



Review

The Influence of Reliable Microbiota Consortia in Probiotic Yogurt on Improving Insulin Sensitivity in Type 2 Diabetes Mellitus Patients

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Abstract

Type 2 diabetes mellitus (T2DM) is a chronic metabolic disorder characterized by progressive insulin resistance, impaired glucose regulation, and elevated cardiometabolic risk. Despite the availability of pharmacological therapies, long-term glycemic control remains suboptimal in many patients, highlighting the need for effective adjunctive nutritional strategies. Probiotic yogurt containing well-characterized bacterial consortia has been proposed as one such approach, given its potential to modulate gut microbiota composition, increase short-chain fatty acid (SCFA) production, improve intestinal barrier integrity, and attenuate low-grade systemic inflammation. A narrative review was conducted by searching PubMed, Scopus, and Google Scholar databases using terms related to probiotic yogurt, synbiotic yogurt, insulin sensitivity, T2DM, gut microbiota, *Lactobacillus*, and *Bifidobacterium*. Priority was given to randomized controlled trials (RCTs), meta-analyses, and systematic reviews, supplemented by mechanistically relevant preclinical studies. The reviewed evidence indicates that probiotic yogurt generally produces more consistent improvements in long-term metabolic markers, particularly glycated hemoglobin (HbA1c) and lipid profile, than in acute fasting glucose responses. Several trials also report reductions in fasting insulin and the homeostatic model assessment of insulin resistance (HOMA-IR), combined with improvement in the quantitative insulin sensitivity check index (QUICKI), particularly when yogurt is enriched with prebiotic substrates such as inulin and konjac glucomannan. Probiotic yogurt formulated with well-selected microbial consortia may serve as a safe complementary intervention for improving insulin sensitivity and overall metabolic control in T2DM patients.

Keywords: probiotic yogurt; *Lactobacillus acidophilus*; *Bifidobacterium*; HbA1c; HOMA-IR; short-chain fatty acids

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1. Introduction

Diabetes mellitus is a chronic metabolic disorder marked by persistent hyperglycemia resulting from insufficient insulin secretion, impaired insulin action, or both. Among its forms, type 2 diabetes mellitus (T2DM) accounts for the majority of cases globally and is characterized by progressive insulin resistance in skeletal muscle, hepatic tissue, and

adipose tissue, coupled with a relative deficiency in pancreatic beta-cell function. The global burden of diabetes continues to increase; the 11th edition of the IDF (International Diabetes Federation) Diabetes Atlas estimated that 11.1% of adults aged 20–79 years were living with diabetes in 2024, underscoring the growing clinical and socioeconomic importance of effective long-term disease control [1]. This combination leads to sustained hyperglycemia, dyslipidemia, and increased susceptibility to cardiovascular complications. At the molecular level, chronic nutrient excess, elevated circulating free fatty acids, oxidative stress, endoplasmic reticulum stress, and inflammatory signaling contribute to progressive impairment of insulin action and pancreatic beta-cell function [2]. Current management strategies encompass lifestyle modification, pharmacological intervention, and evolving nutritional approaches aimed at restoring metabolic homeostasis. Nevertheless, T2DM is heterogeneous and progressive, and many patients do not achieve durable metabolic control, supporting continued investigation of safe adjunctive nutritional strategies that target mechanisms beyond glucose lowering alone.

Despite advances in antidiabetic pharmacotherapy, achieving long-term glycemic targets remains challenging for a substantial proportion of T2DM patients. This factor underscores the need for complementary strategies that address upstream metabolic dysregulation. One emerging area of interest is the role of the gut microbiota in the pathogenesis and management of insulin resistance. Adults with T2DM harbor a gut microbial community that differs qualitatively and quantitatively from that of non-diabetic individuals, with reductions in beneficial butyrate-producing bacteria and increases in opportunistic or pro-inflammatory taxa [2]. These microbiota changes have been linked to increased intestinal permeability, endotoxemia, and systemic low-grade inflammation, all of which impair insulin signaling [3]. More recent multi-omics evidence has further demonstrated that microbial carbohydrate metabolism and altered intestinal metabolite profiles are associated with insulin resistance and host inflammatory signaling, strengthening the biological rationale for microbiota-targeted interventions [4]. However, the direction of causality and the extent to which microbiota modification translates into clinically meaningful improvements in insulin sensitivity remain incompletely resolved.

