gram-positive, rod-shaped bacteria which often appear in chains. They carry out fermentative metabolism and thrive under microaerophilic to anaerobic conditions [3]. *Lactobacilli* inhabit a diversity of ecological niches which are reflected in their reputation of being widely distributed in nature, including plants, animals and raw milk, as well as their long history of application in fermented food products such as dairy products and vegetables.

Several LAB strains have been well studied in clinical and translational contexts. Representative strains include the *Lactobacillus acidophilus* LA1, the *Lactobacillus rhamnosus* GG (LGG), the *Lactobacillus plantarum* Lp01and the *Lactobacillus fermentum* RC-14, and each one is characterized for its survival, functional stability, and colonization ability .

2.1. Intestinal Barrier Enhancement

Among the best-characterized probiotics strains is *L. rhamnosus* GG (LGG). This strain can tolerate acidic and bile conditions similar to those encountered during gastrointestinal transit. It also adheres to epithelial surfaces and produces multiple bioactive factors that influence host signaling. A key mechanism of specific *Lactobacillus* strains is enhancement of the intestinal barrier, which is composed of a mucus layer produced by goblet cells and a monolayer of epithelial cells joined together by tight junctions (TJs), providing the first line of defense against the pathogens and toxins in the gut lumen as seen in Figure1A [4].

Mechanistically, LGG expresses SpaCBA fimbriae, and these structures enhance adhesion to mucin and epithelial cells through high-affinity interactions, therefore reducing pathogen access and modulating inflammatory signaling indirectly seen in Figure1B [5]. For example, LGG had been demonstrated to significantly provide protection to gastric mucosal integrity, resulting in a decrease in urinary excretion of sucrose, a marker of gastric permeability (from 108.5 mg to 47.8 mg, $P < 0.025$) when fed in a human clinical trial using the indomethacin induced injury model, showing a ~56% reduction. However, considering the site-specific action, the rise in small intestinal permeability was not significantly affected by LGG. In a human duodenal model, six hours after administration of *L. plantarum* WCFS1, the mean fluorescence pixel intensities of ZO-1 and occludin at tight junctions were around 54% and 36% higher respectively, than the placebo group ($P < 0.05$), proving that this strain can rapidly stabilize the mucosal barrier at the molecular level seen in Figure1C [6]. Complementary in vitro studies on Caco-2 cells indicate that this protection is TLR2-dependent against a chemically induced barrier disruption. Collectively, these findings highlight both strain dependence and anatomical specificity of barrier effects.

2.2. Immunomodulation and Molecular Mechanisms

In addition to their effects on the intestinal barrier, certain *Lactobacillus* strains can also modulate both innate and adaptive immune responses through surface molecules and secreted factors.

LGG produces functional secreted proteins such as Msp1/p75 and Msp2/p40. These proteins activate the EGFR-Akt signaling pathway and inhibit TNF-induced epithelial apoptosis seen in Figure1D [7]. Apart from this anti-apoptosis effect, LGG also significantly reduces cytokine-induced barrier dysfunction. In a Caco-2 model, Caco-2 cells exposed to IFN-γ and TNF-α mediums had a transepithelial electrical resistance (TER) of 61.8 ± 3.1% of baseline, while cells pretreated with LGG showed a TER of 89.6 ± 6.0%. This protective effect is clearly strain-specific, as other lactobacilli such as *L. plantarum* and *L. farciminis* failed to maintain barrier integrity under the same inflammatory conditions [8]. Moreover, lipoteichoic acid (LTA) in LGG can bind to TLR2–TLR6 heterodimers (co-receptors CD14 and CD36), then activate NF-κB signaling and induce pro-inflammatory IL-8 expression in intestinal epithelial cells [5].

At the human level, a duodenal transcriptome study revealed activation of the pathway related to IFN-γ–STAT4 axis and TH1 associated pathways such as cellular growth, wound healing and ion homeostasis following LGG intake as early as 6 hours [5].

