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Review Article

Probiotic *Lactobacillus* sp. as a strategy for modulation of non-comorbid obesity: A systematic meta-analysis and GRADE assessment of randomized controlled trials

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Abstract

Given the high prevalence of obesity worldwide, effective therapeutic strategies are crucial to prevent and manage obesity-related health conditions. Existing studies indicate that *Lactobacillus* sp. showed beneficial effects on body weight and adiposity by modifying the gut microbiota; however, no meta-analysis has been conducted assessing the efficacy of *Lactobacillus* sp-based probiotics on anthropometric parameters, leptin and adiponectin levels, and gut microbiota composition. The aim of this study was to evaluate the efficacy and safety of probiotic supplementation with *Lactobacillus* sp. in obese individuals without comorbidities. A systematic search was conducted on November 28, 2024, using five databases: PubMed, Wiley, ScienceDirect, Epistemonikos, and Cochrane. Primary outcomes included changes in body mass index (BMI), body weight, waist and hip circumferences, visceral and subcutaneous fat areas, and total body fat content. Secondary outcomes included alterations in leptin and adiponectin levels, gut microbiota composition, and the incidence of adverse events. A total of 1,058 individuals were included across 12 clinical trials. Significant reductions were observed in BMI (mean difference (MD): -0.40 kg/m^2; 95%CI: -0.48–(-0.32), p<0.00001), body weight (MD: -1.16 kg; 95%CI: -1.79–(-0.53), p=0.0003), waist circumference (MD: -1.41 cm; 95%CI: -1.75–(-1.08), p<0.00001), and hip circumference (MD: -0.85 cm; 95%CI: -1.09–(-0.61), p<0.00001) compared to controls. Additionally, compared to control group, significant reductions were observed in visceral and subcutaneous fat mass (MD: -7.35; 95%CI: -9.95–(-4.75); p<0.00001) and overall body fat (MD: -1.11; 95%CI: -1.31–(-0.91); p<0.00001). Leptin levels significantly decreased (MD: -2.11 µg/mL; 95%CI: -3.59–(-0.64), p=0.005) compared to before *Lactobacillus* sp. supplementation, while adiponectin levels increased (MD: 0.71 µg/mL; 95%CI: 0.22–1.20, p=0.004) following *Lactobacillus* sp. supplementation compared to placebo group. No significant adverse events were reported in either the intervention or control groups. In conclusion,

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Lactobacillus sp. probiotic supplementation may serve as an adjuvant therapy to enhance obesity management in non-comorbid obese individuals.

Keywords: Overweight, obesity, *Lactobacillus* sp., body mass index, excessive calorie intake

Introduction

Obesity is a chronic condition that arises when calorie intake consistently exceeds energy expenditure, leading to excessive fat accumulation in the body [1,2]. According to the World Health Organization (WHO), approximately 650 million individuals worldwide are classified as obese, with an additional 1.9 billion categorized as overweight [3]. Obesity is closely associated with a low-grade systemic inflammatory state, which plays a critical role in the initiation and progression of various health complications, including cardiovascular disease (CVD), type 2 diabetes mellitus (T2DM), and cognitive decline [4-6]. These inflammatory processes significantly contribute to the onset and development of obesity-related comorbidities [7]. Central obesity is the most frequently observed component of metabolic syndrome in affected individuals [8].

Hormonal imbalances, such as decreased adiponectin and increased leptin levels, contribute to obesity-related comorbidities [9,10]. Consequently, effective therapeutic strategies are essential to prevent and manage these associated health conditions in individuals with obesity [9]. Emerging evidence highlighted the relationship between alterations in gut microbiota composition and weight loss [10,11]. The gut microbiota has been increasingly recognized as a pivotal determinant in metabolic diseases and obesity [12]. Healthy individuals typically exhibit a higher abundance of Bacteroidetes bacteria, whereas obese individuals show an increased prevalence of Firmicutes bacteria [13]. Alterations in gut microbiota, particularly an elevated Firmicutes-to-Bacteroidetes ratio, are strongly associated with obesity, highlighting the microbiota's role in metabolic diseases and weight regulation [14].

Strategies to address gut microbiota dysbiosis include prebiotics, probiotics, and synbiotics [15,16], with *Lactobacillus* sp. being the most used probiotic to modulate the Firmicutes-to-Bacteroidetes ratio [17]. *Lactobacillus* sp., a Gram-positive, anaerobic bacterium naturally present in the human gastrointestinal tract, is influenced by dietary patterns, which can affect gut microbiome composition, diversity, body weight, and obesity development [15,18,19]. *Lactobacillus* sp. confer several metabolic benefits, including reductions in body fat mass, weight, and cholesterol levels [15,20]. A previous study has demonstrated that *Lactobacillus* sp. supplementation can improve low-density lipoprotein (LDL), total cholesterol, fasting plasma glucose, and triglycerides in overweight or obese individuals under specific conditions [21]. However, a comprehensive meta-analysis is yet to be conducted to evaluate the effects of *Lactobacillus* sp. supplementation on anthropometric parameters, leptin and adiponectin levels, and gut microbiota composition.

The mechanistic role of *Lactobacillus* sp. in mitigating obesity among non-comorbid individuals involves promoting lipid oxidation, improving insulin resistance, modulating inflammatory pathways, regulating gene expression related to leptin and adiponectin, and enhancing immune function [22,23]. However, these mechanisms remain complex and dynamically evolving, particularly in achieving intestinal microbiome homeostasis to prevent metabolic syndrome. The aim of this study was to assess the efficacy and safety of *Lactobacillus* sp. supplementation in obese individuals without comorbidities, focusing on anthropometric parameters, changes in leptin and adiponectin levels, gut microbiota composition, and adverse effects.

Methods

Study design and registration

This systematic review and meta-analysis adhered to the preferred reporting items for systematic reviews and meta-analyses (PRISMA) guidelines [24], and were registered with International

Prospective Register of Systematic Reviews – National Institute for Health Research (PROSPERO-NIHR) under the registered number CRD42023460820.

Search strategy

A systematic literature search was conducted across five databases, including PubMed, Cochrane, Wiley, Epistemonikos, and ScienceDirect, as of November 28, 2024. Randomized controlled trials (RCTs) were retrieved from medical databases using the Boolean operator "Lactobacillus" AND "obesity". Detailed keyword combination used are presented in **Table 1**.

Table 1. Combined keywords employed in each database

Database	Keywords
PubMed	((("lactobacillus"[MeSH Terms] OR "lactobacillus"[All Fields]) AND ("obeses"[All Fields] OR "obesity"[MeSH Terms] OR "obesity"[All Fields] OR "obese"[All Fields] OR "obesities"[All Fields] OR "obesity s"[All Fields] OR ("overweight"[MeSH Terms] OR "overweight"[All Fields] OR "overweighted"[All Fields] OR "overweightness"[All Fields] OR "overweights"[All Fields]))) AND (randomizedcontrolledtrial [Filter])
Cochrane	#1 ("Lactobacillus"):ti,ab,kw AND (obesity):ti,ab,kw AND (overweight):ti,ab,kw #2 ("Lactobacillus"):ti,ab,kw AND (obesity):ti,ab,kw AND (overweight):ti,ab,kw AND ("randomised controlled trials"):ti,ab,kw
Wiley	Lactobacillus anywhere and "Obesity" anywhere; Type of publication: journal [Publication title: Lactobacillus] AND [Publication title: obesity]
Epistemonikos	Lactobacillus AND obesity; Filters: primary study
ScienceDirect	Lactobacillus AND obesity; Filters: article type - research articles, publication title -The Journal of Nutrition, subject areas - medicine and density, and open access.

Eligibility criteria

Eligible studies involved individuals diagnosed with obesity without comorbidities, using *Lactobacillus* sp. probiotic therapy, with no restrictions on dosage or administration methods. Comparisons were made against a placebo or other eligible biomaterials. Primary outcomes included body mass index (BMI), body weight, waist and hip circumferences, visceral and subcutaneous fat areas, and total body fat content, while secondary outcomes were leptin and adiponectin levels, adverse effects, and microbiota composition. Only RCTs were included, while case reports, observational studies, animal studies, technical studies, and reviews were excluded.

Data screening and selection

Duplicate search results were removed using Zotero v.6.0.26 (https://www.zotero.org/). Title and abstract screening were conducted independently by four reviewers according to the predetermined inclusion/exclusion criteria (DV, JAMNL, KBS, and DDCHR). Any discrepancies among the reviewers were resolved through discussion to reach consensus. Studies were then screened, extracted, analyzed, and synthesized to obtain qualitative and quantitative data.

Data extraction

The following data were extracted: (1) author and year of publication; (2) country; (3) study design; (4) participant characteristics and sample size; (5) age of participants; (6) BMI prior to intervention; (7) *Lactobacillus* sp. type strain (*L. plantarum* K50, *L. plantarum* LMT1-48, *L. gasseri* BNR17, *L. gasseri* SBT2055, *L. sakei* CJLS03, *L. rhamnosus* CGMCC1.3724 (LPR), *L. sakei* DW2010, and *L. reuteri*); (8) route of administration; (9) dosage; (10) follow-up duration; and (11) control group. Outcomes of interest were extracted, including BMI, body weight, waist and hip circumferences, visceral and subcutaneous fat areas, total body fat content, leptin and adiponectin levels, adverse effects, and microbiota composition. Low dose was categorized as below ten billion colony-forming units (CFUs), while high dose was categorized as exceeding ten billion CFUs.