Probiotics, defined as live microorganisms that confer a health benefit on the host when administered in adequate amounts [1], have received growing attention as biological agents capable of modulating the gut microbiota and metabolic function. Importantly, fermented foods and probiotics are not interchangeable concepts: a fermented food should not automatically be described as a probiotic unless the microorganisms are adequately characterized and they confer a health benefit [5]. Among available delivery matrices, yogurt is particularly relevant because it provides a physiologically buffered environment that can support probiotic viability through gastrointestinal transit. Furthermore, the fermentation process itself generates bioactive compounds, including organic acids and bacteriocins, that may complement the actions of the live bacteria. In the context of T2DM, the potential benefit of probiotic yogurt is biologically plausible because microbiota-derived metabolites, including short-chain fatty acids, can influence intestinal barrier integrity, immune signaling, bile-acid metabolism, incretin release, and insulin-signaling pathways [6–8]. Yogurt enriched with probiotic strains belonging primarily to *Lactobacillus* and *Bifidobacterium* has therefore been investigated as a functional food approach for improving glycemic and cardiometabolic outcomes [9,10].

A critical limitation of the current evidence is that most commercial yogurt products are formulated primarily for sensory quality rather than therapeutic efficacy. Not all commercially used strains exhibit adequate resistance to gastric acid and bile salts. A consortium approach employing multiple complementary strains may provide functional redundancy and broader metabolic activity; multistrain formulations should not be assumed to be clinically superior to single-strain products without direct comparative trials.

Clinical evidence remains heterogeneous: some randomized trials report improvements in HbA1c, lipid profile, fasting insulin, HOMA-IR, or QUICKI [8,9,11–14], whereas in a meta-analysis focused specifically on probiotic yogurt, researchers found no consistent overall improvement in glycemic markers compared with conventional yogurt [15]. This inconsistency suggests that strain identity, viable dose, intervention duration, background diet, medication use, yogurt composition, and the presence of prebiotic substrates may all modify treatment response [16,17]. Evidence from experimental and clinical studies suggests that fermented milk or soy-milk formulations with selected probiotic strains can modify glucose metabolism, GLUT-4 expression, antioxidant status, and tissue-level biological markers [6,7,18]. However, a critical gap remains in synthesizing how specifically designed microbial consortia within the yogurt matrix affect the full spectrum of insulin sensitivity indices in T2DM patients.

In this review, we aim to synthesize the available scientific evidence on the role of reliable microbiota consortia in probiotic yogurt for improving insulin sensitivity in T2DM patients. Beyond cataloging study outcomes, we critically evaluate the mechanistic plausibility of observed effects, identify key sources of heterogeneity across trials, and highlight unresolved questions that should inform future research. Particular emphasis is placed on distinguishing direct evidence from probiotic yogurt trials from supportive evidence derived from probiotic supplements, synbiotic formulations, and mechanistic pre-clinical studies, because differences in delivery matrix and intervention composition may affect biological and clinical responses. The scope encompasses clinical outcomes including glycemic control, insulin resistance indices (HOMA-IR, QUICKI), lipid profile, oxidative stress, gut barrier function, and microbiota modulation.

2. Methods

In this study, we employed a narrative review design to synthesize the available evidence on probiotic and synbiotic yogurt interventions in the context of insulin sensitivity and T2DM. A narrative approach was selected because the primary objective was to evaluate mechanistic pathways and clinical outcomes across heterogeneous intervention types, rather than to perform a quantitative meta-analytic synthesis.

Scientific sources were identified through systematic searches of PubMed/MEDLINE, Scopus, and Google Scholar databases. Search terms included combinations of the following: “probiotic yogurt,” “synbiotic yogurt,” “fermented milk,” “insulin sensitivity,” “insulin resistance,” “type 2 diabetes mellitus,” “gut microbiota,” “*Lactobacillus acidophilus*,” “*Bifidobacterium*,” “HOMA-IR,” “HbA1c,” and “short-chain fatty acids.” No formal language restriction was applied, though only peer-reviewed publications in English were included. The search covered publications from 2007 to 2025, with specific emphasis on studies published from 2013 onwards, when methodological rigor in probiotic RCTs has generally improved.

