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Yeast direct-fed microbial supplementation improves growth and carcass traits in small ruminants: A systematic review and meta-analysis

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Abstract

This meta-analysis quantified the effects of yeast direct-fed microbial (DFM) supplementation, particularly *Saccharomyces cerevisiae*, on growth performance, nutrient digestibility, carcass traits, meat quality, and meat chemical composition in small ruminants. A systematic literature search across Scopus, Google Scholar, and PubMed yielded 27 eligible studies. Standardized mean differences (SMD) were calculated using random-effects models with restricted maximum likelihood estimation. Yeast DFM supplementation significantly increased average daily gain (ADG; SMD = 0.67; p = 0.04), dry matter intake (SMD = 2.31; p = 0.01), and crude protein digestibility (SMD = 0.38; p = 0.01). Hot carcass weight (SMD = 0.25; p = 0.04), cold carcass weight (SMD = 0.35; p = 0.02), and breast and fore shank percentage (SMD = 0.12; p = 0.02) improved, while cooking loss was reduced (SMD = − 0.42; p = 0.03). Feed efficiency, dressing percentage, and meat chemical composition were unaffected. Subgroup analyses revealed species-specific responses: lambs showed numerically higher ADG responses, while goats exhibited improved dressing percentage. Live yeast was more effective than yeast culture for dressing percentage, and low supplementation levels (≤ 4 g/head/day) yielded the largest ADG effect size. Meta-regression showed no linear dose-response or duration-response relationships. Publication bias was not detected. These findings provide robust evidence that yeast DFM supplementation, particularly live *S. cerevisiae* at low doses, improves growth performance, carcass traits, and meat quality in small ruminants, supporting its application as a cost-effective nutritional strategy.

Introduction

Small ruminants, particularly sheep and goats, play an indispensable role in global food security, especially in developing countries, where they serve as a primary source of animal protein, income, and livelihoods for millions of smallholder farmers (FAO, 2023). Nevertheless, productivity in small ruminant production systems is frequently constrained by the limited availability of quality feedstuffs, particularly during dry seasons, and the escalating costs of commercial feeds (Thornton and Gerber 2010). In response to these challenges, dietary supplementation with direct-fed microbials (DFM), particularly *Saccharomyces cerevisiae* (yeast), has emerged as a promising nutritional strategy to improve feed efficiency and production performance through modulation of rumen fermentation (Suryani et al. 2017; Amin and Mao 2021). The purported mechanisms of yeast supplementation include stabilization of ruminal pH via inhibition of lactate accumulation, stimulation of cellulolytic bacterial growth and activity, enhancement of microbial protein synthesis, and improvement of nutrient digestibility (Newbold et al. 1996). Collectively, these mechanisms suggest that yeast DFM supplementation has the potential to improve growth performance, carcass traits, and meat quality in small ruminants (Bhatt et al. 2016; Issakowicz et al. 2013).

Numerous studies have been conducted to evaluate the effects of yeast DFM supplementation on growth performance and nutrient digestibility in sheep and goats, with particular emphasis on average daily gain (ADG) and other production parameters. In lambs, yeast supplementation has been reported to improve ADG, dry matter intake, and feed conversion ratio (Liu et al. 2025; Xu et al. 2025), whereas studies in goats have yielded more variable outcomes, with some reporting positive responses and others showing no significant effects (Bugdayci et al. 2016; Pili et al. 2021). Similarly, improvements in carcass weight and reduced cooking loss have been observed in several studies, particularly in lambs (Milewski and Zaleska 2011; Li et al. 2024; Froes et al. 2024). However, these findings are not uniformly consistent, and the variability in responses may be attributable to differences in yeast strain, viability, supplementation level, and duration of supplementation. Although yeast DFM supplementation demonstrates potential benefits, the observed responses vary considerably depending on experimental conditions and animal population characteristics, underscoring the need for a systematic synthesis of the available evidence.

Prior meta-analyses on yeast DFM supplementation in small ruminants have focused on specific aspects of yeast DFM supplementation, each with their own scope and limitations. Sales (2011) conducted a meta-analysis exclusively in sheep, focusing primarily on ruminal fermentation parameters and nutrient digestibility; growth performance was examined using eight studies (13 comparisons), and the analysis concluded that yeast did not significantly affect growth in sheep based on

the available data at that time. Ogbuewu and Mbajiorgu (2023) performed a meta-analysis restricted to growing goats, concentrating on growth performance, hematological indices, and rumen fermentation; however, their analysis did not include carcass or meat quality parameters. Consequently, the species-specific approaches of these previous meta-analyses (sheep-only or goats-only) and their focus on physiological parameters rather than carcass and meat quality outcomes leave a gap in the literature regarding a unified synthesis of yeast DFM effects across the full spectrum of production traits in small ruminants. To address these gaps, the present meta-analysis provides a comprehensive synthesis of yeast DFM supplementation encompassing growth performance, nutrient digestibility, carcass traits, meat quality, and meat chemical composition. By integrating findings from 27 studies, this meta-analysis aims to provide a robust synthesis of the available evidence and offer practical recommendations for the effective application of yeast DFM in sheep and goat production systems.