Statistical analysis

Review Manager 5.4 software (Cochrane Collaboration, Oxford, UK) was used for the meta-analysis. Clinical outcomes from continuous data were reported as mean difference (MD) and a 95% confidence interval (95%CI) and presented using a forest plot, with $p<0.05$ considered statistically significant. The I^2 method was used to calculate statistical heterogeneity (25% was

considered low heterogeneity, 25–50% moderate heterogeneity, and >50% high heterogeneity). A random effects model was used for further analysis if significant heterogeneity (I^2>50%) was found.

Quality assessment

Four independent investigators (DV, JAMNL, KBS, and DDCHR) performed the quality assessment, resolving discrepancies through consensus. The risk of bias in the included studies was assessed using the Revised Tool for Risk of Bias in Randomized Trials (RoB 2.0) [25]. The RoB 2.0 tool, a revised version of the Cochrane risk-of-bias tool, specifically assesses bias risk in RCTs, evaluating domains such as the randomization process, deviations from intended interventions, missing outcome data, outcome measurement, and selection of reported results. Each domain is assessed through signaling questions, determining the risk level as low risk, some concerns, or high risk. Studies rated as low risk across all domains are considered reliable, while those with high risk in any domain raise substantial concerns about validity. Low-quality studies were excluded.

Furthermore, the Grading of Recommendations Assessment, Development, and Evaluation (GRADE) methodology [26] was applied to summarize the evidence and assess confidence levels. It evaluated five factors: (1) risk of bias, based on the quality of the primary studies; (2) inconsistency, determined by heterogeneity and I^2 statistics; (3) indirectness, considering the applicability of findings to the studied populations; (4) imprecision, based on sample size and study number; and (5) publication bias, assessed through comparison of effect sizes and funnel plot symmetry. The GRADE assessment was conducted independently by four independent investigators (DV, JAMNL, KBS, and DDCHR), who collectively agreed on the final outcome. Outcomes were categorized as not reported, neutral, serious, or very serious, with meta-analyses downgraded by one or two points accordingly. Final classifications were 'high' (4 points), 'moderate' (3 points), 'low' (2 points), or 'very low' (≤1 point).

Results

Study selection process

A total of 444 records were identified from five databases: PubMed (n=104), Cochrane (n=52), Wiley (n=35), Epistemonikos (n=150), and ScienceDirect (n=103) (**Figure 1**). After removing 19 duplicate records, 425 records were screened. All 406 records were excluded during the screening process. Subsequently, 19 records were sought for retrieval and assessed for eligibility. Of these, three records were excluded due to the inclusion of obese individuals with non-alcoholic fatty liver disease (NAFLD) [27-29], one due to obese individual with polycystic ovary syndrome (PCOS) [30], and three due to the use of probiotic products other than *Lactobacillus* sp. [31-33]. Finally, 12 studies were included in the review [12,13,15,18,34-41].

Study characteristics

Studies conducted between 2010 and 2023 included sample sizes of 21 to 210 individuals and follow-up durations of 8 to 90 days (**Table 2**). The intervention group consisted of 237 females and 183 males, with an average age of 42.69 years and a BMI of 29.18 kg/m^2, while the control group had 212 females and 193 males, averaging 56.6 years and a BMI of 28.15 kg/m^2. All participants were obese without comorbidities (**Table 2**). Lower doses included daily supplementation of 2 billion, 4 billion, and 6 billion CFUs, while higher doses ranged from 10 billion to 50 billion CFUs (**Table 3**). Various *Lactobacillus* strains, including *L. plantarum*, *L. gasseri*, *L. sakei*, *L. rhamnosus*, and *L. reuteri*, were administered orally in forms such as capsules, fermented milk, and probiotic powders, with dosages ranging from 1×10^6 to 5×10^{10} CFU/day. Follow-up periods varied, with most studies lasting 12 weeks. Control groups received placebo treatments that mimicked the probiotic delivery methods, such as non-active capsules or fermented milk (**Table 3**).

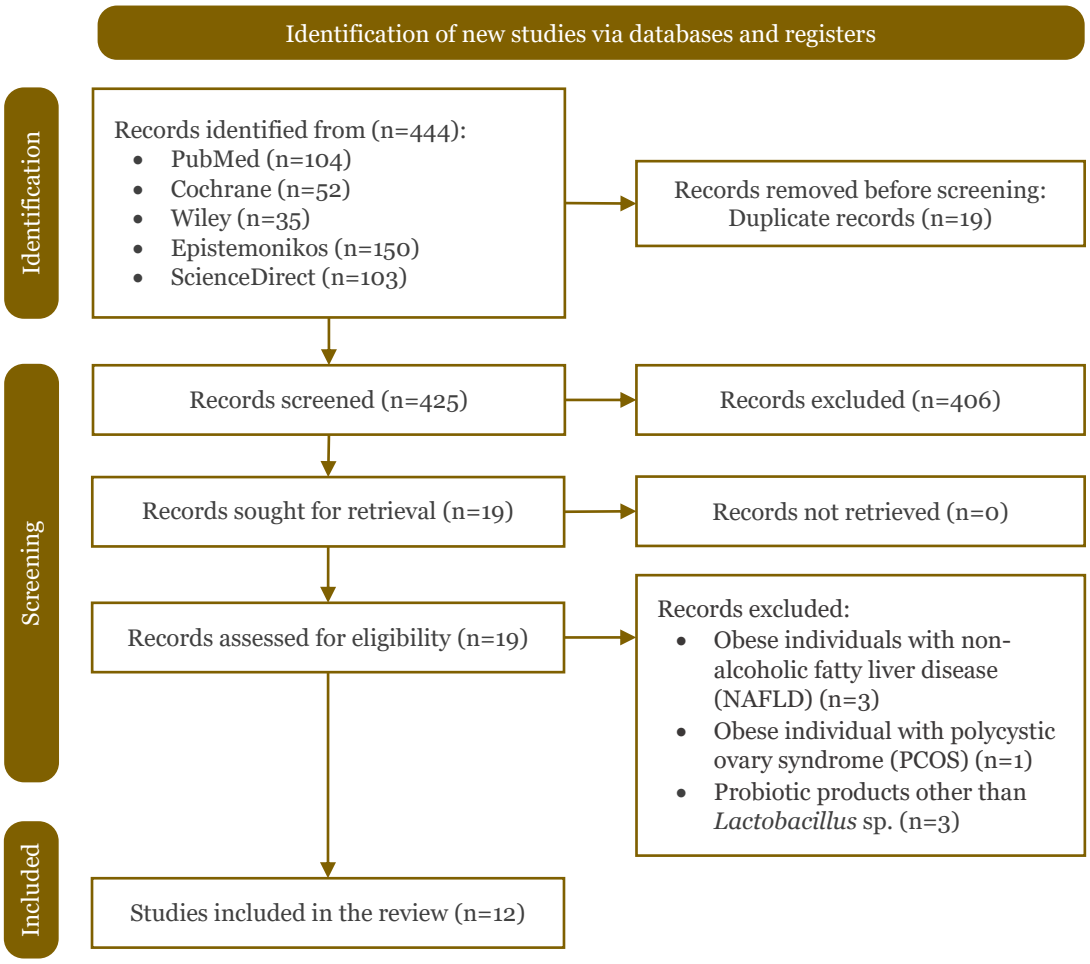

Figure 1. PRISMA flow diagram illustrating the systematic study selection and inclusion process.

Risk of bias

Eight of the 12 included studies had low risk of bias [12,13,18,34,38,39,42,43], ensuring high confidence in the findings, while four studies had some concerns [12,15,35,36], primarily related to deviations from intended interventions (**Figure 2**). The GRADE assessment revealed high-quality evidence for body fat area and weight, and moderate-quality evidence for BMI, waist and hip measurements, body fat percentage, leptin, and adiponectin (**Table 4**). Subgroup analyses were limited by small sample sizes for weight outcomes at weeks 6, 12, and 24 (**Table 4**).

Efficacy of *Lactobacillus* sp. supplementation on anthropometric indicators in non-comorbid obese patients

Body mass index

Meta-analysis comparing BMI between the *Lactobacillus* sp. supplementation group and the placebo group demonstrated a significant reduction in BMI with *Lactobacillus* sp. supplementation group (MD: -0.40 kg/m^2; 95%CI: -0.48–(-0.32), p<0.00001), with data exhibited high heterogeneity (I^2=69%, p-heterogeneity of 0.001) (**Figure 3**).

Body weight

At the 6-week follow-up, *Lactobacillus* sp. supplementation did not demonstrate a significant reduction in weight compared to placebo (MD: 0.40 kg; 95%CI: -18.66–19.46; p=0.970) (**Figure 4**). Similarly, at the 8-week follow-up, while there was a trend toward weight reduction, it was not statistically significant compared to placebo group (MD: -1.00 kg; 95%CI: -20.29–18.29, p=0.920). However, at the 12-week follow-up, *Lactobacillus* sp. supplementation significantly reduced weight compared to placebo (MD: -1.13 kg; 95%CI: -1.80–(-0.45), p=0.001), with data showing low heterogeneity (I^2=0%, p-heterogeneity of 0.510).