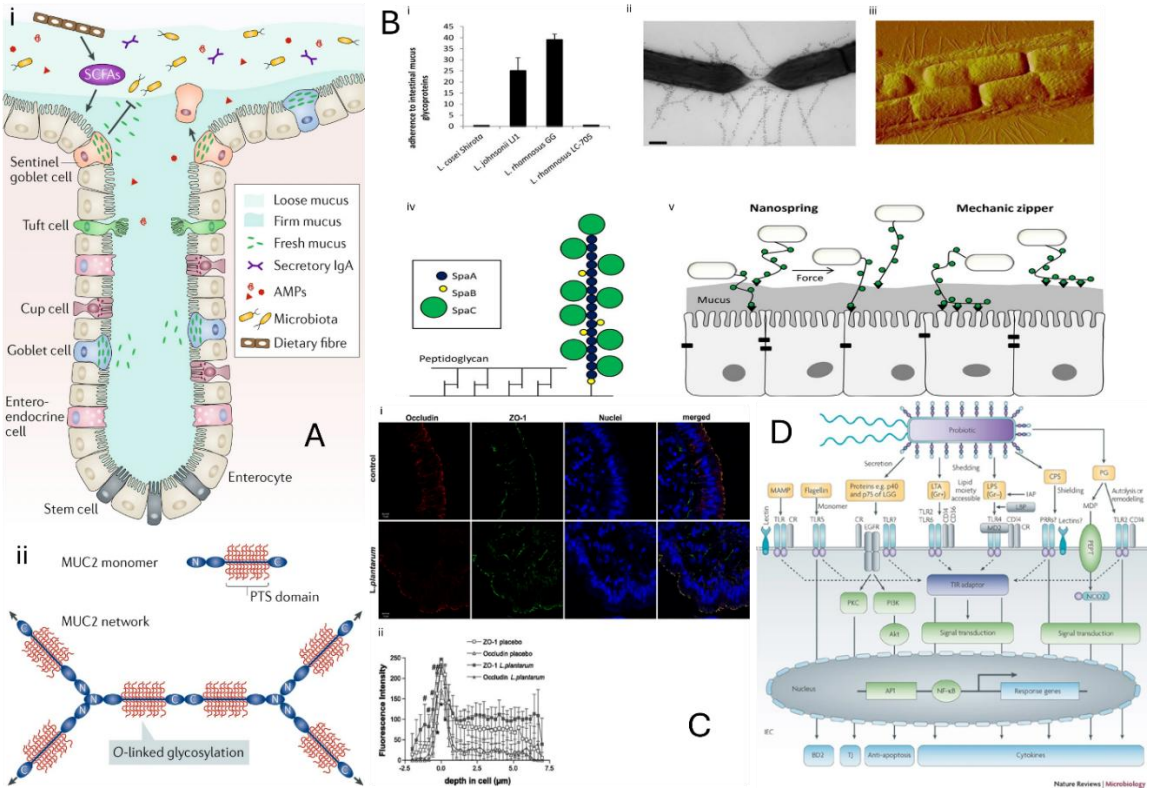

Figure 1. Mechanisms of *Lactobacillus* in maintaining intestinal homeostasis and barrier integrity [4-7]. (A) Structural architecture of the intestinal barrier: Schematic representation of the colonic crypt and mucus layer. Commensal bacteria ferment dietary fibers into short-chain fatty acids (SCFAs), while goblet cells maintain the mucus shield enriched with secretory IgA (sIgA) and antimicrobial peptides (AMPs) to prevent pathogen encroachment [4]. (B) Molecular basis of *L. rhamnosus* GG (LGG) adhesion: Structural model of the SpaCBA pilus system. The SpaA backbone and the mucus binding adhesin SpaC mediate 'molecular zipper' mechanism for strong binding of the bacteria to the intestinal mucosa and to persist in the gut [5]. (C) Reinforcement of tight junction (TJ) proteins: Representative confocal images and fluorescence intensity profiles of human duodenal biopsies. *L. plantarum* administration considerably improves the apical localization and expression of the important TJ proteins occludin (red) and zonula occludens-1 (ZO-1, green) [6]. (D) Intestinal epithelial signaling pathways: Schematic illustration of interactions among different effectors from *Lactobacillus* (such as secreted p40/p75 proteins, cell wall LTA) and host receptors (EGFR, TLR2). These interactions initiate protective pathways including PI3K/Akt that prevent apoptosis and enhance barrier stability [7].

2.3. Translational Evidence and Food Matrices

Most notably, three consecutive meta-analyses of RCT have shown that LGG can reduce the duration of the acute diarrhea in children by approximately 1.05 days. The strongest effect was observed at doses of$\geq 10^{10}$ CFU/day in European pediatric populations [5].

Delivery matrices affect the viability of the cells and functional expression; traditional matrices include fermented vegetables, dairy products (yogurt, fermented milk) and a growing body of literature has shown that plant-based matrices of fruit juices, fruit-vegetable blends and fermented grains are also effective. These matrices are frequently rich in dietary fibers and phenolics with prebiotic activity to help the survival of the probiotics during gastrointestinal digestion and processing, but the health benefits are dependent on the intrinsic properties of the probiotic strain administered.

3. *Bifidobacterium* Species

A major focus of gut microbiome studies is the genus *Bifidobacterium*, which is important for carbohydrate metabolism and cross-feeding with butyrate producers.

3.1. Colonization Niche and Metabolic Role Effects on Gut Environment

The distribution of *Bifidobacteria* species is not random throughout the gut ecosystem; This age-associated dynamic reflects changes in diet, immune development and ecological competition, and highlights the importance of considering life stage when evaluating the role of *Bifidobacteria* and their probiotic potential.

