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Sequential Ecological Relay of a BALIMONT Multi-Strain Probiotic Platform for Weight Management and Metabolic Environment Modulation

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ABSTRACT

We evaluated a BALIMONT multi-strain probiotic platform composed of Bacillus coagulans ATCC 7050, Bifidobacterium animalis ATCC 27536, and Lactobacillus plantarum DSM 20174, and we integrated the original formulation dataset with currently available published evidence relevant to probiotic-based weight management. The platform used a 1:1:1 viable-count ratio and a sequential ecological-relay design in which B. animalis and L. plantarum were pre-incubated in a B. coagulans cell-free metabolite filtrate before final blending with B. coagulans spore powder. In the original comparative dataset, six-month viable-count retention reached 85.2%, versus 52.0% for a same-strain direct-mix comparator. In vivo, B. coagulans first reduced free oxygen from 5.2 mg/L to 0.8 mg/L and shifted the proximal intestinal redox potential from +120 mV to −180 mV, followed by jejunal/ileal enrichment of L. plantarum and distal-colon enrichment of B. animalis. In obese mice, the medium and high doses reduced body weight by 12.3% and 15.7%, body-fat percentage by 18.5% and 22.4%, and colonic short-chain fatty acids by 58% and 72%, respectively, relative to the model pattern reported in the source dataset. Published human studies and meta-analyses further support the plausibility of probiotic-mediated improvement in visceral fat, body weight, insulin resistance, and microbiota-related metabolic markers. Together, these data support BALIMONT as a process-defined probiotic platform for metabolic-environment modulation and justify further randomized human validation.

KEYWORDS

BALIMONT; Bacillus coagulans; Bifidobacterium animalis; Lactobacillus plantarum; Weight management; Metabolic environment; Short-chain fatty acids; Probiotic synergy

1. INTRODUCTION

Obesity remains a major global public-health burden. According to the World Health Organization, 2.5 billion adults were overweight in 2022, including 890 million living with obesity, and 1 in 8 people in the world were living with obesity. The intestinal microbiota is now recognized as an important modulator of host energy balance, barrier integrity, inflammatory tone, and short-chain fatty-acid (SCFA) production, all of which are closely linked to obesity-related metabolic risk [1, 2].

Available evidence also suggests that strain-specific probiotics can affect adiposity and metabolic endpoints. Bacillus coagulans BC69 reduced body-weight gain, pro-inflammatory cytokines, and fecal acetate and butyrate disturbances in a high-sugar/high-fat-diet mouse model [3]. In adults with overweight or obesity, Bacillus coagulans BC99 produced greater weight loss than placebo after 8 weeks and significantly altered gut β-diversity [4]. Bifidobacterium animalis ssp. lactis GCL2505 significantly reduced visceral fat area in overweight or mildly obese adults after 8 and 12 weeks [5],

while Lactobacillus plantarum LMT1-48 reduced body weight, abdominal visceral fat area, insulin resistance, and leptin in overweight subjects [6]. A recent meta-analysis further indicated that L. plantarum supplementation was associated with significant reductions in body weight and BMI, with additional benefits for abdominal fat and inflammatory markers [7].

Against this background, we positioned BALIMONT as a sequential ecological-relay platform rather than a simple direct mixture. The central design logic is that Bacillus coagulans acts as a spore-forming pioneer strain and metabolite donor, Lactobacillus plantarum supports mid-intestinal barrier and inflammatory control, and Bifidobacterium animalis contributes distal-colon metabolic reinforcement and SCFA production. We therefore examined whether this process-defined architecture could generate stronger storage stability, staged colonization, and metabolic readouts than a same-strain direct-mix comparator, and we aligned those findings with currently available published data.

2. MATERIALS AND METHODS

2.1. Platform Composition And Sequential Ecological Relay

We formulated BALIMONT with Bacillus coagulans ATCC 7050, Bifidobacterium animalis ATCC 27536, and Lactobacillus plantarum DSM 20174 at a 1:1:1 viable-count ratio. Bacillus coagulans was used both as a spore biomass and as the source of a cell-free metabolite filtrate characterized in the source dataset as containing at least 1.2 g/L total SCFAs, at least 80 U/mL catalase activity, and at least 0.5 g/L free amino acids. Washed B. animalis and L. plantarum pastes were jointly dispersed into this filtrate, anaerobically conditioned for 4 h at 37 °C, freeze-dried, and then blended with B. coagulans spore powder to obtain the final composition.