Table 2. Characteristics of the included studies

Author, year	Country	Sample			Sex (female/male), n		Age (years), mean±SD/median (min-max)		BMI (kg/m²), mean±SD/median (min-max)	
		Sample characteristic	Number of sample, n							
			IG	CG	IG	CG	IG	CG	IG	CG
Kadooka *et al.*, 2010 [35]	Japan	Men and women with a BMI ranging from 24.2 to 30.7 kg/m² and a visceral fat area of 81.2 to 178.5 cm²	43	44	14/29	14/30	48.3±9.3	49.2±9.1	27.5±1.7	27.2±1.7
Jung *et al.*, 2013 [12]	South Korea	Men and non-pregnant women with a BMI ≥23 kg/m² and fasting blood glucose levels ≥100 mg/dL	28	29	15/13	20/9	37.84±14.49	40.72±17.28	29.6±3.6	28.6±2.2
Kadooka *et al.*, 2013 [35]	Japan	Healthy men and women with visceral fat areas ranging from 80.2 to 187.8 cm²	140	70	36/35	35/35	46.9±7.4 (low dose group 1: 1×10^7 CFU/day), 47.2±7.4 (low dose group 2: 1×10^6 CFU/day)	47.4±7.0	27.5±1.9/27.2±1.8	27·2±1.9
Sanchez *et al.*, 2014 [37]	Canada	Men and women with a BMI ranging from 29 to 41 kg/m²	62	63	38/24	39/34	35.0±10.0	37.0±10.0	33.8±3.3	33.3±3.2
Simon *et al.*, 2015 [40]	Germany	BMI categories of 19–25 kg/m² and 30–45 kg/m²	10	11	5/5	6/5	51.0±7.0	49.0±7.0	35.5±4.9	23.6±1.7
Kim *et al.*, 2018 [38]	South Korea	BMI categories of 25 kg/m² and 35 kg/m²	60	30	24/6 (low dose), 23/7 (high dose)	16/14	39.3 (35.0–43.6)	38.1 (34.1–42.2)	27.9 (27.0–28.7)	28.6 (27.7–29.8)
Lim *et al.*, 2020 [18]	South Korea	Men and women with a BMI ≥25 kg/m²	57	48	NA	NA	46.4±12.2	47.2±11.2	28.5±2.4	28.3±2.4
Rahayu *et al.*, 2021 [39]	Indonesia	Men and women with a BMI ≥25 kg/m²	30	30	28/12	28/12	44.07±6.32	44.67±5.66	32.69±5.07	31.88±3.77
Mo *et al.*, 2022 [34]	South Korea	Men and women with a BMI between ≥23 kg/m² and <35 kg/m²	30	29	5/25	8/21	35.7±1.44	39.34±1.61	26.87±0.52	26.81±0.47
Sohn *et al.*, 2022 [13]	South Korea	Healthy men and women with a BMI ranging from 25 to 30 kg/m²	41	40	25/16	24/16	47.8±11.7	45.5±10.0	27.1±1.5	27.3±1.6
Oh *et al.*, 2023 [41]	South Korea	Men and women with a BMI between ≥25 kg/m² and <30 kg/m²	35	39	24/11	22/17	39.9±9.7	42.1±10.0	27.20±1.53	27.09±1.56
Sohn *et al.*, 2023 [15]	South Korea	BMI between ≥25 and <30 kg/m²	50	49	21/29	21/28	40.2±11.2	40.1±10.5	27.1±1.5	27.3±1.6

BMI: body mass index; CG: control group; IG: intervention group

Table 3. Outcome of interest from the included studies

Author, year	Intervention type	Route of administration	Dosage	Follow-up (weeks)	Control
Kadooka *et al.*, 2010 [35]	Administration of two portions of active *L. gasseri* SBT2055 in fermented milk	Oral	5×10^{10} CFU/day (high dose)	12	Placebo
Jung *et al.*, 2013 [12]	Administration of six *gasseri* BNR17 capsules	Oral	6×10^{9} CFU/day (low dose)	12	Placebo
Kadooka *et al.*, 2013 [35]	Administration of two portions of active *L. gasseri* SBT2055 in fermented milk	Oral	1×10^{7} CFU/day, 1×10^{6} CFU/day (low dose)	12	Administration of non-active fermented milk capsules
Sanchez *et al.*, 2014 [37]	Administration of two LPR capsules (*L. rhamnosus* CGMCC1.3724)	Oral	3.24×10^{8} CFU/day (low dose)	12 and 24	Placebo
Simon *et al.*, 2015 [40]	Administration of one *L. reuteri* caplet encapsulated	Oral	2×10^{9} CFU/day (low dose)	8	Placebo
Kim *et al.*, 2018 [38]	Administration of two *L. gasseri* BNR17 capsules	Oral	1×10^{9} CFU/day, 1×10^{10} CFU/day (low dose and high dose)	12	Placebo
Lim *et al.*, 2020 [18]	Administration of two CJLS03 capsules (*L. sakei* CJLS03)	Oral	1×10^{9} CFU/day (low dose)	12	Placebo
Rahayu *et al.*, 2021 [39]	Administration of one sachet of probiotic powder containing *L. plantarum* Dad-13	Oral	2×10^{9} CFU/day (low dose)	90 days	Placebo
Mo *et al.*, 2022 [34]	Administration of one probiotic capsule containing *L. curvatus* HY7601 and *L. plantarum* KY1032	Oral	5×10^{9} CFU/day (low dose)	12	Placebo
Sohn *et al.*, 2022 [13]	Administration of two LPK capsules (*L. plantarum* K50)	Oral	4×10^{9} CFU/day (low dose)	12	Placebo
Oh *et al.*, 2023 [41]	Administration of one DW2010 capsule (*L. sakei* OK67)	Oral	1×10^{10} CFU/day (high dose)	12	Placebo
Sohn *et al.*, 2023 [15]	Administration of two LMT1-48 capsules (*L. plantarum* LMT1-48)	Oral	1×10^{10} CFU/day (high dose)	12	Placebo

Table 4. GRADE profile of *Lactobacillus* sp. probiotic supplementation for the modulation of non-comorbid obesity: Effect on body mass index (BMI), body weight, waist circumference, hip circumference, body fat mass, fat area, visceral fat, subcutaneous fat, adiponectin, and leptin hormone levels

Variables	Number of studies	Risk of bias	Inconsistency	Indirectness	Imprecision	Publication bias	Total number (intervention/control)	Quality of evidence	Mean difference (95%CI)
Body mass index (BMI)	9	Not serious	Serious[a]	Not serious	Not serious	Not serious limitation	772 (383/389)	⊕⊕⊕◯ Moderate	-0.4 (-0.32, -0.48)
Body weight (kg)	12	Not serious	Not serious	Not serious	Not serious	Not serious limitation	891 (440/451)	⊕⊕⊕⊕ High	-1.16 (-0.53, -1.79)
Waist circumference (cm)	10	Not serious	Serious[a]	Not serious	Not serious	Not serious limitation	878 (439/439)	⊕⊕⊕◯ Moderate	-1.41 (-1.08, -1.75)
Hip circumference (cm)	7	Not serious	Serious[a]	Not serious	Not serious	Not serious limitation	603 (301/302)	⊕⊕⊕◯ Moderate	-0.85 (-0.61, -1.09)
Body fat mass	11	Not serious	Serious[a]	Not serious	Not serious	Not serious limitation	1,395 (690/705)	⊕⊕⊕◯ Moderate	-1.11 (-0.91, -1.31)
Body fat mass (kg)	7	Not serious	Serious[a]	Not serious	Not serious	Not serious limitation	736 (365/371)	⊕⊕⊕◯ Moderate	-1.14 (-0.89, -1.4)
Body fat percentage (%)	8	Not serious	Serious[a]	Not serious	Not serious	Not serious limitation	659 (325/334)	⊕⊕⊕◯ Moderate	-1.1 (-0.71, -1.48)

Variables	Number of studies	Risk of bias	Inconsistency	Indirectness	Imprecision	Publication bias	Total number (intervention/control)	Quality of evidence	Mean difference (95%CI)
Fat mass area (cm^2)	9	Not serious	Serious[a]	Not serious	Not serious	Not serious limitation	1,280 (638/642)	⊕⊕⊕⊕ High	-7.35 (-4.75, -9.95)
Visceral fat	9	Not serious	Serious[a]	Not serious	Not serious	Not serious limitation	832 (414/418)	⊕⊕⊕⊕ High	-8.66 (-5.24, -12.08)
Subcutaneous fat	4	Not serious	Serious[a]	Not serious	Not serious	Not serious limitation	448 (224/224)	⊕⊕⊕⊕ High	-5.3 (-2.59, -8.02)
Adiponectin	5	Not serious	Serious[a]	Not serious	Not serious	Not serious limitation	366 (183/183)	⊕⊕⊕◯ Moderate	0.71 (0.22, 1.2)
Leptin	6	Not serious	Serious[a]	Not serious	Not serious	Not serious limitation	464 (233/231)	⊕⊕⊕◯ Moderate	-2.11 (-0.64, -3.59)

CI: confidence interval

[a]There was significant heterogeneity for BMI (I^2=69%), waist circumference (I^2=76%), hip circumference (I^2=74%), body fat mass (I^2=86%), body fat mass (kg) (I^2=80%), body fat mass (%) (I^2=89%), fat area (cm^2) (I^2=55.9%), visceral fat (I^2=85%), subcutaneous fat (I^2=86%), adiponectin (I^2=77%), and leptin (I^2=78%)