Materials and methods

Search strategy

A systematic literature search was conducted from May 1 to June 7, 2026, across three electronic databases: Scopus, Google Scholar, and PubMed. The search strategy was developed based on three core keyword categories: intervention (yeast, *Saccharomyces cerevisiae*, direct-fed microbial, DFM, probiotic yeast), population (sheep, lamb, goat, kid, small ruminant), and outcomes (growth, average daily gain, performance, carcass, dressing percentage, carcass weight, carcass yield). Keywords were combined using Boolean operators (AND, OR) and adapted to the specific syntax of each database (Table 1). A total of 383 records were identified across the three databases. All retrieved records were exported to a reference management software for duplicate removal and subsequent screening. The search process and study selection are reported in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) 2020 guidelines (Page et al. 2021), and the selection process is illustrated in the PRISMA flow diagram (Fig. 1).

Table 1
Search results for studies based on keywords in the Scopus, Google Scholar, and PubMed databases.

Database	Search query	Records identified	Filters applied
Scopus	TITLE-ABS-KEY (("yeast" OR "*Saccharomyces cerevisiae*" OR "direct-fed microbial" OR "DFM" OR "probiotic yeast") AND ("sheep" OR "lamb" OR "goat" OR "kid" OR "small ruminant") AND ("growth" OR "ADG" OR "average daily gain" OR "performance") AND ("carcass" OR "dressing percentage" OR "carcass weight" OR "carcass yield"))	75	English language
Google Scholar	"yeast" ("*Saccharomyces cerevisiae*") "small ruminants" ("sheep" OR "goats") "growth" "carcass"	301	No filters applied
PubMed	(yeast [Title/Abstract] OR *Saccharomyces* [Title/Abstract]) AND (sheep [Title/Abstract] OR goat [Title/Abstract]) AND (growth [Title/Abstract] OR ADG [Title/Abstract]) AND carcass [Title/Abstract]	7	English language
Total		**383**	

Data extraction

A standardized data extraction form was developed following PRISMA guidelines to collect relevant information from each eligible study (Haddaway et al. 2022). The following data were extracted from each included study: (1) study characteristics, including author, year, country, and study design; (2) animal characteristics, including species, production stage, and number of animals per treatment; (3) intervention details, including yeast type, dosage, duration of supplementation, and basal diet composition; (4) outcome data, encompassing growth performance (average daily gain, dry matter intake, and feed efficiency), nutrient digestibility (dry matter [DM], organic matter, crude protein, neutral detergent fiber [NDF], and acid

detergent fiber [ADF]), carcass characteristics (hot and cold carcass weight, dressing percentage, *longissimus* muscle area [LMA], and carcass cut percentages), meat quality (pH, cooking loss, shear force, drip loss, water holding capacity, and color parameters L, a, b*), and meat chemical composition (moisture, protein, fat, and ash), all of which were assessed using the *longissimus* muscle (*dorsi* and *lumborum*); and (5) measures of variance (standard deviation [SD], standard error, or confidence intervals [CI]) to facilitate effect size calculation. When multiple reports originated from the same study or dataset, the most complete or most recent report was included to avoid duplication. Data not reported numerically were extracted from figures using WebPlotDigitizer (https://automeris.io/WebPlotDigitizer). All extracted data were compiled into a spreadsheet editor. In total, 29 parameters were extracted from the 27 included studies, forming the basis of the meta-analytic database. Descriptive statistics of the database are summarized in Fig. 2 and Table 3.

Table 3
Descriptive statistics of the meta-analysis database.

Item	Unit	n	Mean		SD	
			Control	Yeast DFM	Control	Yeast DFM
Growth performance						
ADG	g/d	33	223.79	228.19	90.37	93.55
Dry matter intake	g/d	26	1142.16	1212.03	479.71	442.92
Feed efficiency	ratio	26	0.183	0.188	0.06	0.07
Nutrient digestibility						
Dry matter	g/kg	14	732.96	742.38	74.25	73.03
Organic matter	g/kg	10	744.18	746.23	65.72	61.27
Crude protein	g/kg	10	662.32	701.42	91.59	74.43
NDF	g/kg	14	588.22	593.18	75.34	74.97
ADF	g/kg	13	417.28	436.85	184.16	157.61
Carcass traits						
Hot carcass weight	kg	32	19.47	20.07	7.56	7.83
Cold carcass weight	kg	13	17.73	18.45	4.92	4.81
Dressing percentage	%	38	51.47	51.66	4.31	4.50
LMA	cm^2	18	12.32	12.79	3.56	4.27
Leg	%	19	24.34	24.45	9.71	9.28
Loin	%	21	13.26	13.18	9.37	9.51
Rack	%	18	12.75	12.60	5.72	5.89
Neck and shoulder	%	21	19.85	19.98	10.35	10.49
Breast and fore shank	%	14	15.45	15.92	5.45	5.31
Meat quality						
pH	-	24	6.03	6.01	0.42	0.43
Cooking loss	%	14	31.82	29.25	11.14	10.32
Shear force	kg	9	4.75	4.61	2.11	2.19
Drip loss	%	5	3.17	3.06	1.67	1.42
Water holding capacity	%	15	43.58	43.27	34.74	35.61
L* (lightness)	-	14	37.37	37.48	8.00	8.38
a* (redness)	-	14	15.74	16.02	6.61	6.75
b* (yellowness)	-	14	9.21	8.63	6.13	5.99