2.2. Stability, Colonization, And Metabolic-Efficacy Assessment

We retained the original platform endpoints, including six-month storage stability at 25 °C/60% RH, intestinal colonization sequencing in C57BL/6J mice, proximal-intestinal oxygen and redox measurements, and an 8-week high-fat-diet mouse model assessing body weight, body-fat percentage, serum lipids, and colonic SCFAs. We also reviewed published human and preclinical evidence related to Bacillus coagulans, Bifidobacterium animalis, Lactobacillus plantarum, and probiotic weight-management interventions in order to integrate the source results with external data [3-8].

Table 1. Sequential ecological-relay architecture and key source readouts

Strain	Platform role	Key readouts
Bacillus coagulans ATCC 7050	Pioneer spore former; oxygen depletion; metabolite filtrate donor	1.2×10^7 CFU/g at 6 h; free oxygen 5.2→0.8 mg/L; redox +120→−180 mV
Lactobacillus plantarum DSM 20174	Mid-intestinal barrier-supporting strain	8.5×10^6 CFU/g in jejunum/ileum at 12 h; IL-6 ↓42%; TNF-α ↓38%
Bifidobacterium animalis ATCC 27536	Distal-colon metabolic amplifier	9.2×10^6 CFU/g in distal colon at 24 h; total SCFAs ↑65%

3. RESULTS

3.1. Platform Characteristics, Storage Stability, And Ecological Relay

The sequential ecological-relay design produced strong formulation stability in the source dataset. Total viable-count retention remained 85.2% after six months, whereas the direct-mix same-strain comparator retained only 52.0%. In vivo, Bacillus coagulans first colonized the proximal small

intestine, where its abundance reached 1.2×10^7 CFU/g contents at 6 h, while free oxygen declined from 5.2 mg/L to 0.8 mg/L and redox potential shifted from +120 mV to −180 mV. At 12 h, Lactobacillus plantarum reached 8.5×10^6 CFU/g contents in the jejunum and ileum and was accompanied by decreases in IL-6 and TNF-α of 42% and 38%, respectively. At 24 h, distal-colon Bifidobacterium animalis reached 9.2×10^6 CFU/g contents, with a 65% increase in distal-colon total SCFAs relative to the blank pattern described in the source dataset.