Study inclusion prioritized the following: (i) randomized controlled trials involving adult participants with T2DM or metabolic syndrome receiving probiotic or synbiotic yogurt; (ii) meta-analyses or systematic reviews summarizing RCT evidence on probiotics and glycemic or metabolic outcomes; and (iii) preclinical studies providing mechanistic insight into gut microbiota-mediated pathways relevant to insulin resistance. Studies were excluded if they involved probiotic supplementation in forms other than fermented dairy or yogurt without also reporting yogurt-specific or biologically comparable data or if they failed to report any quantitative metabolic outcome. The relevant gray literature and the reference lists of included publications were also reviewed to identify additional sources.

Data from selected studies were evaluated qualitatively by comparing the direction, magnitude, and consistency of reported effects on key outcomes: fasting plasma glucose

(FPG), HbA1c, fasting insulin, HOMA-IR, QUICKI, lipid profile (TC, LDL, HDL, TG), oxidative stress markers, incretin response, and microbiota or gut barrier-related parameters. Because this study was a narrative synthesis, no quantitative pooling or formal risk-of-bias scoring (e.g., Cochrane RoB tool) was performed; however, study quality was considered qualitatively in interpreting the findings.

For clinical interpretation, greater evidential weight was given to human RCTs involving T2DM or closely related metabolic populations. Preclinical data were used primarily to support mechanistic explanations, particularly for pathways not yet directly assessable in human trials, such as specific microbiota compositional changes, SCFA flux, and tight junction protein expression. Studies evaluating non-probiotic interventions were included only when they clarified the biological basis of microbiota involvement in insulin resistance.

3. Results and Discussion

3.1. Effects on Glycemic Control and Insulin Sensitivity

The reviewed studies collectively indicate that probiotic yogurt and related interventions can improve long-term glycemic control in T2DM, although the direction and magnitude of effects differ across clinical outcomes. Improvements appear more consistent for HbA1c, a marker of average glycemic exposure over two to three months, than for fasting plasma glucose, which reflects shorter-term metabolic regulation and is more susceptible to dietary and medication confounding. This pattern is clinically meaningful, as HbA1c is a primary endpoint in T2DM management guidelines and a stronger predictor of long-term complication risk.

Early seminal work by Ejtahed et al. [8,9,19] established proof-of-concept for probiotic yogurt in T2DM. The labels La5, Bb12, and SD5865 are retained as strain identifiers rather than interpreted as accession numbers; this factor is important because probiotic effects are strain-specific and should not be generalized from the species level alone [7]. In a randomized controlled trial, T2DM patients consuming 300 g per day of yogurt containing *Lactobacillus acidophilus* La5 and *Bifidobacterium lactis* Bb12 for six weeks exhibited significant improvements in glycemic control and lipid profile compared to those receiving conventional yogurt. In a companion trial by the same group, the results demonstrated improved antioxidant status, including superoxide dismutase activity, glutathione peroxidase activity, and reduced malondialdehyde levels, indicating that probiotic yogurt may simultaneously address oxidative stress, a key pathophysiological driver of insulin resistance [9]. These findings introduced the mechanistic premise that probiotic-mediated antioxidant effects and glycemic improvements are interlinked and may reinforce each other.

In metabolic syndrome patients, daily consumption of 300 g of probiotic yogurt containing La5 and Bb12 for eight weeks improved antioxidant capacity and exhibited metabolic correlations with insulin resistance measures [11,20]. Although this population was not limited to T2DM patients, the findings remain relevant because metabolic syndrome shares core pathophysiological features with T2DM, including oxidative stress and insulin resistance. The results suggest that probiotic yogurt may affect insulin sensitivity indirectly through improvement of redox balance and attenuation of inflammatory signaling.