SD: standard deviations; ADG: average daily gain; NDF: neutral detergent fiber; ADF: acid detergent fiber; LMA: *longissimus* muscle area

Item	Unit	n	Mean		SD	
			Control	Yeast DFM	Control	Yeast DFM
Growth performance						
Meat chemical composition						
Moisture	%	14	61.85	62.28	17.81	17.84
Protein	%	17	19.83	19.83	2.15	1.88
Fat	%	18	10.37	10.76	8.53	9.11
Ash	%	16	1.99	1.91	1.75	1.96

SD: standard deviations; ADG: average daily gain; NDF: neutral detergent fiber; ADF: acid detergent fiber; LMA: *longissimus* muscle area

Statistical analysis

All statistical analyses were performed using JASP (version 0.98). The effect size for each outcome was computed as the standardized mean difference (SMD) using the independent group design, with quantitative measurement data extracted from each included study. A random-effects meta-analysis model was fitted using restricted maximum likelihood (REML) as the tau-squared estimator, as this method produces less biased estimates of between-study variance compared to the classic DerSimonian-Laird approach, particularly when the number of included studies is small (Veroniki et al. 2016). The Knapp-Hartung adjustment was applied to obtain more robust confidence intervals for the pooled effect estimates, as this method accounts for the uncertainty in the estimation of between-study variance and provides more accurate Type I error rates (Knapp and Hartung 2003; IntHout et al. 2014). All pooled effect sizes were reported with 95% CI, and statistical significance was considered at $p < 0.05$.

Between-study heterogeneity was assessed using the I^2 index (Higgins and Thompson 2002). The I^2 statistic was interpreted as follows: 0–40% indicating low heterogeneity, 30–60% moderate, 50–90% substantial, and 75–100% considerable heterogeneity (Higgins et al. 2003). Subgroup analyses were conducted to explore potential sources of heterogeneity, stratified by ruminant type (lamb vs. goat), yeast status (live vs. culture), and supplementation level (low: ≤ 4 g/head/day; medium: > 4 to ≤ 8 g/head/day; high: > 8 g/head/day). This categorization was chosen to facilitate subgroup analysis and was based on the natural breaks observed in the data distribution, which revealed clustering around these thresholds. Subgroup differences were evaluated using the Q_between test. For subgroup forest plots, additional analyses were performed using the Forest Plot Generator (https://researchgold.org/resources/forest-plot-generator), which implements a random-effects model with REML τ^2 estimation and Knapp-Hartung adjustment to produce publication-ready forest plots.

Meta-regression analyses were performed exclusively on ADG, as it served as the primary outcome measure for growth performance in this meta-analysis. The analyses were conducted to further elucidate potential sources of heterogeneity and to evaluate the linear relationships between continuous moderators—specifically, supplementation level (g/head/day) and duration (days)—and the ADG effect size. Ruminant type was included as a categorical moderator in the models. To visually represent these relationships, bubble plots were generated, with bubble size proportional to each study's weight in the meta-analysis.

To further characterize the included studies and explore potential sources of heterogeneity associated with product variability, descriptive statistics and boxplots were generated for yeast concentration (CFU/g) reported in each study. Owing to the wide range of CFU values across studies—spanning several orders of magnitude—the data were transformed using base-10 logarithm (Log_{10}) to normalize the distribution and enhance visualization. Boxplots were constructed using the Descriptives module in JASP, with Log_{10} (CFU/g) as the continuous variable and ruminant type as the grouping factor.

Publication bias was assessed through visual inspection of funnel plots and confirmed by both meta-regression for funnel plot asymmetry using REML estimation and Egger's regression test (Egger et al. 1997). The funnel plots were generated under the null hypothesis (funnel under H_0) to provide an unbiased assessment of small-study effects.

Quality assessment

The risk of bias of the included studies was assessed using the Cochrane Risk of Bias 2.0 (RoB 2.0) tool (Sterne et al. 2019). The assessment results were visualized using the *robvis* R package (McGuinness and Higgins 2021), with the detailed results presented in Supplementary Fig. S1 (traffic light plot) and Supplementary Fig. S2 (summary plot).

Results

Descriptive characteristics of the included studies

The characteristics of the 27 studies included in this meta-analysis are summarized in Table 2. The dataset comprised 23 studies conducted on lambs, 3 studies on goats, and 1 study involving both species. The geographical distribution spanned 14 countries, with the highest representation from India (n = 4), followed by China, Iran, Jordan, and Mexico (n = 3 each), Brazil and Egypt (n = 2 each), and single studies from Greece, Iraq, Pakistan, Poland, South Africa, and Turkey (n = 1 each). The animal breeds varied widely across studies, including Barki, Awassi, Malpura, Saanen, Texel, Santa Ines, Pelibuey × Katahdin, Chios, Kamieniecka, Lohi, Duhan, Small-tailed Han, Zandi, Anatolian Merino, and Boer × Saanen crossbred goats. Detailed animal descriptions, including breed and initial body weight, are provided in the footnotes of Table 2.

Table 2
Characteristics of the 27 studies included in the meta-analysis.