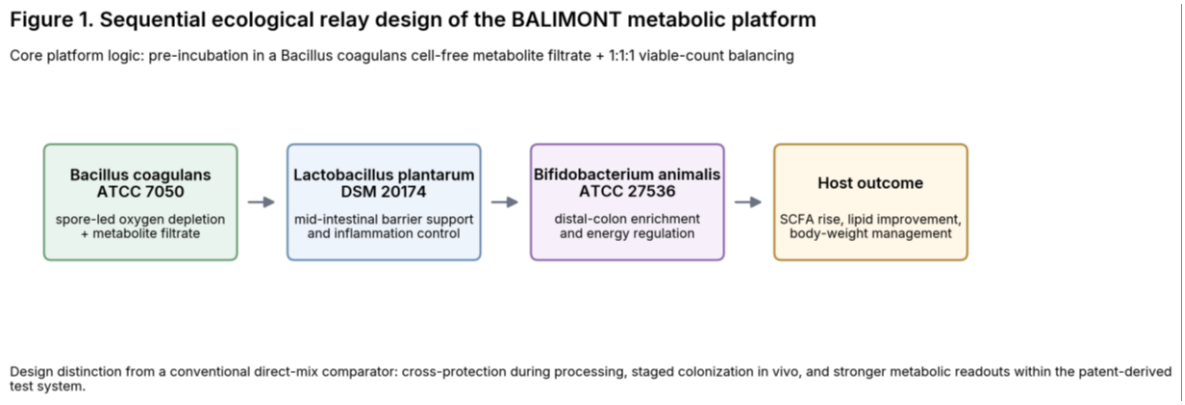

Figure 1. Sequential ecological relay design of the BALIMONT metabolic platform

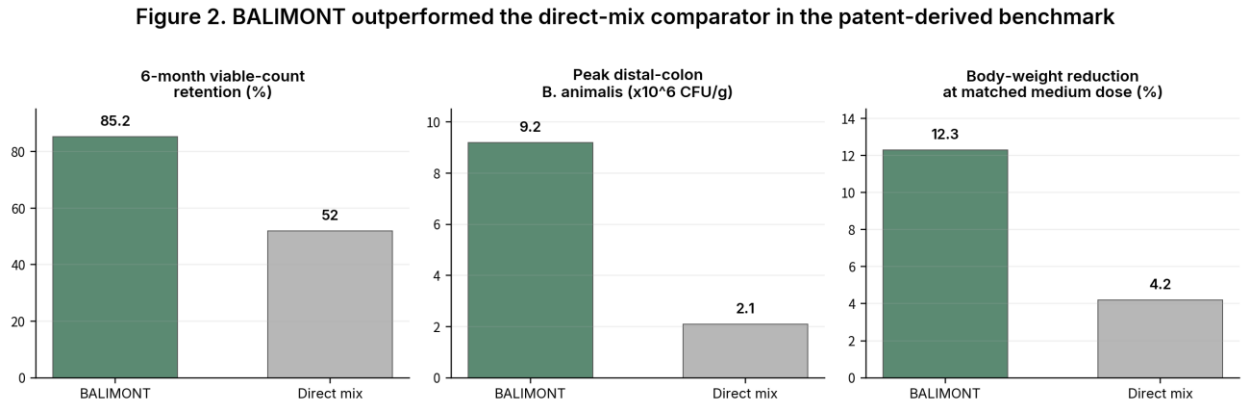

Figure 2. BALIMONT outperformed the same-strain direct-mix comparator in the benchmark comparison

3.2. Dose-dependent Metabolic Outcomes and Comparator Advantage

In the high-fat-diet mouse model, the medium and high doses of BALIMONT reduced body weight by 12.3% and 15.7% and body-fat percentage by 18.5% and 22.4%, respectively. Colonic SCFAs increased by 58% and 72%, total cholesterol declined by 21.2% and 25.6%, and triglycerides declined by 18.7% and 22.3%, respectively. Importantly, the matched medium-dose direct-mix comparator produced only 4.2% body-weight reduction, supporting the view that the BALIMONT technical route—not merely the strain list—drove the stronger functional signal.