⊕⊕⊕⊕: High quality of evidence for all critical outcomes

⊕⊕⊕◯: Moderate quality of evidence for all critical outcomes

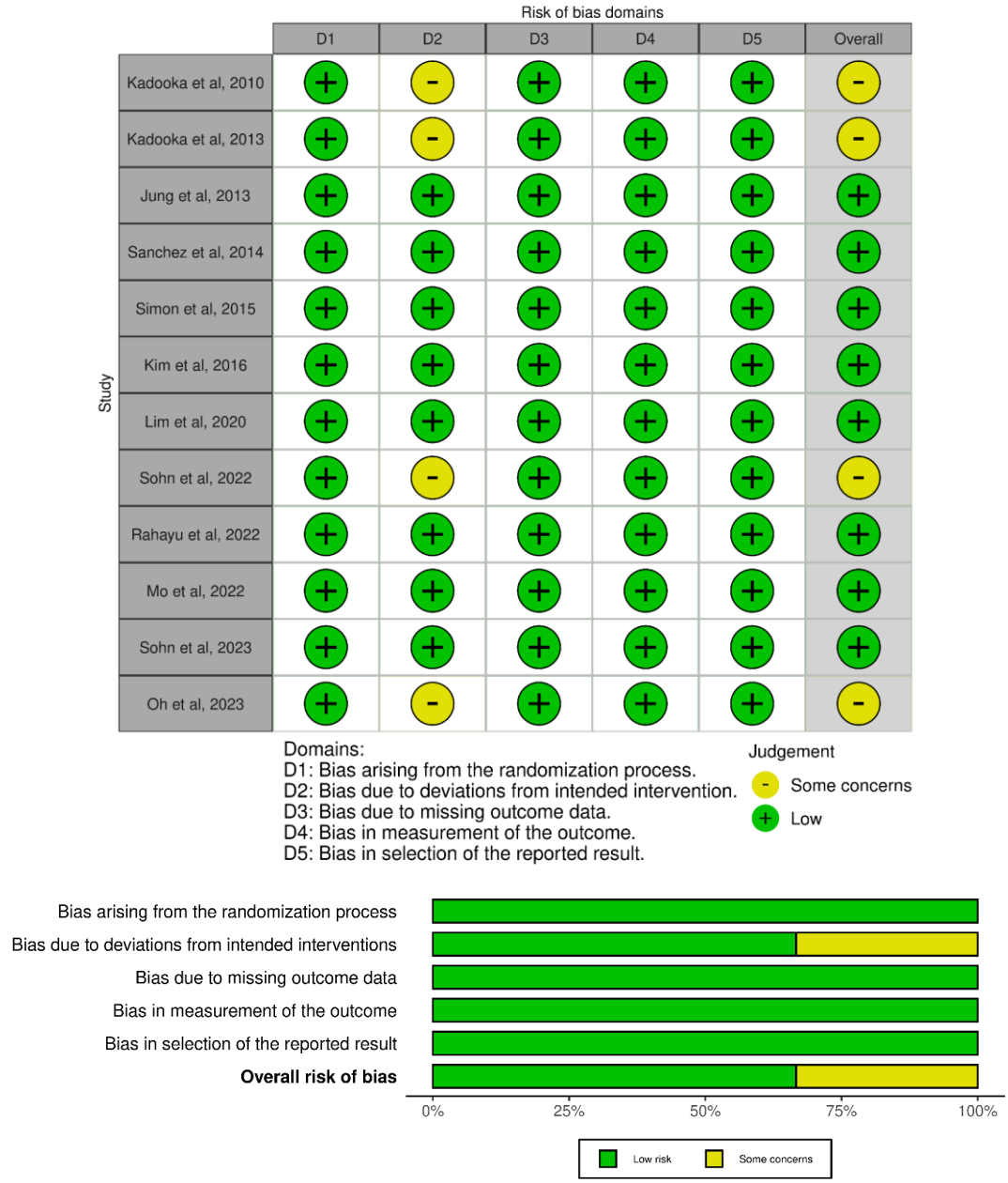

Figure 2. Traffic light plot depicting risk of bias assessment summarizing the risk of bias evaluation for the included studies using Revised Tool for Risk of Bias in Randomized Trials (RoB 2.0).

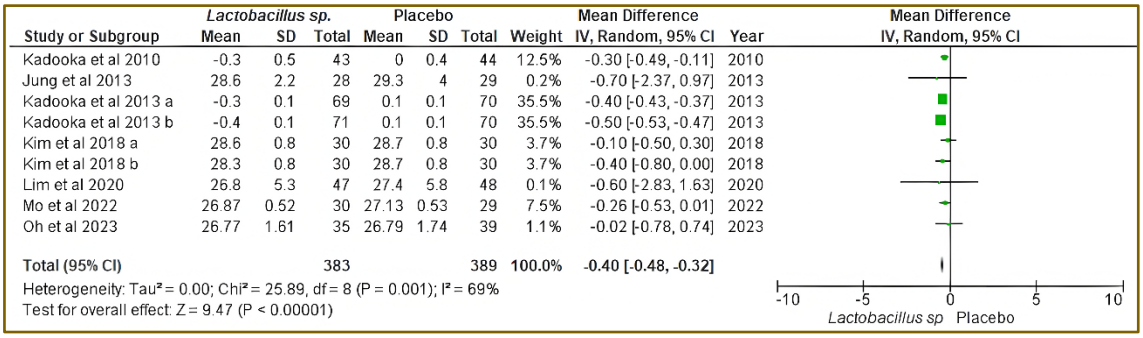

Figure 3. Forest plot showing the efficacy of *Lactobacillus* sp. supplementation compared to placebo in reducing body mass index (BMI) in non-comorbid obese patients.

At the 24-week follow-up, *Lactobacillus* sp. supplementation again showed a trend toward weight reduction, but this result was not statistically significant (MD: -1.40 kg; 95%CI: -3.13–0.33, p=0.110). Overall, the pooled analysis indicated that *Lactobacillus* sp. supplementation significantly reduced body weight compared to placebo (MD: -1.16; 95%CI: -1.79–(-0.53), p=0.0003), with low heterogeneity observed across the studies (I^2=0%, p-heterogeneity of 0.770) (**Figure 4**). These findings suggest that *Lactobacillus* sp. supplementation may be effective for body weight reduction, particularly with longer follow-up durations, with a significant reduction in body weight observed at 12 weeks.

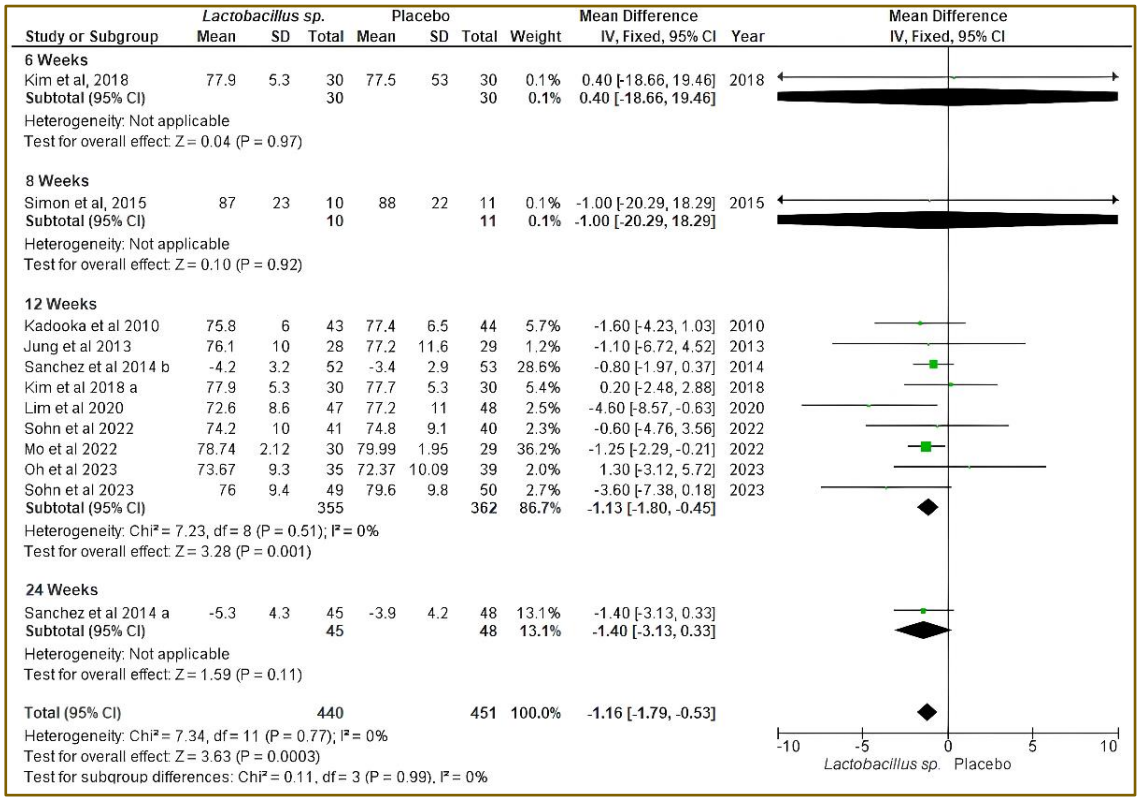

Figure 4. Forest plot showing the efficacy of *Lactobacillus* sp. supplementation compared to placebo in reducing body weight at 6, 8, 12, and 24 weeks of administration in non-comorbid obese patients.

Waist circumference

Meta-analysis comparing waist circumference between the *Lactobacillus* sp. and placebo groups at 12 weeks demonstrated that *Lactobacillus* sp. supplementation significantly reduced waist circumference (MD: -1.41 cm; 95%CI: -1.75–(-1.08), p<0.00001) compared to placebo group, with high heterogeneity was observed (I^2=76%, p-heterogeneity of 0.00001) (**Figure 5**).