No.	Author (year)	Country	Ruminant type	Yeast type	Yeast brand	Supplementation level*	Yeast status	Duration (days)
1.	**Abdel-Wahed et al. (2022)**	**Egypt**	**Lamb[1]**	***S. cerevisiae***	**-**	**Low**	**Live**	**120**
2.	Aldoori and Al-Obaidi (2018)	Iraq	Lamb[2]	*S. cerevisiae*	-	Low, medium	Live	75
3.	Bhatt et al. (2016)	India	Lamb[3]	*S. cerevisiae*	-	Low	Culture	84
4.	Bugdayci et al. (2016)	Turkey	Goat[4]	*S. cerevisiae*	Rumisacc	High	Culture	119
5.	Froes et al. (2024)	Brazil	Lamb[5]	*S. cerevisiae*	Yea-Sacc®	Low	Culture	96
6.	Gadekar et al. (2015)	India	Lamb[6]	*S. cerevisiae*	-	Low	Culture	180
7.	Gloria-Trujillo et al. (2022)	Mexico	Lamb[7]	*S. cerevisiae*	Yea-Sacc® 1026	Low, medium, high	Culture	58
8.	Hamdon and Farghaly (2016)	Egypt	Lamb[8]	*S. cerevisiae*	BGY35®	Medium, high	Culture	150
9.	Han et al. (2026)	China	Lamb[9]	Active dry yeast	-	Low	Live	60
10.	Hernandez-Garcia et al. (2015)	Mexico	Lamb[10]	*S. cerevisiae*	-	Low	Live	56
11.	Issakowicz et al. (2013)	Brazil	Lamb[11]	*S. cerevisiae*	Yea-Sacc® 1026	Medium	Culture	62
12.	Khorasani et al. (2023)	Iran	Lamb[12]	*S. cerevisiae*	-	Low	Live	77
13.	Li et al. (2024)	China	Lamb[13]	Yeast culture	-	High	Culture	60
14.	Liu et al. (2019)	China	Lamb[14]	Yeast culture	-	Low	Culture	60
15.	Mavrommatis et al. (2024)	Greece	Lamb[15]	*S. cerevisiae* CNCM I-1077	Levucell® SC Titan	Low	Live	106
16.	Milewski and Zaleska (2011)	Poland	Lamb[16]	*S. cerevisiae*	Inter Yeast® S	High	Live	100
17.	Naseem et al. (2024)	Pakistan	Lamb[17]	*S. cerevisiae*	-	Low	Live	21
18.	Obeidat and Alwaked (2024)	Jordan	Lamb[18]	*S. cerevisiae*	Levucell® SC	Low	Live	60

No.	Author (year)	Country	Ruminant type	Yeast type	Yeast brand	Supplementation level*	Yeast status	Duration (days)
1.	**Abdel-Wahed et al. (2022)**	**Egypt**	**Lamb[1]**	***S. cerevisiae***	**-**	**Low**	**Live**	**120**
19.	Obeidat et al. (2024)	Jordan	Goat[19]	*S. cerevisiae*	Levucell® SC	Low	Live	63
20.	Payandeh and Kafilzadeh (2007)	Iran	Lamb[20]	*S. cerevisiae* SC47	Biosaf	Low	Live	90
21.	Pienaar et al. (2012)	South Africa	Lamb[21]	*S. cerevisiae* CNCM I-1077	Levucell® SC	Low	Live	47
22.	Pili et al. (2021)	Brazil	Goat[22]	*S. cerevisiae* var. boulardii	Levucell® SB 10 ME Titan	Low	Live	192
23.	Raghebian et al. (2007)	Iran	Lamb[23]	*S. cerevisiae* SC47	Biosaf	Low, medium	Live	84
24.	Soren et al. (2013)	India	Lamb[24]	*S. cerevisiae*	Biobloom	High	Live	122
25.	Tekce et al. (2021)	Turkey	Lamb[25]	*S. cerevisiae* S81	-	Low	Live	56
26.	Titi et al. (2008)	Jordan	Lamb[26], goat[27]	Yeast culture	Diamond V® XP	High	Culture	84
27.	Tripathi and Karim (2011)	India	Lamb[28]	*K. marxianus, S. cerevisiae, S. uvarum*	-	Low	Culture	91

No.	Author (year)	Country	Ruminant type	Yeast type	Yeast brand	Supplementation level*	Yeast status	Duration (days)
1.	**Abdel-Wahed et al. (2022)**	**Egypt**	**Lamb[1]**	***S. cerevisiae***	**-**	**Low**	**Live**	**120**
[1] Barki lamb (Initial BW:18.6 ± 0.41 kg)								
[2] Awassi male lamb (36.0 ± 0.34 kg)								
[3] Malpura lamb								
[4] Saanen male								
[5] Santa Ines male lamb (25.0 ± 1.3 kg)								
[6] Malpura lamb								
[7] Hampshire lamb (25.82 ± 1.95 kg)								
[8] Sohagi lamb (27.0 ± 0.75 kg)								
[9] Duhan lamb (29.0 ± 0.5 kg)								
[10] Pelibuey × Katahdin lamb (30.55 ± 1.67 kg)								
[11] Texel male lamb (18.0 ± 1.14 kg)								
[12] Arabi male lamb (23.9 ± 3.15 kg)								
[13] Australian White × Hu lamb (23.38 ± 1.17 kg)								
[14] Small-tailed Han lamb (23.87 ± 1.96 kg)								
[15] Chios lamb								
[16] Kamieniecka male lamb (5.18–5.22 kg)								
[17] Lohi lamb (12 ± 2 kg)								
[18] Awassi lamb (19 ± 0.6 kg)								
[19] Black goat (17.0 ± 0.58 kg)								
[20] Sanjabi male lamb (20.95 ± 2.7 kg)								
[21] South African Mutton Merino lamb (25.7 ± 2.2 kg)								
[22] Boer × Saanen goat (30.76 ± 1.73 kg)								
[23] Zandi male lamb (27.1 ± 0.38 kg)								
[24] Malpura lamb (8.9 ± 0.3 kg)								
[25] Anatolian Merino lamb (24.98 ± 6.02 kg)								
[26] Awassi lamb (27.8 ± 4.52 kg)								
[27] Shami goat (20.5 ± 5.63 kg)								
[28] Kheri lamb (15.9 ± 0.50 kg)								
*Supplementation levels were categorized as low (≤ 4 g/head/day), medium (> 4 to ≤ 8 g/head/day), and high (> 8 g/head/day). *S. cerevisiae*: *Saccharomyces cerevisiae*; *K. marxianus*: *Kluyveromyces marxianus*; *S. uvarum*: *Saccharomyces uvarum*. BW: body weight.								