In a proof-of-concept trial using *Lactobacillus reuteri* SD5865 in glucose-tolerant adults, the findings demonstrated increased GLP-1 and GLP-2 secretion, in addition to higher insulin and C-peptide concentrations following supplementation [12]. Although peripheral and hepatic insulin sensitivity did not change significantly in the aforementioned study—likely because participants were normoglycemic at baseline—increased incretin and insulin secretion indicate that certain probiotic strains can influence enteroendocrine pathways. For T2DM patients, in whom incretin responses are often attenuated, this

mechanism could contribute meaningfully to postprandial glucose regulation if replicated with appropriate strains in a compromised metabolic context.

Recent RCT evidence more directly addresses T2DM populations. In a multistrain probiotic RCT involving 130 T2DM patients, researchers reported significant improvement in HbA1c and HDL cholesterol after supplementation with 14 probiotic strains at 30 billion colony-forming units per day for 24 weeks (Table 1), suggesting a stronger effect on long-term metabolic regulation than on acute glucose parameters [13]. In a separate RCT of probiotic yogurt containing *Lactobacillus acidophilus* and *Bifidobacterium lactis* in 72 T2DM patients (Table 1), researchers reported improved HbA1c and lipid outcomes after 12 weeks, with less consistent between-group changes in fasting glucose [13–15]. Taken together, these trials reinforce the pattern that probiotic consortia in yogurt preferentially improve long-term glycemic markers over acute glucose measures in T2DM [17–19].

The synbiotic approach may further amplify metabolic effects by providing fermentable prebiotic substrates that stimulate the activity and growth of the probiotic organisms. In a notable RCT, yogurt enriched with konjac glucomannan and inulin for eight weeks reduced fasting insulin and HOMA-IR while increasing QUICKI in T2DM patients [14,19]. These indices are direct measures of insulin sensitivity rather than indirect glycemic proxies, representing a methodologically stronger demonstration that the intervention improved the insulin signaling environment [20]. The addition of prebiotic substrates likely increases colonic SCFA yield, which in turn supports gut barrier integrity and reduces inflammatory activation—pathways that directly influence peripheral insulin sensitivity.

Table 1. Selected clinical studies of probiotic or synbiotic yogurt relevant to insulin sensitivity and glycemic control in T2DM, with reported viable cell count or probiotic dose.

Study	Population	Intervention	Duration	Key Outcomes
Ejtahed et al. [13]	T2DM patients ($n = 64$)	300 g/day probiotic yogurt containing <i>L. acidophilus</i> La5 and <i>B. lactis</i> Bb12; reported counts on day 7: 1.05×10^6 CFU/g and 1.19×10^6 CFU/g, respectively.	6 weeks	Improved glycemic control (FPG, HbA1c) and lipid profile; no significant change in HOMA-IR reported.
Ejtahed et al. [13]	T2DM patients ($n = 64$)	300 g/day probiotic yogurt containing La5 + Bb12; trial summaries report approximately 1.8×10^6 CFU/g for the probiotic strains.	6 weeks	Improved antioxidant markers (SOD, GPx, MDA); antioxidant effects linked to improved redox balance.
Rezazadeh et al. [15]	Metabolic syndrome ($n = 44$)	300 g/day probiotic yogurt containing La5 + Bb12; exact viable count was not consistently specified in the reviewed source.	8 weeks	Improved antioxidant capacity; metabolic correlations with insulin resistance measures observed.
Simon et al. [16]	Glucose-tolerant adults ($n = 21$)	<i>L. reuteri</i> SD5865 supplementation; 2×10^{10} CFU/day. This was included as supportive mechanistic evidence and was not a yogurt matrix.	4 weeks	Increased GLP-1, GLP-2, insulin, and C-peptide; peripheral and hepatic insulin sensitivity not significantly changed.
Chaithanya et al. [17]	T2DM patients ($n = 130$)	Multistrain probiotic supplement containing 14 strains; total dose 30 billion CFU/day.	24 weeks	HbA1c significantly decreased; HDL improved; FPG and postprandial glucose trends less consistent.
Mirjalili et al. [18]	T2DM patients ($n = 72$)	200 g/day probiotic yogurt containing <i>L. acidophilus</i> and <i>B. lactis</i> ; 4.65×10^6 CFU/g.	12 weeks	HbA1c and lipid profile improved after covariate adjustment; between-group glucose changes less consistent.
Babajafari et al. [19]	T2DM patients	Low-fat yogurt enriched with konjac glucomannan and inulin; probiotic viable count was not the primary reported exposure.	8 weeks	Fasting insulin and HOMA-IR decreased; QUICKI, TC, and TG improved, indicating enhanced insulin sensitivity.