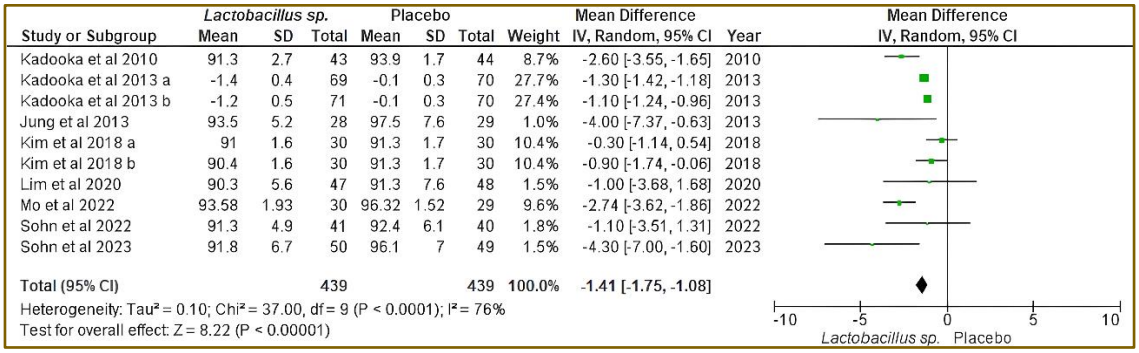

Figure 5. Forest plot showing the efficacy of *Lactobacillus* sp. supplementation compared to placebo in reducing waist circumference at 12 weeks of administration in non-comorbid obese patients.

Hip circumference

Meta-analysis comparing hip circumference between the *Lactobacillus* sp. supplementation and placebo groups at 12 weeks indicated that *Lactobacillus* sp. supplementation significantly reduced hip circumference (MD: -0.85 cm; 95%CI: -1.09–0.61, p<0.00001) compared to placebo group, with high heterogeneity was observed (I^2=74%, p-heterogeneity of 0.0009) (**Figure 6**).

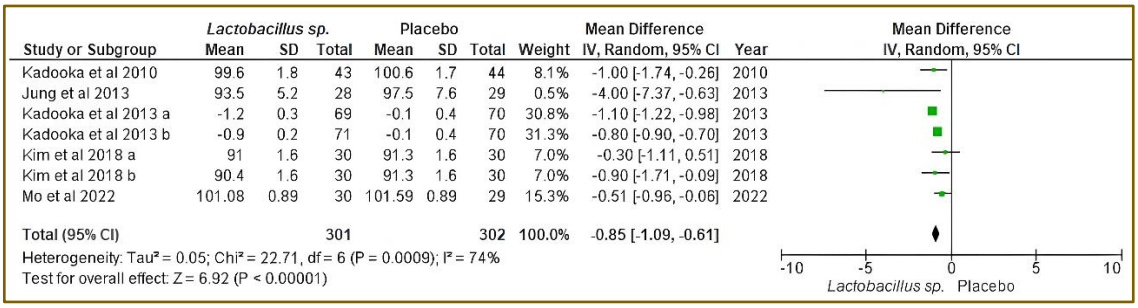

Figure 6. Forest plot showing the efficacy of *Lactobacillus* sp. supplementation compared to placebo in reducing hip circumference at 12 weeks of administration in non-comorbid obese patients.

Visceral, subcutaneous, and body fat mass

Meta-analysis of visceral and subcutaneous fat mass at 12 weeks showed that *Lactobacillus* sp. supplementation significantly reduced both visceral fat (MD: -8.66; 95%CI: -12.08–(-5.24), p<0.00001) and subcutaneous fat (MD: -5.30; 95%CI: -8.02–(-2.59), p=0.0001) compared to placebo group (**Figure 7**). Overall, *Lactobacillus* sp. supplementation reduced visceral and subcutaneous fat mass (MD: -7.35; 95%CI: -9.95–(-4.75), p<0.00001), with high heterogeneity across all studies (I^2=55.9%, p-heterogeneity of 0.130).

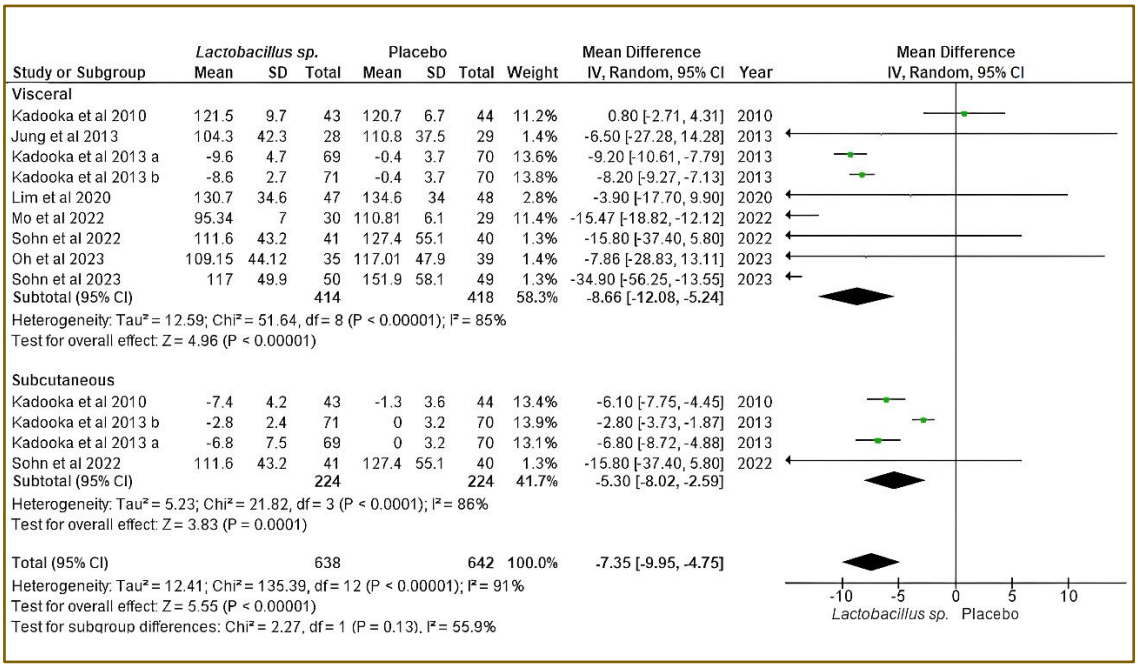

Figure 7. Forest plot showing the efficacy of *Lactobacillus* sp. supplementation compared to placebo in reducing visceral and subcutaneous fat mass at 12 weeks of administration in non-comorbid obese patients.

The meta-analysis of body fat mass and percentage at 12 weeks showed that *Lactobacillus* sp. supplementation significantly reduced body fat mass (MD: -1.14; 95%CI: -1.40–(-0.89), p<0.00001) and body fat percentage (MD: -1.10; 95%CI: -1.48–(-0.71), p<0.00001) compared to placebo group, with high heterogeneity was observed (I^2=80%, p-heterogeneity<0.0001)

(**Figure 8**). Overall, *Lactobacillus* sp. supplementation significantly reduced body fat (MD: -1.11; 95%CI: -1.31–(-0.91), p<0.00001), with high heterogeneity across all studies (I^2=96%, p-heterogeneity<0.0001).

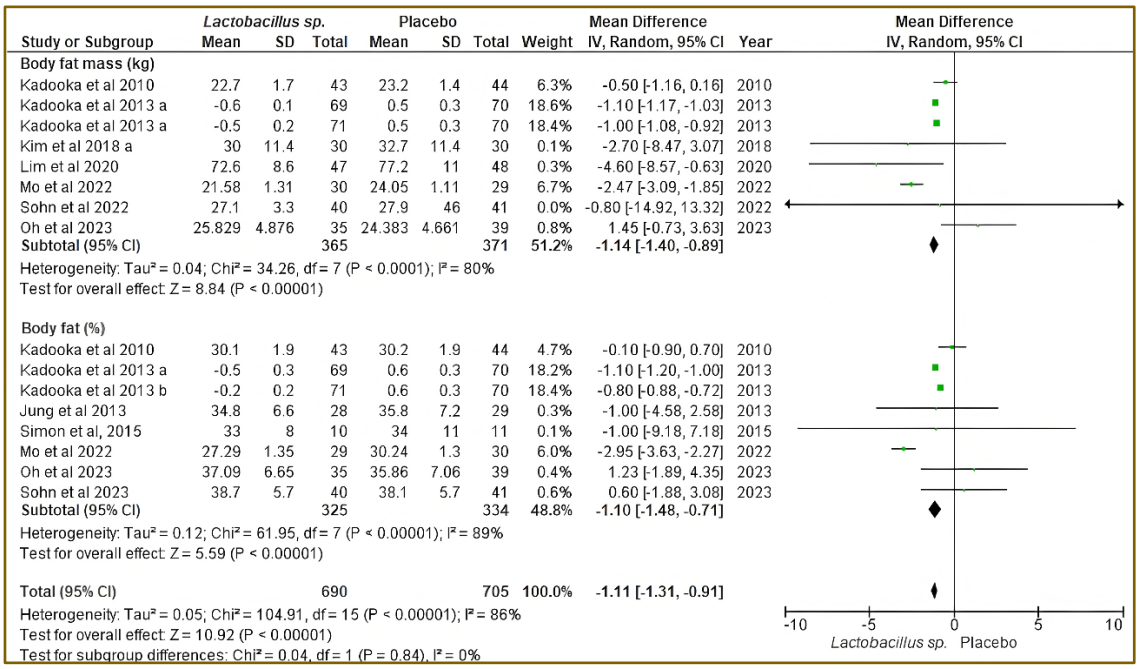

Figure 8. Forest plot showing the efficacy of *Lactobacillus* sp. supplementation compared to placebo in reducing body fat mass and body fat percentage at 12 weeks of administration in non-comorbid obese patients.