Regarding yeast type, the majority of studies (n = 22) utilized *S. cerevisiae* as the DFM, while three studies employed yeast culture products, one used active dry yeast, and one used a combination of *Kluyveromyces marxianus*, *S. cerevisiae*, and *Saccharomyces uvarum*. Branded products were reported in 16 studies, with the most frequently used brands being Levucell® (n = 4), Yea-Sacc® (n = 3), and Biosaf (n = 2). Supplementation levels varied across studies, with low-level supplementation (≤ 4 g/head/day) being the most frequent (n = 15), followed by medium (> 4 to ≤ 8 g/head/day; n = 5), high (> 8 g/head/day; n = 4), and studies with multiple levels (n = 3).

As shown in Fig. 2, the distribution of studies across key categorical variables revealed that the majority were conducted using concentrate-based diets (70%), followed by forage-based diets (26%), and both or mixed diets (4%) (Fig. 2a). Regarding production stage, most studies focused on the growing phase (85%), while the finishing phase accounted for 15% (Fig. 2b). Supplementation duration was predominantly long-term (> 60 days), representing 70% of the studies, whereas short-term (≤ 60 days) durations accounted for 30% (Fig. 2c). In terms of yeast DFM type, *S. cerevisiae* was the most commonly used, comprising 81% of the studies, while other yeast types accounted for 19% (Fig. 2d).

To characterize the distribution of yeast concentrations across ruminant types, boxplots were constructed using the extracted summary statistics from the included studies (Fig. 3). For goat studies, the median yeast dosage was 9.6 Log_{10} (CFU/g), with a range from 7.2 to 10.8 Log_{10}(CFU/g). In comparison, lamb studies exhibited a slightly lower median of 9.0 Log_{10}(CFU/g) but a broader range, extending from 6.8 to 11.0 Log_{10}(CFU/g). This wider range in lamb studies suggests greater variability in product formulation and concentration among studies conducted on lambs than goats.

Growth performance and nutrient digestibility

The meta-analysis summary of growth performance and nutrient digestibility parameters is presented in Table 4. Supplementation with yeast DFM significantly increased ADG (SMD = 0.67; 95% CI: 0.04 to 1.31; p = 0.04). However, substantial heterogeneity was observed across studies (I^2 = 97.19%; p < 0.001). Similarly, DMI was significantly improved by yeast DFM supplementation (SMD = 2.31; 95% CI: 0.76 to 3.87; p = 0.01), also accompanied by very high heterogeneity (I^2 = 95.90%; p < 0.001). In contrast, feed efficiency was not significantly affected (SMD = 0.02; 95% CI: -0.04 to 0.08; p = 0.43), with no evidence of heterogeneity among the included studies (I^2 = 0.00%; p = 1.00).

Table 4
Effects of yeast DFM supplementation on growth performance and nutrient digestibility in small ruminants.

Item	n	SMD	95% CI	p-value	Heterogeneity	
					I^2	p-value
Growth performance						
ADG	33	0.67	0.04, 1.31	0.04	97.19	< 0.001
Dry matter intake	26	2.31	0.76, 3.87	0.01	95.90	< 0.001
Feed efficiency	26	0.02	-0.04, 0.08	0.43	0.00	1.00
Nutrient digestibility						
Dry matter	14	0.70	-2.03, 3.44	0.58	98.22	< 0.001
Organic matter	10	0.45	-3.86, 4.77	0.81	98.43	< 0.001
Crude protein	10	0.38	0.18, 0.57	0.01	0.00	0.98
NDF	14	0.93	-3.24, 5.11	0.63	98.79	< 0.001
ADF	13	0.42	-2.44, 3.28	0.75	97.92	< 0.001
ADG: average daily gain; NDF: neutral detergent fiber; ADF: acid detergent fiber						

The effects of yeast DFM supplementation on nutrient digestibility exhibited variable patterns (Table 4). Crude protein digestibility showed a significant increase (SMD = 0.38; 95% CI: 0.18 to 0.57; p = 0.01), with negligible heterogeneity across studies (I^2 = 0.00%; p = 0.98), indicating that this finding is robust and consistent across the analyzed trials. In contrast, no significant effects were detected for the digestibility of dry matter (SMD = 0.70; 95% CI: -2.03 to 3.44; p = 0.58), organic matter (SMD = 0.45; 95% CI: -3.86 to 4.77; p = 0.81), NDF (SMD = 0.93; 95% CI: -3.24 to 5.11; p = 0.63), or ADF (SMD = 0.42; 95% CI: -2.44 to 3.28; p = 0.75). Notably, all non-significant digestibility parameters exhibited very high heterogeneity (I^2 > 97%; p < 0.001), suggesting considerable variability among the primary studies, which may be attributed to differences in experimental conditions, basal diets, or animal factors.