By strain level, there are specific *Bifidobacterium* strains that have unique ecological niches and functional profiles, which highlights the need to functionally assess strains. Key species include *B. longum*, *B. breve*, *B. bifidum* and *B. adolescentis*, among others, and commercially used strains (e.g. *B. longum* subsp. *infantis* or *B. animalis* subsp. *lactis*) differ a lot in their carbohydrate-active enzyme complements and substrate preferences.

Bifidobacteria are key carbohydrate-metabolizing members of the gut microbiota, colonizing the gut based on the availability of substrates, and are genetically regulated by a transcription factor, NagR, that controls a reconstructed regulon of about 25-30 genes required for carbohydrate transport and catabolism [1]. Many bifidobacterial taxa have specialized gene clusters enabling utilization of human milk oligosaccharides (HMOs), plant-derived arabinogalactans and resistant starches. For example, *B.longum* has been shown to be highly efficient at using arabinose containing plant polysaccharides while other taxa have complementary arrays of enzymes that allow them to degrade resistant starch (Figure 2A). This substrate specificity allows the colonization of different bifidobacteria in different niches in the gut.

3.2. *Bifidobacterium* Species Metabolic Outputs

Some *Bifidobacterium* strains express extracellular glycoside hydrolases and other enzymes that can break down complex polysaccharides and improve community level carbohydrates utilization. As a key probiotic group in the human gut, *Bifidobacteria* produce metabolites that affect the physiology of the host, such as motility and transport of nutrients. The short-chain fatty acids (SCFAs) produced in the course of bifidobacterial fermentation are mainly acetate, and propionate and butyrate also may be produced by cross-feeding, which affect energy metabolism of the host as well as expression of metabolic enzymes.

Bifidobacteria engage in cross-feeding interactions that underpin community assembly and metabolic output. Fermentation products like acetate and lactate will be the substrates for butyrate-producing taxa and thus support the production of butyrate as a colonic health metabolite seen in Figure 2C [9].

Beyond serving as a cross-feeding substrate, bifidobacterial acetate can also act as a direct host-protective mediator. In a germ-free mouse model, mice colonized with a protective *Bifidobacterium*

strain (e.g. *B. longum* subsp. *longum*) showed nearly 100% survival after *E. coli* O157:H7 infection while those colonized with non-protective strains showed a 0% survival rate within 7 days. Protective strains, including *B. infantis* 157F, produced significantly higher levels of acetate than did non-protective strains (approximately 4-6 mM for the former versus 1-2 mM for the latter). The supplementation with acetylated starch caused an increase in the level of acetate and greatly improved the survival of mice colonized with non-protective strains, this effect was linked to ABC-type carbohydrate transporters, which mediate the utilization of fructose and therefore sustain the continuous production of acetate [10].

3.3. Downstream Immune Effects

Bifidobacterial abundance and strain-specific activities play key role in immunoregulation. For example, *B. longum* 1714™ significantly inhibits LPS-induced systemic and splenic (both $p < 0.05$) NF-κB activity. This modulatory effect is partly related to indolelactic acid (ILA) released by this strain that directly inhibits the NF-κB signaling pathway activation. In addition, the branched hexasaccharide EPS secreted by the strain, stimulates the PBMCs to release the anti-inflammatory cytokine, IL-10 in a dose-dependent manner (0.0025–0.04 mg) [11]. Moreover, *Bifidobacteria* help in establishing immune homeostasis by supporting regulatory T cell (Treg) induction and function, which helps to prevent hyper-inflammatory response as observed in Figure 2B [12].

Collectively, the results clearly indicate that *B. longum* 1714™ has an immunomodulatory effect via various mechanisms. Importantly, evidence from a randomized, placebo-controlled human trial indicated that supplementation with *B. longum* 1714™ (1×10^9 CFU/day, 8 weeks) significantly elevated the levels of the circulating tryptophan and kynurenic acid, as well as the ratio of kynurenic acid/kynurenine [11]. These metabolic changes suggest a systemic bias toward neuroprotective and anti-inflammatory tryptophan metabolism. Although the trial did not directly measure immune endpoints, the findings offer indirect clinical evidence that this strain can influence host immune regulation through the gut–immune–metabolic axis.

4. *Streptococcus* Species

More than a hundred kinds of *Streptococcus* have been identified so far, and they all show different physiological and host traits. While some species are pathogenic, many strains are commensal members of environmental and human microbiomes and have been developed as probiotics. Among these, *Streptococcus thermophilus* (belonging to the *S. salivarius* group) is a canonical probiotic and a mainstay starter culture in the food industry. Lactose can also influence the survival and colonization potential of *S. thermophilus*. For example, lactose has been reported to mitigate bile-salt induced stress in certain strains, promoting transient persistence and increased abundance in the gut microbiota [13].