Efficacy of *Lactobacillus* sp. supplementation on adiponectin and leptin hormone levels in non-comorbid obese patients

Meta-analysis showed a significant increase in adiponectin levels after *Lactobacillus* sp. supplementation (MD: 0.71 µg/mL; 95%CI: 0.22–1.20; p=0.004) compared to before *Lactobacillus* sp. supplementation, with high heterogeneity (I^2=77%, p-heterogeneity of 0.002) (**Figure 9**). Furthermore, *Lactobacillus* sp. supplementation significantly reduced leptin levels (MD: -2.11 µg/mL; 95%CI: -3.59–(-0.64), p=0.005) compared to placebo, with high heterogeneity (I^2=78%, p-heterogeneity of 0.0004) (**Figure 10**).

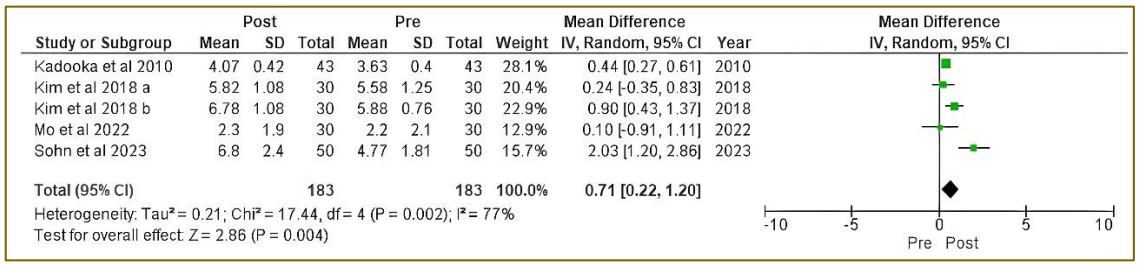

Figure 9. Forest plot showing the efficacy of *Lactobacillus* sp. supplementation in increasing adiponectin levels before and after treatment in non-comorbid obese patients.

Adverse effects of *Lactobacillus* sp. supplementation in non-comorbid obese patients

No significant adverse events were identified in either the intervention or placebo groups (**Table 5**). Mild adverse effects, including diarrhea, skin rash, and abdominal discomfort, were occasionally reported but were not directly attributed to the probiotic supplementation. Compliance with the intervention was notably high, with adherence rates exceeding 94%, and no participants withdrew due to serious adverse events. Routine health evaluations, such as vital signs and laboratory assessments, revealed no significant differences between the intervention

and placebo groups. These findings indicate that *Lactobacillus* sp. supplementation was well tolerated in non-comorbid obese individuals, with no major safety concerns observed.

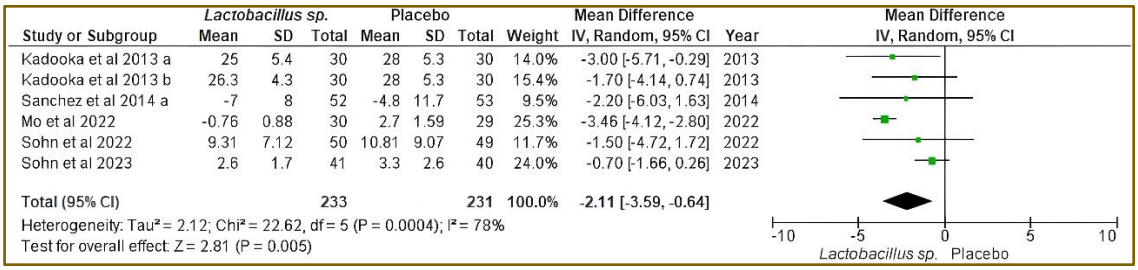

Figure 10. Forest plot showing the Efficacy of *Lactobacillus* sp. supplementation compared to placebo in reducing leptin levels in non-comorbid obese patients.

Table 5. Adverse effects of *Lactobacillus* sp. supplementation in non-comorbid obese patients

Author, year	Adverse effects
Sohn *et al.*, 2023 [15]	• No significant differences in the incidence of adverse events, including gastrointestinal, skin, eye, psychiatric, and cardiac disorders, as well as general weakness, were observed between the groups throughout the 12-week study. • No serious adverse events were reported during the study period. • Vital signs remained within normal limits for participants in both groups during physical examinations.
Mo *et al.*, 2022 [34]	• No adverse events were identified as reasons for participant dropout. • Among participants who completed the 12-week treatment, adherence to the medication regimen was 98.64% in the treatment group and 96.48% in the placebo group. • The difference in adherence rates between the groups was not statistically significant (p=0.476).
Sohn *et al.*, 2022 [13]	• No significant differences were observed between groups regarding the incidence, type, or severity of symptoms, or their relation to the intervention. • Reported adverse reactions, including pruritus, facial laceration, low back pain, insomnia, and vasovagal syncope, were mild and showed no significant association with the intervention. • No deaths or hospitalizations occurred due to serious adverse events.
Oh *et al.*, 2022 [41]	• No serious adverse events were reported in the study. • Mild adverse effects in the *Lactobacillus sakei* OK67 (DW2010) group included contact dermatitis, skin rash, and abdominal pain. • A total of seven mild adverse events were reported in the DW2010 group, compared to four in the placebo group. • No significant differences were observed in parameters between the DW2010 and placebo groups. • The mild adverse events were not directly associated with DW2010 consumption.
Kim *et al.*, 2018 [38]	None of the participants reported significant adverse events during the study
Simon *et al.*, 2015 [40]	No adverse events, including gastrointestinal disturbances, were reported by any patients
Sanchez *et al.*, 2014 [37]	No adverse events were reported as reasons for discontinuing participation
Jung *et al.*, 2013 [12]	• No significant changes in blood pressure or pulse rate were observed between the groups during the study. • Blood parameters remained stable across groups, except for a slight alteration in hematocrit levels in the *Lactobacillus gasseri* BNR17 (BNR17) group. • Mild adverse effects included: diarrhea in the BNR17 group (n=1), and unrelated nausea in the placebo group (n=1). • No serious adverse reactions were reported.
Kadooka *et al.*, 2013 [35]	• No abnormalities in daily life or adverse events related to fermented milk consumption were identified through daily records and physician interviews. • Blood test results, including parameters such as triglycerides, cholesterol levels, and others, consistently remained within normal ranges, with no significant physiological changes observed.
Kadooka *et al.*, 2010 [36]	No deviations in daily routines or adverse events were associated with the consumption of the fermented milk throughout the study

Alterations in gut microbiota composition following *Lactobacillus* sp. supplementation in non-comorbid obese patients

The changes in microbiota composition post-intervention in obese patients without comorbidities were assessed. LMT1-48 supplementation significantly increased microbiota richness and diversity, as measured by the Shannon index, alongside shifts in phylum-level composition, including increases in Actinobacteria and Firmicutes, and a decrease in Bacteroidetes (**Table 6**) [15]. The rise in the Firmicutes-to-Bacteroidetes ratio was associated with metabolic alterations in obesity [17]. Probiotic intervention enhanced the abundance of beneficial taxa, such as Bifidobacteriaceae and Akkermansiaceae, which contribute to gut barrier integrity and metabolic regulation, while reducing taxa associated with dysbiosis, such as Oscillospiraceae and Selenomonadaceae [34]. The placebo group also exhibited compositional changes, indicating the possible influence of baseline dietary or environmental factors [29]. *L. plantarum* K50 (LPK) supplementation selectively targeted Lactobacillales order genera, particularly *Lactobacillus plantarum* and *Enterococcus hirae*, which were inversely correlated with obesity markers, including visceral fat and body weight [13]. Despite these changes, there were no significant alterations in overall microbiota diversity (alpha and beta), suggesting that the intervention specifically modulated certain microbial populations without affecting global diversity metrics. Another study identified consistent trends in dominant phyla across treatment and placebo groups, with the treatment group showing a significant decrease in Firmicutes and an increase in Bacteroidetes, indicative of shifts towards a potentially healthier microbial profile [34]. However, the decrease in Verrucomicrobia, a phylum associated with glucose regulation and gut health, requires further exploration to understand its implications in metabolic health [39].