Abbreviations: CFU, colony-forming units; FPG, fasting plasma glucose; HbA1c, glycated hemoglobin; HOMA-IR, homeostatic model assessment of insulin resistance; QUICKI, quantitative insulin sensitivity check index; TC, total cholesterol; TG, triglycerides; GLP-1, glucagon-like peptide 1; GLP-2, glucagon-like peptide 2. Viable counts are reported when available from the cited article or trial summary; “not specified” indicates that the count was not clearly reported in the source reviewed.

3.2. Lipid Profile, Oxidative Stress, and Gut Barrier Mechanisms

In response to the reviewer's request, this section was expanded beyond a descriptive discussion of lipid profile outcomes to include the principal lipid classes in yogurt, their generalized chemical structures, and the oxidative reactions through which lipids can participate in metabolic stress [20–22]. The major lipid fraction in whole-milk yogurt is derived from milk fat, which is dominated by triacylglycerols, while smaller but biologically relevant fractions include phospholipids, cholesterol, free fatty acids, monoacylglycerols, diacylglycerols, and sphingolipids located partly within or derived from the milk-fat globule membrane [23–25]. Although the exact lipid profile depends on milk source, fat level, processing, starter culture, storage, and fortification, the relevant chemical consideration for T2DM is not simply total fat content but the susceptibility of different lipid species to oxidation and their ability to modulate inflammation, bile-acid signaling, membrane function, and insulin signaling.

In brief, yogurt lipids are dominated by triacylglycerols, which consist of a glycerol backbone esterified with three fatty acyl chains. These acyl chains may include saturated fatty acids such as palmitic acid (C16:0), monounsaturated fatty acids such as oleic acid (C18:1 *cis*-9), and polyunsaturated fatty acids such as linoleic acid (C18:2 *n*-6). This distinction is mechanistically important because polyunsaturated fatty acids contain bis-allylic hydrogen atoms that are more vulnerable to radical-mediated oxidation, whereas saturated fatty acids are chemically less prone to peroxidation but may still contribute to inflammatory and ectopic lipid signaling when consumed in excess [26–28].

The oxidative involvement of yogurt lipids can therefore be explained through a lipid-peroxidation chain process rather than by listing complex formulas in the narrative. Under hyperglycemic and inflammatory conditions, mitochondrial overload, NADPH oxidase activity, and metal-catalyzed reactions increase reactive oxygen species generation [29]. These reactive species initiate hydrogen abstraction from susceptible polyunsaturated fatty-acyl chains, producing lipid radicals that react with oxygen and propagate damage to neighboring lipids [30]. The resulting lipid hydroperoxides may decompose into malondialdehyde, 4-hydroxy-2-nonenal, and oxidized phospholipids, which can modify proteins, disturb membranes, amplify NF- κ B/JNK-related inflammation, and impair insulin-receptor substrate signaling [31–33].

A simplified lipid-peroxidation pathway linking yogurt lipid chemistry, oxidative stress, and insulin signaling in T2DM.

Step 1—ROS generation: Hyperglycemia, mitochondrial overload, NADPH oxidase activity, and transition-metal reactions increase superoxide, hydrogen peroxide, and hydroxyl-radical formation.

Step 2—Initiation: Reactive species abstract hydrogen from susceptible polyunsaturated fatty-acyl chains, forming lipid radicals.

Step 3—Propagation: Lipid radicals react with oxygen and attack neighboring lipids, producing lipid hydroperoxides and sustaining the oxidative chain reaction.

Step 4—Decomposition: Lipid hydroperoxides break down into malondialdehyde, 4-hydroxy-2-nonenal, and oxidized phospholipids.