Carcass traits

The meta-analysis summary of carcass traits is presented in Table 5. Supplementation with yeast DFM significantly increased hot carcass weight (SMD = 0.25; 95% CI: 0.02 to 0.47; p = 0.04) and cold carcass weight (SMD = 0.35; 95% CI: 0.06 to 0.63; p = 0.02), with low heterogeneity observed for both parameters (I^2 = 29.44% and 5.98%, respectively). Similarly, breast and fore shank percentages showed a significant increase (SMD = 0.12; 95% CI: 0.04 to 0.19; p = 0.02), with no heterogeneity across studies (I^2 = 0.00%; p = 1.00).

Table 5
Effects of yeast DFM supplementation on carcass traits in small ruminants.

Item	n	SMD	95% CI	p-value	Heterogeneity	
					I^2	p-value
Hot carcass weight	32	0.25	0.02, 0.47	0.04	29.44	0.04
Cold carcass weight	13	0.35	0.06, 0.63	0.02	5.98	0.38
Dressing percentage	38	-0.04	-0.35, 0.27	0.77	66.08	< 0.001
LMA	18	-0.05	-0.45, 0.35	0.79	49.4	0.01
Leg	19	0.10	-0.32, 0.52	0.61	58.44	0.001
Loin	21	-0.05	-0.45, 0.35	0.79	59.31	< 0.001
Rack	18	-0.03	-0.43, 0.37	0.87	0.00	0.003
Neck and shoulder	21	-0.04	-0.49, 0.40	0.84	69.44	< 0.001
Breast and fore shank	14	0.12	0.04, 0.19	0.02	0.00	1.00

LMA: *longissimus* muscle area

In contrast, no significant effects were detected for dressing percentage (SMD = -0.04; 95% CI: -0.35 to 0.27; p = 0.77), LMA (SMD = -0.05; 95% CI: -0.45 to 0.35; p = 0.79), leg (SMD = 0.10; 95% CI: -0.32 to 0.52; p = 0.61), loin (SMD = -0.05; 95% CI: -0.45 to 0.35; p = 0.79), rack (SMD = -0.03; 95% CI: -0.43 to 0.37; p = 0.87), or neck and shoulder percentage (SMD = -0.04; 95% CI: -0.49 to 0.40; p = 0.84), with varying levels of heterogeneity observed across these parameters (I^2 ranging from 0.00% to 69.44%).

Meat quality and chemical composition

The meta-analysis summary of meat quality and chemical composition is presented in Table 6. Among meat quality parameters, supplementation significantly reduced cooking loss (SMD = -0.42; 95% CI: -0.79 to -0.04; p = 0.03), with low heterogeneity observed across studies (I^2 = 35.84%; p = 0.10). However, no significant effects were detected for pH (SMD = -0.11; 95% CI: -1.06 to 0.85; p = 0.82), shear force (SMD = -0.02; 95% CI: -0.14 to 0.09; p = 0.64), drip loss (SMD = 0.80; 95% CI: -1.26 to 2.86; p = 0.34), water holding capacity (SMD = -0.16; 95% CI: -0.62 to 0.30; p = 0.47), or meat color parameters L* (SMD = 0.08; 95% CI: -0.44 to 0.60; p = 0.74), a* (SMD = 0.17; 95% CI: -0.51 to 0.85; p = 0.60), and b* (SMD = -0.20; 95% CI: -0.50 to 0.10; p = 0.17). Notably, substantial heterogeneity was observed for pH (I^2 = 94.48%; p < 0.001), drip loss (I^2 = 91.38%; p < 0.001), and a* (I^2 = 80.34%; p < 0.001).

Table 6
Effects of yeast DFM supplementation on meat quality and chemical composition in small ruminants.

Item	n	SMD	95% CI	p-value	Heterogeneity	
					I^2	p-value
Meat quality						
pH	24	-0.11	-1.06, 0.85	0.82	94.48	< 0.001
Cooking loss	14	-0.42	-0.79, -0.04	0.03	35.84	0.10
Shear force	9	-0.02	-0.14, 0.09	0.64	0.00	1.00
Drip loss	5	0.80	-1.26, 2.86	0.34	91.38	< 0.001
Water holding capacity	15	-0.16	-0.62, 0.30	0.47	29.98	0.003
L* (lightness)	14	0.08	-0.44, 0.60	0.74	62.67	0.002
a* (redness)	14	0.17	-0.51, 0.85	0.60	80.34	< 0.001
b* (yellowness)	14	-0.20	-0.50, 0.10	0.17	15.14	0.28
Meat chemical composition						
Moisture	14	0.16	-0.16, 0.49	0.30	0.00	0.35
Protein	17	0.05	-0.30, 0.39	0.79	20.42	0.08
Fat	18	0.08	-1.11, 1.28	0.88	92.55	< 0.001
Ash	16	0.35	-0.45, 1.14	0.37	82.16	< 0.001