4.1. Support for Lactose Digestion

Streptococcus thermophilus is an important starter culture for dairy fermentation due to its rapid acidification, which is achieved by converting lactose into lactic acid [14]. This species preferentially utilizes lactose as its principal carbon and energy source, and many strains exhibit high β-galactosidase activity that directly participates in lactose hydrolysis in the gut. In a controlled human trial, a single intake of fresh yogurt containing live *S. thermophilus* reduced breath-hydrogen AUC from 6465 to 2400 ppm·3h in lactose malabsorbers, compared with 2174 ppm·3h after heated yogurt; most importantly, after 15 days of consumption, fresh yogurt further reduced breath-hydrogen AUC to 1461 ppm·3h versus 3007 ppm·3h in the heated yogurt group ($P < 0.01$), confirming that this benefit depends on the viability of the bacterial cultures [15].

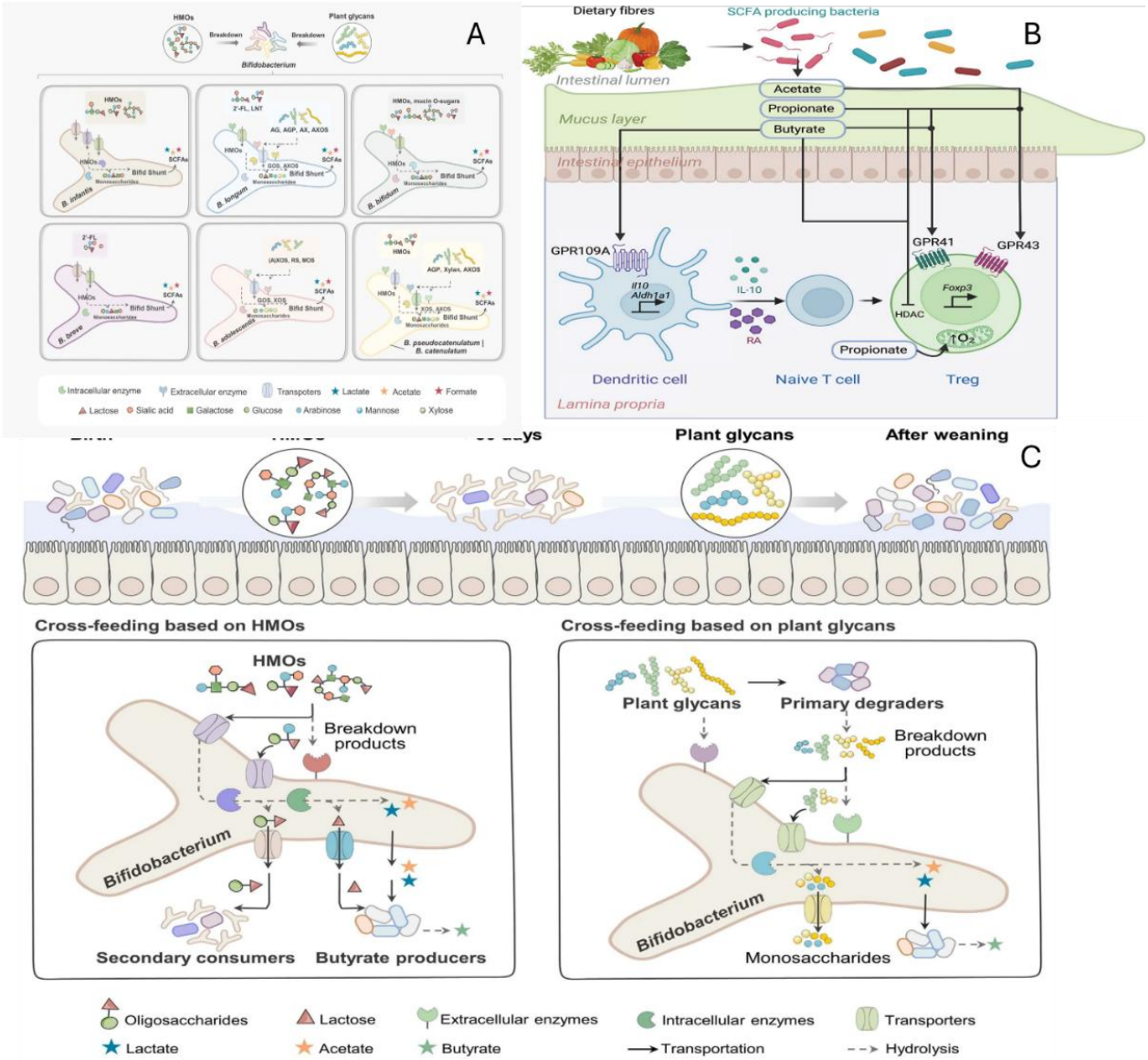

Figure 2. Metabolic specialization, cross-feeding networks, and immunomodulatory effects of *Bifidobacterium* species [9,12]. (A) Strain-specific carbohydrate utilization: Many ways have emerged by which *Bifidobacteria* break down complex glycans. *B. infantis* and *B. bifidum* focus on human milk oligosaccharides (HMOs) through either intracellular or extracellular pathways, while other species such as *B. adolescentis* and *B. longum* are good at utilizing resistant starch and phytoglycans, respectively [9]. (B) SCFA-mediated Treg modulation: Mechanisms of SCFA regulation of immune homeostasis. Acetate, propionate and butyrate all act on G-protein coupled receptors (GPR41/43/109A) and HDAC inhibition to promote the expression of Foxp3 and differentiate peripheral regulatory T cells (pTregs) [12]. (C) Metabolic cross-feeding dynamics: *Bifidobacterium* is a typical taxon that hydrolyzes complex polysaccharides to generate metabolic intermediates. These products support the growth of non-degrading commensals and butyrate-producing bacteria, establishing a stable microbial trophic network throughout the host's life cycle [9].

4.2. Support for Gut Comfort

As a key component of traditional yogurt production, *S. thermophilus* acts synergistically with other probiotic species to influence product properties and host physiology. Fermentation by mixtures that include *S. thermophilus* can generate SCFAs such as acetic acid, which contribute to intestinal homeostasis and support epithelial barrier function. Moreover, conditioned media from yogurt fermented with *S. thermophilus* has been shown to increase expression of MUC2 and CDX2 in intestinal epithelial models; MUC2 is the principal secreted mucin of the mucus layer, while CDX2 regulates MUC2 expression.

S. thermophilus has the ability to exert a modulation of the gut microbiota composition under certain conditions. Some studies have shown that it promotes the growth of *Bacteroides dorei* and exhibits competitive behavior against *Escherichia coli* in co-culture systems, thereby reshaping microbial community structure. The strain could also produce xylan-degrading enzymes, and synthesize vitamin B (e.g., riboflavin and folate), which can provide carbon and micronutrient sources to specific gut commensals through cross-feeding [16].