Step 5—Metabolic consequence: Lipid-derived oxidation products activate inflammatory signaling, alter membrane and mitochondrial function, and weaken insulin signaling and GLUT4-mediated glucose uptake.

These reactions are relevant to probiotic yogurt as changes in lipid profile and oxidative stress markers have been reported in several studies; however, the interpretation requires caution. Ejtahed et al. [13] reported improved antioxidant status and reduced MDA after probiotic yogurt intake, whereas Ruan et al. [25] observed reduced TNF- α com-

bined with improved HbA1c. Such findings are consistent with lower oxidative and inflammatory stress, yet they do not prove that milk lipids themselves were the direct mediators. A more plausible model is that yogurt affects multiple compartments simultaneously: microbial modulation may reduce endotoxin-driven inflammation; antioxidant enzyme activity may reduce lipid peroxidation; and changes in bile acid or cholesterol handling may influence serum lipid profile [29,32].

Lipids also mediate insulin resistance through non-oxidative and oxidative mechanisms. Excess intracellular diacylglycerol and ceramide can activate protein kinase C isoforms, stress kinases, or inflammatory signaling, leading to inhibitory serine phosphorylation of insulin receptor substrate proteins and reduced PI3K-Akt signaling [4,5]. Oxidized lipids and aldehydes such as MDA and 4-HNE can form adducts with proteins and phospholipids, amplify NF- κ B-related inflammatory signaling, and impair membrane and mitochondrial function [34–37]. Therefore, probiotic yogurt may improve lipid-related metabolic risk only when its formulation reduces oxidative/inflammatory tone or improves lipid handling sufficiently to overcome the potential adverse contribution of excess saturated fat, added sugar, or energy intake.

From a review perspective, the lipid evidence supports a balanced conclusion. Favorable changes in total cholesterol, LDL-C, triglycerides, HDL-C, antioxidant enzymes, or MDA suggest biological activity in some trials [13–18,38]; however, these effects are not universal and cannot be generalized to all probiotic yogurts. The authors of future studies should report the yogurt lipid composition, fat percentage, fatty-acid profile, phospholipid/cholesterol content, added sugar, viable probiotic counts, and oxidative markers at baseline and follow-up. Without these data, improvements in serum lipid profile cannot be confidently attributed to probiotic action, dairy lipid chemistry, reduced inflammation, dietary substitution, or changes in total energy intake.

3.3. Effect of GLUT4, Tumor Necrosis Factor-Alpha (TNF-alpha), and Interleukin-6 (IL-6): Critical Interpretation

The previous version of this section incorporated author–year citations and included material that was not sufficiently connected to T2DM. The section has therefore been rewritten using numerical citations and a more critical comparison of evidence. GLUT4 is the major insulin-responsive glucose transporter in skeletal muscle and adipose tissue; its metabolic relevance depends not only on gene expression but also on insulin receptor activation, IRS-1/PI3K/Akt signaling, AS160/TBC1D4 regulation, vesicle trafficking, and translocation of GLUT4 protein to the plasma membrane [7,39,40]. Therefore, changes in blood glucose should not be interpreted as evidence of improved GLUT4 function unless transporter abundance, translocation, or insulin-signaling intermediates are directly assessed.

The preclinical study by Setiawan et al. [11] is noteworthy because the authors examined fermented cow- and soy-milk yogurt formulations in relation to blood glucose and GLUT4 gene expression in rat soleus muscle. However, its relevance to T2DM patients must be framed carefully. First, the study was conducted in an animal model rather than in human participants. Second, the reported glucose-lowering effects were not uniformly accompanied by parallel increases in GLUT4 expression across all treatment groups. This discrepancy suggests that the metabolic effect of fermented yogurt may involve post-transcriptional GLUT4 regulation, GLUT4 translocation, improved insulin receptor sensitivity, changes in hepatic glucose output, altered gut-derived metabolites, or reduced oxidative stress rather than simple upregulation of GLUT4 mRNA alone [5,41–43].