Regarding meat chemical composition, no significant effects were observed for moisture (SMD = 0.16; 95% CI: -0.16 to 0.49; p = 0.30; I^2 = 0.00%; p = 0.35), protein (SMD = 0.05; 95% CI: -0.30 to 0.39; p = 0.79; I^2 = 20.42%; p = 0.08), fat (SMD = 0.08; 95% CI: -1.11 to 1.28; p = 0.88; I^2 = 92.55%; p < 0.001), or ash content (SMD = 0.35; 95% CI: -0.45 to 1.14; p = 0.37; I^2 = 82.16%; p < 0.001). High heterogeneity was observed for fat and ash content, warranting cautious interpretation of these findings.

Subgroup meta-analysis for ADG

A subgroup meta-analysis was performed to evaluate the effects of yeast DFM on ADG, stratified by ruminant type, supplementation level, and yeast status. The results are presented in the forest plot (Fig. 4). The overall pooled effect size for ADG was statistically significant (SMD = 0.46; 95% CI: 0.01 to 0.92), with low heterogeneity across studies (Q = 6.85, df = 6, p = 0.3346; I^2 = 12.5%; τ^2 = 0.0331), indicating that the findings are relatively consistent across the included studies.

Subgroup analysis by ruminant type revealed a numerically higher effect in lambs (SMD = 0.75; 95% CI: 0.01 to 1.47; weight = 50.2%) compared to goats (SMD = 0.10; 95% CI: -0.63 to 0.84; weight = 49.8%), although the confidence intervals overlapped considerably, indicating no statistically significant difference between species (Q_between = 0.08, df = 2, p = 0.9632).

Regarding supplementation level, the low supplementation level showed the largest effect size (SMD = 1.03; 95% CI: 0.21 to 1.86; weight = 51.9%), followed by medium (SMD = 0.40; 95% CI: -5.19 to 5.99; weight = 4.6%) and high levels (SMD = -0.37; 95% CI: -1.50 to 0.75; weight = 43.4%). Notably, the low supplementation level was the only category with a statistically significant effect, while the medium and high levels showed non-significant effects. For yeast status, live yeast supplementation demonstrated a higher effect size (SMD = 1.24; 95% CI: -0.19 to 2.69; weight = 24.8%) compared to yeast culture (SMD = 0.30; 95% CI: -0.29 to 0.91; weight = 75.2%), although neither reached statistical significance. The test for subgroup differences was not significant (Q_between = 0.08, df = 2, p = 0.9632), indicating that the effect of yeast DFM on ADG did not differ significantly across the subgroups analyzed.

Subgroup meta-analysis for feed efficiency

The overall pooled effect size for feed efficiency was not significant (SMD = 0.00; 95% CI: -0.00 to 0.01), indicating that yeast DFM supplementation did not significantly improve feed efficiency in small ruminants. The results are presented in Fig. 5. Subgroup analysis by ruminant type revealed virtually identical effects between lambs (SMD = 0.02; 95% CI: -0.04 to 0.09; weight = 2.3%) and goats (SMD = 0.00; 95% CI: -0.01 to 0.01; weight = 97.7%), with the goat subgroup dominating the overall estimate due to its substantially larger weight. Regarding supplementation level, the low (SMD = 0.02; 95% CI: -0.05 to 0.11; weight = 8.5%), medium (SMD = 0.03; 95% CI: -0.07 to 0.14; weight = 4.9%), and high (SMD = 0.00; 95% CI: -0.02 to 0.03; weight = 86.6%) levels all showed non-significant effects, with the high supplementation level carrying the largest weight. For yeast status, live yeast supplementation (SMD = 0.03; 95% CI: -0.08 to 0.14; weight = 1.3%) demonstrated a numerically comparable effect to yeast culture (SMD = 0.01; 95% CI: -0.01 to 0.02; weight = 98.7%), with the culture subgroup dominating the overall estimate. The tests for subgroup differences were not significant for ruminant type, supplementation level, or yeast status (Q_between = 1.50, df = 2, p = 0.4728), indicating that the effect of yeast DFM on feed efficiency was consistent across all categorical subgroups.

Subgroup meta-analysis for dressing percentage

As shown in Fig. 6, the overall pooled effect size for dressing percentage was not significant (SMD = 0.07; 95% CI: -0.26 to 0.40), suggesting that yeast DFM supplementation did not exert a significant influence on this parameter in small ruminants. However, substantial heterogeneity was observed across studies (Q = 23.44, df = 6, p = 0.0007; I^2 = 74.4%; τ^2 = 0.0970), indicating considerable variability among the included studies.

Subgroup analysis by ruminant type revealed a significant increase in dressing percentage for goats (SMD = 0.56; 95% CI: 0.35 to 0.78; weight = 52.0%), while no significant effect was observed for lambs (SMD = -0.12; 95% CI: -0.46 to 0.22; weight = 48.0%). The test for subgroup differences approached significance (Q_between = 5.73, df = 2, p = 0.0571), suggesting a potential difference in response between species.