S. thermophilus has been suggested to have anti-tumor and preventive benefits. For example, the β-galactosidase from certain strains has been found to be linked to the regulation of signaling pathways (including Hippo-pathway kinases), which are relevant to tumorigenesis. Additionally, metabolites present in culture supernatants, such as folate produced by *S. thermophilus* and its symbionts, may inhibit growth of colorectal cancer–associated pathogens and alleviate pathogen-induced dysbiosis while sparing beneficial bacteria, thus supporting community stability [16].

4.3. Yogurt as a Probiotic Delivery Model

The strains of *S. thermophilus* and *L. delbrueckii* subsp. *bulgaricus* are among the bacteria that have been approved for use in the production of yogurt, and both of these strains are lactase positive, which can help to improve lactose digestion. Human studies demonstrate that yogurt containing live cultures enhances lactose digestion and reduces gastrointestinal symptoms in lactose-intolerant individuals [17]. In lactose malabsorbers, after 15 days of fresh yogurt intake, the area under the curve (AUC) for breath hydrogen (1461 ppm·3h) was significantly lower than after intake of the heated yogurt (3007 ppm·3h) ($P < 0.01$). In addition to lactose digestion, fresh yogurt also elevated plasma butyrate AUC in lactose-normal subjects to 1196 μmol·3h/L compared with 1060 μmol·3h/L in the heated group ($P < 0.03$), suggesting that metabolically active cultures play a role in colonic fermentation beyond the site of lactase activity [15].

5. Comparative Overview of *Lactobacillus*, *Bifidobacterium*, and *Streptococcus Thermophilus*

The three bacterial probiotic groups discussed above differ fundamentally in colonization strategy, primary site of action, and mechanistic logic. Nevertheless, they exhibit complementary functional profiles that collectively cover the major axes of gastrointestinal health (Table 1). *Lactobacillus* mainly exerts localized effects in the small intestine. It reinforces tight junction architecture and triggers immune signaling through surface molecules, with lactic acid providing immediate pathogen inhibition via local acidification. *Bifidobacterium* functions as a keystone metabolizer in the colon. And its carbohydrate fermentation outputs, particularly acetate, serve dual roles as cross-feeding substrates for butyrate-producing bacteria and as direct host-protective mediators. And its strain-specific immunomodulatory capacity extends to systemic NF-κB suppression and regulatory T cell induction. *S. thermophilus* occupies a distinctly different niche. Rather than colonizing the gut, it acts transiently during gastrointestinal transit via β-galactosidase activity. This provides immediate enzymatic relief from lactose malabsorption. At the same time, it supports downstream commensal growth by producing B vitamin and oligosaccharide breakdown products. From an ecological perspective, these three groups are not redundant but are sequential, with *S. thermophilus* helping to make substrate available, *Bifidobacterium* converting those substrates into community-level metabolic outputs, and *Lactobacillus* strengthening the barrier function and immune protection at the mucosal interface. These complementary profiles offer a strong mechanistic rationale for the use of combined probiotic formulations. However, the translational evidence base remains uneven: *Lactobacillus* carries the strongest clinical support, *Bifidobacterium* stands out for its mechanistic depth, and *S. thermophilus* has the clearest evidence within its primary indication of lactose malabsorption. Rigorous characterization of strain identity, dose, and delivery matrix remains prerequisite for any evidence-based combined application.