The inflammatory pathway requires similar critical interpretation. TNF-alpha and IL-6 can impair insulin action by activating JNK, IKK-beta, SOCS proteins, and NF- κ B-related pathways, which can promote inhibitory serine phosphorylation of IRS proteins

and weaken downstream insulin signaling [37–39,44]. However, cytokines are not interchangeable endpoints. TNF-alpha, IL-6, hs-CRP, IL-1beta, and resistin differ in tissue source, half-life, assay variability, and responsiveness to diet. Thus, a probiotic yogurt intervention may reduce one inflammatory marker without producing parallel changes in all markers.

In the T2DM yogurt trial by Ruan et al. [25], consumption of probiotic yogurt significantly reduced HbA1c and TNF-alpha, whereas IL-6 and hs-CRP responses were not equally robust. This pattern strengthens the argument that probiotic yogurt may influence inflammatory tone; however, it also prevents overgeneralization. Rather than claiming a broad anti-inflammatory effect, the evidence should be interpreted as marker-specific and formulation-specific. The result is compatible with reduced endotoxin/TLR4-related inflammatory signaling. However, the trial did not directly measure LPS translocation, TLR4 activation, NF-kB activity, or microbiome-mediated metabolites; therefore, the causal pathway remains inferential [9,14,39].

Comparison with the antioxidant yogurt trial by Ejtahed et al. [13] provides an important mechanistic bridge. Reduced MDA and improved antioxidant enzyme activities may preserve insulin-signaling proteins from oxidative modification, while reduced TNF-alpha may lessen inflammatory interference with IRS-1 and Akt. Nevertheless, the two trials measured different endpoints and cannot be combined as if they demonstrated a single complete mechanism. The current literature supports a coherent hypothesis linking probiotic yogurt, redox balance, inflammation, and insulin sensitivity; however, it does not yet establish a fully demonstrated causal sequence in humans.

3.4. Integrated Mechanistic Overview and Research Gaps

The mechanisms by which probiotic yogurt may influence insulin sensitivity should be viewed as an integrated gut–metabolic network rather than a single linear pathway (Figure 1). The first component is microbial ecology. Administered strains may compete with pathobionts, produce organic acids or bacteriocins, alter luminal pH, participate in cross-feeding, and shift substrate availability for resident microorganisms [45,46]. When fermentable substrates such as inulin or konjac glucomannan are present, colonic fermentation may increase short-chain fatty acid (SCFA) production, particularly acetate, propionate, and butyrate [18,46,47].

The second component is the gut barrier. Butyrate supports colonocyte energy metabolism and can strengthen tight-junction integrity, while reduced barrier permeability may decrease systemic exposure to lipopolysaccharide (LPS) and other microbial products [9,48,49]. This factor is important for insulin sensitivity because LPS can activate TLR4/NF-kB signaling, increase TNF-alpha and IL-6 production, and promote stress-kinase pathways that interfere with insulin receptor substrate signaling [9,37–39]. Thus, improved barrier function is a plausible upstream mechanism linking yogurt-associated microbiota changes to systemic metabolic effects.

The third component is redox and lipid chemistry. Hyperglycemia, inflammation, and mitochondrial overload promote reactive oxygen species formation, while susceptible polyunsaturated lipids undergo peroxidation to generate lipid hydroperoxides, MDA, 4-HNE, and oxidized phospholipids [34–40]. These products may impair membrane function, mitochondrial activity, and insulin signaling [41–45]. Probiotic yogurt trials reporting lower MDA or improved antioxidant enzymes therefore fit the proposed mechanism; however, direct mediation remains unproven unless oxidative markers are measured in combination with microbiome, lipid [46–48], and insulin-sensitivity endpoints [48].

The fourth component is enteroendocrine and glucose-transport signaling. Some probiotics can modulate GLP-1, GLP-2, insulin, and C-peptide responses in humans [19,49]. GLP-1 may improve glucose-dependent insulin secretion, whereas GLP-2 may support intestinal barrier function. Downstream, improved inflammatory and redox status could

preserve IRS-1/PI3K/Akt signaling and support GLUT4 translocation in muscle and adipose tissue [5,44,45]. However, the direct clinical evidence for yogurt-induced GLUT4 improvement remains indirect; preclinical GLUT4 findings should be used to support mechanistic plausibility rather than to claim direct clinical efficacy [47,49].