Table 6. Alterations in gut microbiota composition following *Lactobacillus* sp. supplementation in non-comorbid obese patients

Author, year	Composition of intestinal microbiota changes
Sohn *et al.*, 2023 [15]	• *Lactobacillus plantarum* LMT1-48 (LMT1-48) supplementation significantly increased microbiome richness and diversity (Shannon index) from 1.64 to 1.78 (p<0.050) at the family level compared to placebo. • LMT1-48 supplementation increased Actinobacteria by 0.23%, Firmicutes by 7.24%, and reduced Bacteroidetes by 6.98% (p<0.050) at the phylum level compared to placebo. • The Firmicutes-to-Bacteroidetes ratio increased from 0.53 to 0.80 after 12 weeks of LMT1-48 consumption, with significant differences between groups (p<0.050). • Other phyla remained unaffected by LMT1-48 supplementation.
Mo *et al.*, 2022 [34]	• In the probiotic group, post-intervention, Bifidobacteriaceae and Akkermansiaceae increased, while Oscillospiraceae, Selenomonadaceae, and Prevotellaceae decreased at the family level. • In the placebo group, Actinobacteria members (Coriobacteriia class, Coriobacteriaceae and Eggerthellaceae families, *Collinsella* and *Senegalimassilia* genera) significantly increased, while Bacteroidetes members (Tannerellaceae and Bacteroidaceae families, *Bacteroides, Phocaeicola*, and *Parabacteroides* genera) significantly decreased compared to baseline (p<0.050). • In the probiotic group, Actinobacteria members (*Bifidobacterium* genus) and Verrucomicrobia (*Akkermansia* genus) significantly increased compared to placebo, while members of the Firmicutes phylum (*Ruminococcoides* genus) and Proteobacteria (Sutterellaceae and Desulfovibrionaceae *families*, *Desulfovibrio* genus) significantly decreased (p<0.050) compared to placebo.
Sohn *et al.*, 2022 [13]	• *Lactobacillus plantarum* K8 (LPK) supplementation led to a significant reduction in Actinobacteria at the phylum level compared to the placebo group, with a positive correlation to visceral fat area (VAT) (r=0.24; p=0.051). • No significant differences in overall diversity (alpha and beta) were observed between the LPK and placebo groups (p<0.050). • LPK supplementation significantly increased the abundance of *L. plantarum*, with levels of 0.05%±0.18% in the LPK group versus -0.01%±0.05% in the placebo group (p<0.050). • Changes in the raw counts of *L. plantarum* were inversely correlated with changes in abdominal adipose tissue area, with a borderline level of significance (r=-0.25; p=0.073). • In the Lactobacillales order, *Enterococcus* abundance was significantly higher in the LPK group compared to the placebo group (0.70%±2.32% vs 0.09%±0.28%; p<0.050).

Rahayu *et al*., 2021 [39]	• The relative abundance of *Lactobacillales* was similar between the groups, but significant differences in specific genera composition were noted (PERMANOVA=0.003). • The abundance of *Enterococcus hirae* significantly increased in the LPK group (0.70%±2.33% vs 0.09%±0.28%; $p<0.05$) and showed a positive correlation with *L. plantarum* abundance ($r=0.22$; $p=0.047$) compared to placebo. • The three dominant genera, Firmicutes, Bacteroidetes, and Actinobacteria, were consistently present in most participants. • Phyla such as Proteobacteria and Fusobacteria were found in only a few participants. • Bacteroidetes significantly increased in both the treatment and placebo groups ($p<0.05$). • Firmicutes significantly decreased in the treatment group ($p<0.050$) compared to placebo. • Fusobacteria remained rare, and Verrucomicrobia significantly decreased in both groups after the consumption period ($p<0.050$), although these phyla were associated with gastrointestinal health and glucose regulation. • No significant changes were observed in the phyla Cyanobacteria, Elusimicrobia, Lentisphaerae, and Synergistetes between the probiotic-treated and placebo groups before and after consumption ($p>0.050$).

Discussion

The present study compares *Lactobacillus* spp. supplementation to placebo in obese patients demonstrated significant reductions in body weight, waist circumference, hip circumference, body fat mass, and body fat percentage. Adiponectin levels significantly increased, while leptin levels significantly decreased, with no adverse effects reported. Gut microbiota analysis revealed enhanced diversity following *Lactobacillus* spp. supplementation, characterized by an increase in Bacteroidetes and a decrease in Firmicutes [14,15,17,20,29-36].

The findings of this study suggested that *Lactobacillus* spp. supplementation was both effective and safe for weight management in overweight and obese individuals, allowing for several clinical recommendations. The target population included healthy adults aged 18 years and older with a BMI of 25 kg/m^2 or higher, specifically those classified as overweight or obese. A daily dosage of *Lactobacillus* spp. probiotics ranged from 10^9 to 10^{12} CFU, prioritizing strains such as *L. rhamnosus* CGMCC1.3724, *L. gasseri* (including BNR17 and SBT2055), *L. plantarum* (including LMT-48 and K50), *L. sakei* (OK 67), and a combination of *L. curvatus* HY7601 and *L. plantarum* KY1032. Administration occurred once daily for 8 to 12 weeks via oral routes such as capsules or powders. Indications for use included weight management, improvement of gut microbiota composition, reduction of body fat and waist circumference, enhancement of metabolic health, and support for overall digestive health. However, several contraindications were noted, including known allergies to probiotic components and severe immunocompromised states. Regular monitoring of patient progress and adherence to the regimen was essential for optimizing outcomes.

Recent studies have elucidated the multifactorial determinants of gut microbiota diversity across different populations [44-48]. Changes in gut microbiota, influenced by factors such as aging, sex differences, ethnicity, urban lifestyles, and poor sanitation, contribute to obesity by promoting dysbiosis, inflammation, and metabolic dysfunction. While sex, age, and BMI exert some influence, enterotypes—distinct microbial communities—emerged as the primary factor driving variability in microbiota composition [46]. Notably, older adults and individuals with higher BMI displayed a decrease in beneficial Firmicutes and an increase in potentially harmful microbes, underscoring a complex relationship that warrants further investigation [46]. Furthermore, aging is also associated with elevated inflammation and cytokine levels, which alter gut microbiota, replacing beneficial bacteria with those that degrade toxic metabolites [45]. Sex differences were observed, with obese males showing increased Fusobacteria and obese females exhibiting higher Actinobacteria, potentially associated with metabolic changes [44]. A large study conducted in Amsterdam, involving 5,193 participants, revealed concerning trends among second-generation Moroccans, Turks, and younger Dutch individuals, who displayed reduced gut microbiome diversity [47]. This shift was characterized by a decrease in the *Prevotella* cluster and an increase in the Western-associated *Bacteroides/Blautia/Bifidobacterium* (BBB) cluster, both associated with urban lifestyle diseases [47]. Moreover, in regions such as Indonesia and

Malaysia, poor sanitation practices contribute to the introduction of harmful bacteria via contaminated food, further disrupting gut microbiota composition [48].

The present study's findings were aligned with previous studies that incorporated obese patients with comorbidities [49]. Probiotic interventions in obese patients, including those with T2DM and NAFLD, significantly reduced BMI, body weight, abdominal circumference, fat mass, fasting blood sugar, HbA1c, insulin levels, HOMA-IR, and liver enzymes (alanine and aspartate aminotransferase) compared to placebo [49]. Supplementation with *Lactobacillus* spp. and *Bifidobacterium* spp. further demonstrated metabolic benefits, including reduced leptin levels and increased adiponectin [44-48]. Gut microbiota composition differs between lean and obese individuals, with obesity characterized by a higher proportion of Firmicutes and a lower proportion of Bacteroidetes [39], contributing to energy imbalance and chronic inflammation that promote metabolic disorders such as obesity and T2DM [50,51].

The studies included in the present meta-analysis predominantly utilized probiotic delivery systems in the form of capsules or powders. Probiotic delivery systems, including powders, capsules, tablets, and fermented milk, offer various benefits and limitations related to efficacy, stability, and safety [52]. Probiotic powders are convenient in handling, storage, and formulation versatility; however, maintaining bacterial viability during dehydration can be challenging–encapsulation enhances stability and facilitates targeted delivery to the gastrointestinal tract [53]. Capsules, commonly used in dietary supplements, protect probiotics from stomach acidity, improving viability and enabling controlled release [54]. Tablets are stable and cost-effective but may result in bioactivity loss during manufacturing, making them less suitable for probiotics [55,56]. Fermented milk, which provides bioactive compounds such as essential amino acids and fatty acids, offers health benefits, though raw versions may contain harmful microorganisms, such as coliforms, increasing the risk of foodborne illness [57]. Therefore, the choice of delivery system must balance these factors to ensure optimal probiotic efficacy and patient safety.

Understanding the relationship between gut microbiota and obesity is essential for developing effective interventions, as it highlights factors influencing microbiota composition and its role in metabolism and weight regulation, thereby shedding light on its contribution to obesity development (**Figure 11**) [58]. Short-chain fatty acids (SCFAs) produced by *Lactobacillus* strains originating from the human gut have the potential to influence the body's energy metabolism [58]. Specifically, fecal acetic acid, one of the prominent SCFAs, plays a significant role in regulating metabolic disturbances and maintaining the balance of glucose and insulin levels, as influenced by the gut microbiota [59]. The fermentation of dietary fiber by gut microbiota produces SCFAs that yield multiple beneficial effects on mammalian energy metabolism [60]. These SCFAs can enter the systemic circulation, exerting immediate effects on the metabolism and function of peripheral tissues, including the liver, skeletal muscle, and adipose tissue [61]. Additionally, SCFAs such as propionate and butyrate can alter the epigenome by activating the acetyltransferase P300, leading to increased histone acetylation [62]. Therefore, SCFA production by *Lactobacillus* strains modulates energy metabolism and influences various physiological processes within the human body [63].

Lactobacillus strains can produce bioactive peptides that modulate appetite regulation [64]. Heat-treated *Lactobacillus brevis* SBC8803 has been shown to stimulate serotonin secretion and increase intracellular Ca^{2+} concentrations, suggesting potential effects on gastrointestinal hormones such as ghrelin [65]. Regular consumption of yogurt containing *Lactobacillus* species was associated with weight stability and reduced consumption of unhealthy foods [66]. Moreover, the intake of fermented soybeans (*tempeh*), which contained *Lactobacillus*, elicited a stronger response in regulating appetite hormones compared to unfermented soy [63]. Peptide hormones such as ghrelin, GLP-1, and leptin play essential roles in appetite control and weight management [67]. Specific *Lactobacillus* strains, including *L. fermentum*, *L. plantarum* L-14, and *L. amylovorus* KU4, improved adipose tissue function in obese individuals with insulin resistance [68]. Furthermore, *L. fermentum* enhanced oxidative phosphorylation in adipose tissue, leading to increased energy expenditure and protection against diet-induced obesity [68]. *L. plantarum L-14* extract inhibited adipogenesis via Toll-like receptor 2 (TLR2) and AMP-activated protein kinase (AMPK) signaling pathways, reducing adipocyte differentiation and mitigating obesity and associated diseases [69]. Additionally, *L. amylovorus* KU4 promoted the browning of white

adipocytes by enhancing PPARγ and PGC-1α interaction, increasing Ucp1 expression and mitochondrial function [70]. These molecular and cellular mechanisms contributed to improve adipose tissue function in individuals with insulin resistance [69].