Table 1. Summary and comparison of characteristics, mechanisms, and health benefits of the key probiotic genera discussed in this review.

Characteristic	*Lactobacillus*	*Bifidobacterium*	*Streptococcus thermophilus*
Main Metabolites	Primarily lactic acid [3]	SCFAs (acetate, propionate) and lactic acid	Lactic acid, B vitamins (folate, riboflavin) and EPS [14,16]
Core Mechanism	Directly enhances tight junction proteins (e.g., ZO-1, occludin) to repair the physical barrier [4,6]	Indirectly maintains barrier and immune balance through SCFA production and cross-feeding [9,12]	Directly degrades lactose during intestinal transit via high β-galactosidase activity [14]
Primary Site of Action	Small intestine and upper digestive tract	Colon (large intestine)	Entire gastrointestinal tract during transit
Ecological Role	Rapidly lowers local pH to provide immediate protection against pathogens	Acts as a core carbohydrate metabolizer and provides nutrients for beneficial bacteria such as butyric acid-producing bacteria and regulates long-term metabolism [9]	Serves as a fermentation starter and supports the growth of other beneficial bacteria via cross-feeding and by secreting vitamins and enzymes [16]
Key Health Benefits	Enhanced immune defense, barrier integrity, and anti-inflammatory effects [6,7]	Regulation of chronic inflammation, metabolic balance, and intestinal homeostasis [11,12]	Alleviation of lactose intolerance, improved immune response, and enhanced product texture [15]

6. Yeast Probiotics

6.1. Unique Traits Compared to Bacterial Probiotics

Research on yeast probiotics focuses primarily on *Saccharomyces boulardii*, a eukaryotic probiotic that differs fundamentally from bacterial probiotics in cellular organization, lifecycle, and mechanistic logic. Unlike bacterial probiotics — which typically require stable gut colonization and longer-term community modulation to exert their effects — *S. boulardii* does not colonize the gut; instead, it has a transient effect and is involved in rapid symptom-oriented responses by directly interacting with pathogens or toxins, or by modulating mucosal immune response. This transient mode of action is not a disadvantage, but rather a mechanistic advantage. Because *S. boulardii* can have measurable effects during acute episodes without relying on colonization efficiency, host microbiota composition, or competitive exclusion, factors that often limit many bacterial probiotics.

6.2. Effects on Diarrhea and Gut Health

Among the yeast probiotics, *Saccharomyces boulardii* has the best clinical evidence to prevent or treat antibiotic associated diarrhea (AAD). Its rapid, short-term action and resilience during antibiotic therapy make it particularly suitable for concurrent administration with antibiotics to mitigate AAD. In the ten controlled trials in adults, 80% showed statistically significant reductions in AAD incidence, with relative risk reductions ranging from 7.4% to 25%; in pediatric populations, two RCTs reported relative improvements in AAD prevention of 7.6% to 30.1% compared with control groups [18].

Mechanistically, *S. boulardii* interferes with pathogen adhesion, neutralizes toxins, and regulates local inflammatory responses. It can reduce adherence of pathogens like *Clostridioides difficile* and pathogenic *Escherichia coli* to the intestinal mucosa, thus decreasing the risk of colonization and invasion [4]. *S. boulardii* secretes a ~54 kDa serine protease that can degrade the toxins A and B produced by *C. difficile* and can also inactivate the intestinal receptor for toxin A, thereby limiting toxin-mediated epithelial injury [19]. It also promotes mucosal IgA secretion, antitoxin antibody production and modulates MAP kinase signaling to reduce secretion of pro-inflammatory mediators such as IL-8 in a dose-dependent manner.

6.3. Resistance to Antibiotics

S. boulardii is resistant to many antibiotics — including clinically important such as metronidazole and vancomycin used in *Clostridioides difficile* infection treatment, and rifaximin used to manage

ulcerative colitis— and it typically does not disrupt normal gut microbiota, in contrast, many bacterial probiotics will be affected by antibiotics and may be depleted during treatment [18]. This property allows *S. boulardii* to maintain functional activity throughout antibiotic treatment and to promote the recovery of the disrupted microbiota. It is therefore ideally suited for concurrent use with antibiotics rather than a sequential supplementation.