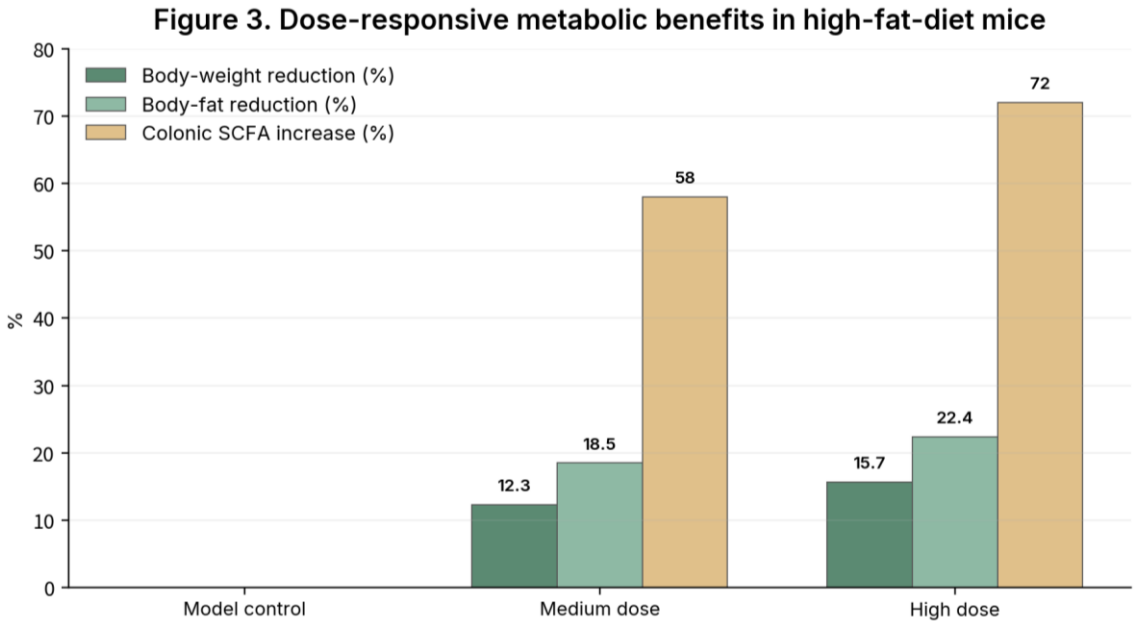

Figure 3. Dose-responsive metabolic benefits in high-fat-diet mice

Table 2. Key comparative endpoints in the BALIMONT dataset

Endpoint	BALIMONT medium dose	BALIMONT high dose	Direct-mix comparator
6-month viable-count retention	85.2%	85.2%	52.0%
Body-weight reduction	12.3%	15.7%	4.2%
Body-fat reduction	18.5%	22.4%	—
Colonic SCFA increase	58%	72%	—
Peak distal-colon B. animalis	9.2×10^6 CFU/g	9.2×10^6 CFU/g	2.1×10^6 CFU/g

3.3. Alignment with Published Evidence

The source results were broadly consistent with published evidence. In a 2024 meta-analysis of 11 randomized controlled trials in overweight or obese women, probiotics significantly reduced waist circumference, insulin, and LDL-C, although effects on body weight were heterogeneous [8]. Human studies of B. animalis and L. plantarum have shown reductions in visceral fat and body weight [5,6], and human or translational studies of B. coagulans also support effects on body weight or adiposity-related endpoints [4,9]. These external data do not replace direct head-to-head validation of BALIMONT, but they strengthen the biological plausibility of the sequential ecological-relay concept.

Table 3. Representative published evidence aligned with the BALIMONT platform

Study / source	Population or model	Main findings	Relevance to BALIMONT
WHO 2025 [1]	Global adults	2.5 billion adults were overweight in 2022; 890 million were living with obesity.	Establishes the public-health need for microbiota-directed weight management.
Probiotic meta-analysis 2024 [8]	11 RCTs in overweight/obese women	Significant reductions in waist circumference, insulin, and LDL-C.	Supports the broader metabolic relevance of probiotic interventions.
B. coagulans BC99 2025 [4]	Overweight/obese adults, 8 weeks	Greater weight loss than placebo; gut β-diversity improved.	Strengthens the clinical plausibility of the Bacillus pioneer module.
B. animalis GCL2505 2016 [5]	Overweight /mildly obese adults, 12 weeks	Visceral fat area significantly decreased at 8 and 12 weeks.	Supports the distal-colon metabolic role of bifidobacterial enrichment.
L. plantarum LMT1-48 2023 [6]	Overweight adults, 12 weeks	Body weight, abdominal visceral fat, insulin resistance, and leptin decreased.	Supports the barrier-metabolic role of the mid-intestinal relay component.
L. plantarum meta-analysis 2024 [7]	9 RCTs	Significant reductions in body weight and BMI; abdominal fat and inflammatory markers also improved.	Supports multi-strain, process-defined positioning for metabolic health.

4. DISCUSSION

We found that BALIMONT is best understood as a process-defined probiotic platform with three complementary layers of differentiation. First, Bacillus coagulans functions as an oxygen-depleting pioneer strain and cross-protective metabolite donor, creating a more permissive ecological niche for the other strains. Second, Lactobacillus plantarum appears to occupy the mid-intestinal window, where barrier-support and inflammatory control are particularly relevant to obesity-associated gut dysfunction. Third, Bifidobacterium animalis acts as a distal-colon metabolic amplifier that supports higher SCFA output and more favorable ecological remodeling. This staged model is more mechanistically coherent than a standard direct mixture and explains why the same strain set can perform differently when formulation logic changes.

5. CONCLUSION

We conclude that the BALIMONT combination of Bacillus coagulans ATCC 7050, Bifidobacterium animalis ATCC 27536, and Lactobacillus plantarum DSM 20174 constitutes a differentiated weight-management probiotic platform characterized by strong storage stability, staged intestinal colonization, enhanced SCFA output, and stronger metabolic-environment modulation than a same-strain direct-mix comparator. The concordance between the original dataset and the published probiotic literature supports the translational relevance of this design and justifies future randomized human validation.

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