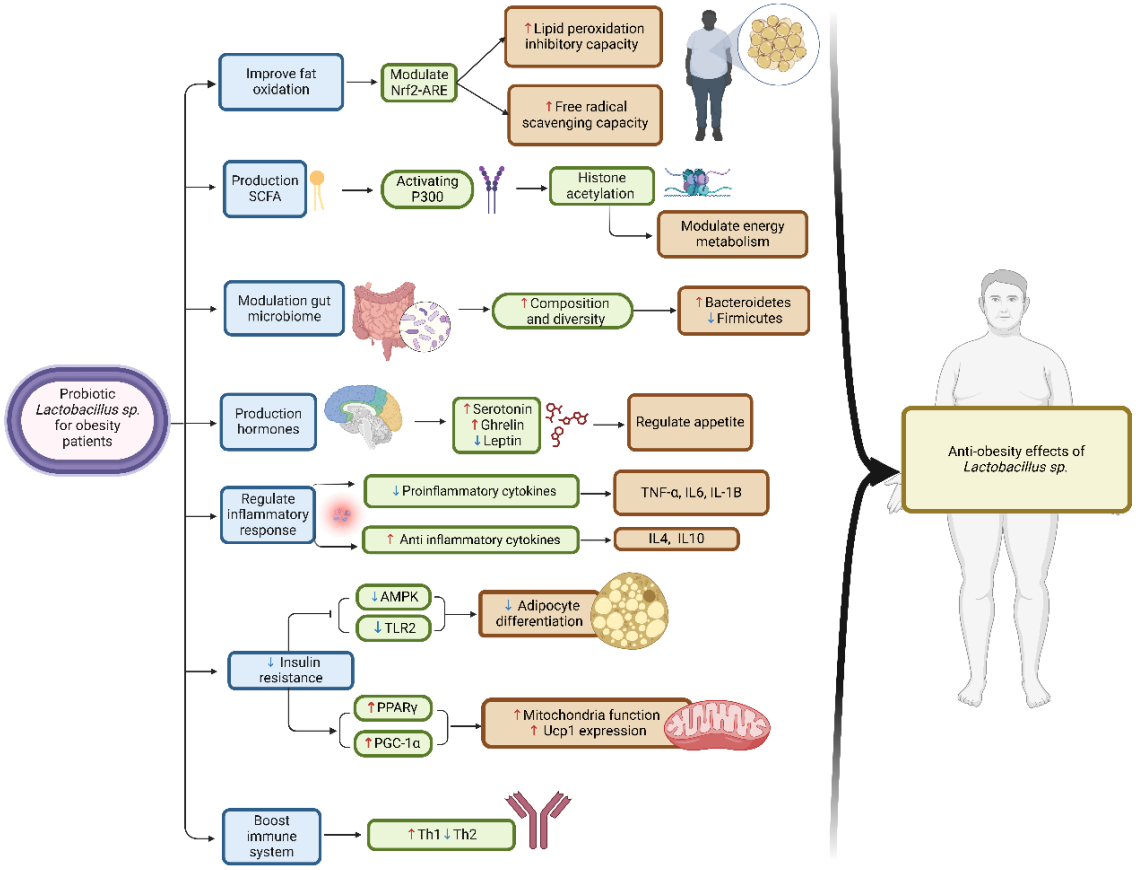

Figure 11. Mechanisms by which gut microbiota contribute to obesity involve multiple pathways influencing metabolic processes that regulate body weight and obesity development. AMPK: AMP-activated protein kinase; IL1β: interleukin 1 beta; IL4: interleukin 4; IL6: interleukin 6; IL10: interleukin 10; NrF2-ARE: nuclear factor erythroid 2-related factor 2-antioxidant response element; P300: histone acetyltransferase; PGC-1α: peroxisome proliferator-activated receptor gamma coactivator 1 alpha; PPARγ: peroxisome proliferator-activated receptor gamma; SCFA: short-chain fatty acids; Th1: T helper 1; Th2: T helper 2; TLR2: toll-like receptor 2; TNF-α: tumor necrosis factor alpha; Ucp1: uncoupling protein 1.

Lactobacillus strains interact with immune cells in both obese and non-obese individuals. Consumption of probiotic yogurt has been shown to modulate T cell subset-specific gene expression in peripheral blood mononuclear cells of overweight and obese individuals [71]. Certain *Lactobacillus* strains, including MP137 and MP108, enhance Th1 immune responses while inhibiting Th2 responses. Additionally, *Lactobacillus fermentum* has been shown to interact with immune cells, modulating both innate and adaptive immune response pathways [72]. The anti-inflammatory effects of *Lactobacillus* strains in obese individuals are mediated through various mechanisms [22]. *Lactobacillus fermentum CQPC05 (LF-CQPC05)* and *Lactobacillus plantarum CQPC02 (LP-CQPC02)* have been found to reduce obesity-induced inflammation and improve lipid profiles by decreasing pro-inflammatory cytokines such as TNF-α, IL-6, and IL-1, while simultaneously increasing anti-inflammatory cytokines like IL-4 and IL-10 [72,73].

Probiotics, particularly *Lactobacillus* strains, are widely utilized in functional foods such as yogurt, kefir, cheese, and fermented beverages, contributing to enhanced flavor, probiotic content, digestibility, and nutritional value. *Lactobacillus* strains are also employed in wine production to improve flavor and in coffee products to enhance taste and aroma [74]. Fermentation with *Lactobacillus paracasei* has been shown to increase the antioxidant content

in mango and pineapple, with one cookie formulation achieving a vitamin C concentration of 107.90 mg/100 g and antioxidant activity of 44.70%, providing a nutritious snack option [75]. Furthermore, *Lactobacillus gasseri* in soy-based tempeh has demonstrated paraprobiotic effects, alleviating fatigue and reducing anxiety through enhanced protein synthesis [76]. Kombucha enriched with sea grapes (*Caulerpa racemosa*) has shown significant benefits, including improved lipid profiles, reduced obesity markers, and weight loss in both in vitro and in vivo models [77]. Additionally, butterfly pea flower kombucha has alleviated metabolic disorders in high-fat diet-induced mice by improving lipid profiles, increasing gut microbiota diversity, and inhibiting ABTS, lipase, α-amylase, and α-glucosidase activities, indicating potential for managing lipid and carbohydrate metabolism [78]. These findings highlight the substantial potential of probiotics and associated bioactive compounds in improving metabolic health and their diverse applications in functional foods for addressing inflammation, obesity, and metabolic disorders.

The present study has several limitations that warrant careful consideration. The effects of supplementation were primarily assessed over a 12-week period, which may not fully capture the long-term efficacy or potential adverse effects of *Lactobacillus* sp. supplementation. The significant heterogeneity in findings, likely due to the use of diverse *Lactobacillus* sp. strains across studies, complicates the interpretation of overall effectiveness. Additionally, some studies were limited by small sample sizes, which may restrict the generalizability of the results [12,34,40]. Variations in diet could also influence outcomes, with ethnic groups from Asian countries, such as Japan [35,36], South Korea [12,13,15,18,34,38,41], and Indonesia [39], potentially showing different results compared to studies conducted in Western countries such as Canada [43] and Germany [42]. Furthermore, differences in dosage may contribute to inconsistencies in observed outcomes.

Despite these limitations, the study presents notable strengths. Oral supplementation was uniformly administered, promoting consistency, though only one study used fermented milk [35]. Subgroup analysis offered valuable insights into the differential impacts of supplementation strategies. Most studies exhibited low risk of bias and employed rigorous designs, enhancing the reliability and validity of the findings. The quality of evidence was also formally assessed using the GRADE approach.

Future research should focus on longitudinal studies beyond the 12-week period to assess the long-term effects of *Lactobacillus* sp. supplementation. Investigations targeting specific *Lactobacillus* strains may reduce variability and clarify efficacy. Larger sample sizes and more specific ethnic demographics are needed to improve external validity. Furthermore, standardized protocols for oral dosage and administration will facilitate reliable cross-study comparisons.

Conclusion

Probiotic *Lactobacillus* sp. supplementation demonstrated a reduction in BMI, body weight, waist and hip circumference, visceral and subcutaneous fat areas, overall body fat, and leptin levels, while increasing adiponectin in non-comorbid obese patients, with no adverse effects. However, to optimize its use in obesity management, standardized protocols and large-scale trials are necessary. Future research should focus on determining the ideal dosage, duration, and potential synergistic effects with conventional treatments, while also considering factors such as age, ethnicity, sex, and diet. These findings suggest that integrating *Lactobacillus* sp. supplementation may enhance obesity management.

Ethics approval

Not required.

Acknowledgments

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Competing interests

All the authors declare that there are no conflicts of interest.

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Underlying data

Derived data supporting the findings of this study are available from the corresponding author on request.

Declaration of artificial intelligence use

We hereby confirm that no artificial intelligence (AI) tools or methodologies were utilized at any stage of this study, including during data collection, analysis, visualization, or manuscript preparation. All work presented in this study was conducted manually by the authors without the assistance of AI-based tools or systems.

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