6.4. Food Matrix Applications and Viability

S. boulardii can be used as a fermentation adjunct, and as a functional ingredient in the final product. In dairy systems, it can work together with lactic acid bacteria to enhance antioxidant properties. It exhibits an antioxidant potential 6 to 10 times higher than that of conventional *S. cerevisiae*, with extracellular total phenolic and flavonoid contents approximately 70-fold and 20-fold higher, respectively, than ordinary yeast [20]. This collaboration also improves flavor profiles and the survival of co-cultured strains.

S. boulardii shows strong viability across a wide range of food matrices and storage conditions. In synbiotic ice cream, viable counts remained at 6.16 $\log_{10}$ CFU/g after 120 days at -18°C. In low-alcohol beer, counts were maintained at 8.3×10^6 CFU/mL after 45 days at 4°C [20]. Both values meet the minimum threshold required for probiotic efficacy. Maintenance of viable counts above therapeutic thresholds across different matrices is essential for the anti-diarrheal and immunomodulatory effects described earlier.

7. Conclusion

This review provides an overview of recent advances in probiotic applications within food science, with a focus on strain-specific functions and emerging opportunities for targeted dietary interventions. Evidence shows that *Lactobacillus* and *Bifidobacterium* species support intestinal barrier integrity, immune modulation and metabolic regulation through strain-dependent mechanisms, including the production of short-chain fatty acid (SCFA) and extracellular polysaccharide (EPS). These functional properties help explain the growing market interest in more tailored probiotic formulations.

Plant-based carriers and symbiotic approaches can improve probiotic efficacy, while postbiotics, such as microbial metabolites or inactivated microbial preparations, provide practical advantages in terms of stability and storage. However, claims about their universal safety and efficacy should be approached with caution, as well-designed clinical evaluations of postbiotic formulations and direct head-to-head comparisons with live probiotics remain still limited. Despite these advantages, several important limitations persist. These include heterogeneity in strain annotation and dosing, high variability in host responses, and the lack of long-term safety data. These gaps make it difficult to generalize study findings and slow both clinical and industrial translation.

Looking forward, three priority directions deserve attention: systematic clinical validation of strain-specific effects and dose–response relationships; the development of standardized pipelines for personalized probiotic recommendations that integrate microbiome diagnostics with solid clinical evidence; and cautious exploration of engineered probiotic chassis and metabolite-based products, along with thorough assessment of their technical feasibility, regulatory requirements and safety. Together, these efforts will help realize the potential for transforming routine foods into evidence-based, precision nutritional interventions.

References

[1] Arzamasov, A. A., Rodionov, D. A., Hibberd, M. C., Guruge, J. L., Kent, J. E., Kazanov, M. D., Leyn, S. A., Elane, M. L., Sejane, K., Furst, A., Bode, L., Barratt, M. J., Gordon, J. I., & Osterman, A. L. (2025). Integrative genomic reconstruction reveals heterogeneity in carbohydrate utilization across human gut bifidobacteria. Nature Microbiology. https://doi.org/10.1038/s41564-025-02056-x

[2] Gasbarrini, G., Bonvicini, F., & Gramenzi, A. (2016). Probiotics History. Journal of Clinical Gastroenterology, 50, S116–S119. https://doi.org/10.1097/mcg.0000000000000697

[3] Giraffa, G., Chanishvili, N., & Widyastuti, Y. (2010). Importance of lactobacilli in food and feed biotechnology. Research in Microbiology, 161(6), 480–487. https://doi.org/10.1016/j.resmic.2010.03.001

[4] Martens, E. C., Neumann, M., & Desai, M. S. (2018). Interactions of commensal and pathogenic microorganisms with the intestinal mucosal barrier. Nature Reviews Microbiology, 16(8), 457–470. https://doi.org/10.1038/s41579-018-0036-x

[5] Segers, M. E., & Lebeer, S. (2014). Towards a better understanding of *Lactobacillus rhamnosus* GG - host interactions. Microbial Cell Factories, 13(Suppl 1), S7. https://doi.org/10.1186/1475-2859-13-s1-s7

[6] Karczewski, J., Troost, F. J., Konings, I., Dekker, J., Kleerebezem, M., Brummer, R.-J. M., & Wells, J. M. (2010). Regulation of human epithelial tight junction proteins by *Lactobacillus plantarum* in vivo and protective effects on the epithelial barrier. American Journal of Physiology. Gastrointestinal

[7] Lebeer, S., Vanderleyden, J., & De Keersmaecker, S. C. J. (2010). Host interactions of probiotic bacterial surface molecules: comparison with commensals and pathogens. Nature Reviews Microbiology, 8(3), 171–184. https://doi.org/10.1038/nrmicro2297