Integrated Mechanism Linking Probiotic Yogurt to Insulin Sensitivity in T2DM

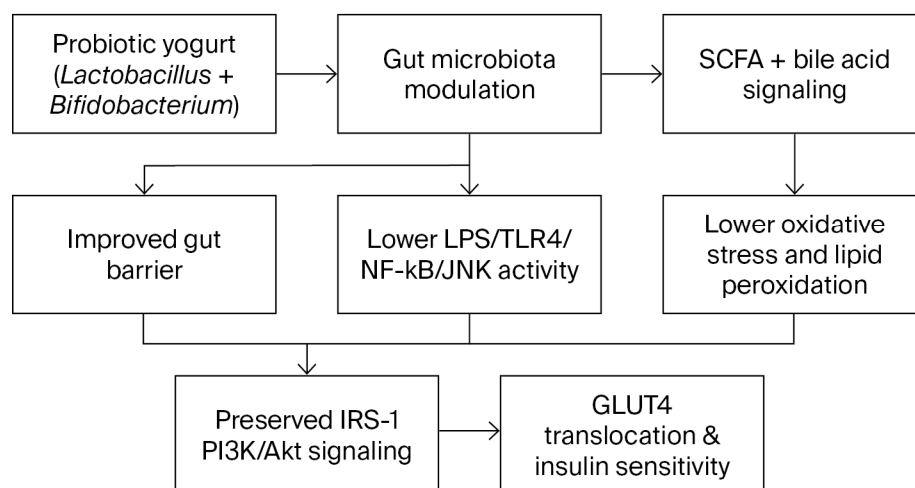


Figure 1. Integrated mechanistic overview of how probiotic yogurt may influence insulin sensitivity in T2DM through microbiota modulation, SCFA production, gut barrier reinforcement, inflammatory signaling, oxidative stress control, lipid-peroxidation reduction, incretin signaling, and GLUT4-mediated glucose uptake.

4. Conclusions

In this review, we synthesized evidence from clinical trials, meta-analyses, and mechanistically relevant preclinical studies to evaluate the role of reliable microbiota consortia in probiotic yogurt for improving insulin sensitivity in T2DM patients. The available evidence indicates that probiotic yogurt containing selected *Lactobacillus* and *Bifidobacterium* consortia contributes to improved metabolic control in T2DM, primarily through more consistent reductions in HbA1c and improvements in lipid profile, with additional benefits in fasting insulin, HOMA-IR, and QUICKI observed particularly in synbiotic formulations enriched with prebiotic substrates such as inulin and konjac glucomannan.

The mechanistic plausibility of these effects is substantiated by multiple interrelated pathways: restoration of gut microbiota balance, increased SCFA production, reinforcement of intestinal barrier function, attenuation of systemic inflammation and endotoxemia, incretin-mediated improvements in insulin and C-peptide secretion, and enhancement of antioxidant capacity. Synbiotic formulations that pair probiotic organisms with selectively fermentable substrates appear to amplify these mechanisms, suggesting that prebiotic inclusion should be prioritized in the design of functional probiotic yogurt for metabolic health.

Probiotic yogurt can serve as an alternative functional food that supports efforts to control blood glucose levels due to the ability of probiotics such as *Lactobacillus* and *Bifidobacterium* to improve the balance of the gut microbiota, reduce inflammation, and increase insulin sensitivity, thus improving glucose metabolism. Furthermore, the protein and fat content in yogurt also aids in slowing carbohydrate absorption and reducing post-meal blood glucose spikes. However, the authors believe that these benefits are not independent of the type of yogurt consumed, with low- or no-sugar products being preferred for optimal blood glucose control. Public efforts to reduce sugar consumption are also an important step in maintaining stable blood glucose levels. High sugar consumption can induce rapid increases in blood glucose and, when sustained over time, can trigger insulin

resistance and increase the risk of type 2 diabetes mellitus. Therefore, the authors believe that shifting consumption patterns toward low-sugar foods, including probiotic yogurt without added sugar, is not simply a healthy lifestyle trend but rather a rational preventive measure to maintain public metabolic health.

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