[8] Donato, K. A., Gareau, M. G., Wang, Y. J. J., & Sherman, P. M. (2010). *Lactobacillus rhamnosus* GG attenuates interferon-{gamma} and tumour necrosis factor-alpha-induced barrier dysfunction and pro-inflammatory signalling. Microbiology (Reading, England), 156(Pt 11), 3288–3297. https://doi.org/10.1099/mic.0.040139-0

[9] Xiao, M., Zhang, C., Duan, H., Arjan Narbad, Zhao, J., Chen, W., Zhai, Q., Yu, L., & Tian, F. (2024). Cross-feeding of bifidobacteria promotes intestinal homeostasis: a lifelong perspective on the host health. Npj Biofilms and Microbiomes, 10(1). https://doi.org/10.1038/s41522-024-00524-6

[10] Fukuda, S., Toh, H., Hase, K., Oshima, K., Nakanishi, Y., Yoshimura, K., Tobe, T., Clarke, J. M., Topping, D. L., Suzuki, T., Taylor, T. D., Itoh, K., Kikuchi, J., Morita, H., Hattori, M., & Ohno, H. (2011). *Bifidobacteria* can protect from enteropathogenic infection through production of acetate. Nature, 469(7331), 543–547. https://doi.org/10.1038/nature09646

[11] Groeger, D., Yao, L., Collins, F., Larsen, I. S., Tan, H.-T. T., Healy, S., Ambrogi, V., Tykwinska, K., Schmidt, M., Golletz, P., Kiely, B., Clarke, G., Dinan, T. G., Murphy, E. F., & O'Mahony, L. (2025). Complementary immunoregulatory effects of *Bifidobacterium longum* 1714TM associated exopolysaccharide and tryptophan metabolism. Current Research in Microbial Sciences, 9, 100481. https://doi.org/10.1016/j.crmicr.2025.100481

[12] Sharma, A., Sharma, G., & Im, S.-H. (2025). Gut microbiota in regulatory T cell generation and function: mechanisms and health implications. Gut Microbes, 17(1). https://doi.org/10.1080/19490976.2025.2516702

[13] Pan, Y., Yu, P., Jiang, Y., Liu, X., Zhao, J., Zhang, H., & Chen, W. (2023). The protective effect of lactose on the bile salt stress response of *Streptococcus thermophilus* is strain dependent. Food Bioscience, 53, 102560–102560. https://doi.org/10.1016/j.fbio.2023.102560

[14] Yu, P., Pan, Y., Pei, Z., Guo, M., Yang, B., Lee, Y.-K., Liu, X., Zhao, J., Zhang, H., & Chen, W. (2023). Influence of Lactose Supplementation on Regulation of Streptococcus thermophilus on Gut Microbiota. Nutrients, 15(22), 4767–4767. https://doi.org/10.3390/nu15224767

[15] Rizkalla, S. W., Luo, J., Kabir, M., Chevalier, A., Pacher, N., & Slama, G. (2000). Chronic consumption of fresh but not heated yogurt improves breath-hydrogen status and short-chain fatty acid profiles: a controlled study in healthy men with or without lactose maldigestion. The American Journal of Clinical Nutrition, 72(6), 1474–1479. https://doi.org/10.1093/ajcn/72.6.1474

[16] Nam, E. H., Lee, M., Kim, H., Kim, D., Lee, Y., Jung, Y. H., Yang, J., & Shin, M. (2025). The impact of *Streptococcus thermophilus* IDCC 2201 on gut microbiota and its potential as a prophylactic agent for colorectal cancer. Scientific Reports, 15(1). https://doi.org/10.1038/s41598-025-20976-w

[17] Guarner, F., Perdigon, G., Corthier, G., Salminen, S., Koletzko, B., & Morelli, L. (2005). Should yoghurt cultures be considered probiotic? British Journal of Nutrition, 93(6), 783–786. https://doi.org/10.1079/bjn20051428

[18] Kelesidis, T., & Pothoulakis, C. (2012). Efficacy and safety of the probiotic *Saccharomyces boulardii* for the prevention and therapy of gastrointestinal disorders. Therapeutic Advances in Gastroenterology, 5(2), 111–125. https://doi.org/10.1177/1756283X11428502

[19] Castagliuolo, I., Riegler, M. F., Valenick, L., LaMont, J. T., & Pothoulakis, C. (1999). *Saccharomyces boulardii* Protease Inhibits the Effects of *Clostridium difficile* Toxins A and B in Human Colonic Mucosa. Infection and Immunity, 67(1), 302–307. https://doi.org/10.1128/iai.67.1.302-307.1999

[20] Dmitrii Manshin, Kuntsova, M., Alexey Shilenko, & Andreeva, A. (2025). Probiotic yeast *Saccharomyces cerevisiae var. boulardii*: properties and peculiarities of use in functional foods development. Functional Foods in Health and Disease, 15(5), 296–315. https://doi.org/10.31989/ffhd.v15i5.1482