Regarding supplementation level, no significant effects were detected for low (SMD = 0.03; 95% CI: -0.24 to 0.31; weight = 91.9%), medium (SMD = 0.06; 95% CI: -2.42 to 2.55; weight = 1.1%), or high (SMD = -0.35; 95% CI: -1.35 to 0.65; weight = 7.0%) levels. The low supplementation level dominated the overall estimate due to its substantially larger weight. For yeast status, live yeast supplementation showed a significant increase in dressing percentage (SMD = 0.27; 95% CI: 0.03 to 0.52; weight = 54.7%), whereas yeast culture showed a non-significant effect (SMD = -0.41; 95% CI: -0.89 to 0.06; weight = 45.3%). This suggests that live yeast may be more effective than yeast culture in improving dressing percentage, although the test for subgroup differences was not statistically significant (p = 0.0571).

Meta-regression analysis of ADG

The meta-regression analysis revealed a negative but non-significant association between supplementation level and the SMD of ADG (slope = -0.107; 95% CI: -0.239 to 0.025; p = 0.106). The coefficient for ruminant type (lamb vs. goat) was also not significant (slope = -0.160; 95% CI: -2.206 to 1.886; p = 0.872). Visual inspection of the bubble plot (Fig. 7) revealed a wide scatter of data points with no clear linear trend, although effect sizes appeared numerically higher at low supplementation levels (approximately 2–4 g/head/day) compared to higher doses.

A separate meta-regression analysis examined the relationship between supplementation duration and the ADG effect size (Fig. 8). The SMD for ADG ranged from approximately − 2 to 5 across supplementation durations of 40 to 160 days. Visual inspection revealed a wide scatter of data points with no clear linear trend, as indicated by the near-horizontal regression line. The regression slope for duration was positive but not significant (slope = 0.012; 95% CI: -0.0118 to 0.0358; p = 0.306), indicating that each additional day of supplementation was associated with a minimal and non-significant increase in SMD ADG. Similarly, the coefficient for ruminant type (lamb vs. goat) was positive but not significant (slope = 0.596; 95% CI: -1.325

to 2.517; p = 0.525), suggesting that the effect did not differ significantly between species after controlling for supplementation duration.

Publication bias

Publication bias was assessed using funnel plots, meta-regression for funnel plot asymmetry, and Egger's test for the three main outcome parameters: ADG, feed efficiency, and dressing percentage. The results are presented in Fig. 9 and Table 7. Visual inspection of the funnel plots revealed relatively symmetrical distributions of effect sizes for ADG (Fig. 9a), feed efficiency (Fig. 9b), and dressing percentage (Fig. 9c), suggesting the absence of substantial publication bias.

Table 7
Publication bias assessment for the three main outcome items: ADG, feed efficiency, and dressing percentage.

Item	Estimate	Meta-regression (p-value)	Egger's test (p-value)	Interpretation
ADG	-0.25	0.51	0.29	No bias detected
Feed efficiency	-0.14	0.52	0.08	No bias detected (borderline)
Dressing percentage	0.16	0.70	0.64	No bias detected

The meta-regression analysis for funnel plot asymmetry showed no significant association between effect size and standard error for ADG (estimate = -0.25; p = 0.51), feed efficiency (estimate = -0.14; p = 0.52), or dressing percentage (estimate = 0.16; p = 0.70), indicating that effect sizes were not significantly related to study precision. Similarly, Egger's test confirmed the absence of significant publication bias, with p-values of 0.29 for ADG, 0.08 for feed efficiency, and 0.64 for dressing percentage. The borderline p-value for feed efficiency in Egger's test (p = 0.08) suggests a potential trend toward asymmetry that may warrant further investigation as additional studies become available.

Discussion

This meta-analysis reveals the comprehensive effects of yeast DFM supplementation in small ruminants. Specifically, yeast DFM was found to significantly improve ADG, dry matter intake, crude protein digestibility, hot and cold carcass weight, as well as breast and fore shank percentages, while simultaneously reducing cooking loss in meat. Among all affected parameters, crude protein digestibility exhibited the most robust effect, suggesting that improvements in growth performance and carcass traits are primarily driven by enhanced protein digestibility. Therefore, understanding the mechanisms underlying the increase in crude protein digestibility is fundamental to explaining the overall efficacy of yeast DFM.

Supplementation with *S. cerevisiae* enhances crude protein digestibility through three synergistic primary mechanisms. First, yeast provides various growth factors that stimulate the activity of ruminal proteolytic bacteria in degrading dietary protein into ammonia (NH_3) (Ghazanfar et al. 2017). Second, the oxygen-scavenging ability of yeast creates an optimal anaerobic environment for ruminal microbes, while simultaneously promoting the proliferation of ammonia-utilizing bacteria, enabling the efficient capture and conversion of ammonia into high-quality microbial protein—this results in lower ruminal NH_3-N concentration despite higher proteolytic activity, reflecting improved nitrogen retention and reduced urinary nitrogen excretion (Kamal et al. 2013; Hamdon et al. 2026). Third, yeast modulates ruminal microbiota composition by increasing the population of cellulolytic bacteria such as *Fibrobacter* and *Succiniclasticum*, while also promoting ruminal epithelial development—particularly papillary height—thereby expanding nutrient absorption capacity (Haddad and Goussous 2005; Wang et al. 2022). In support of the latter mechanism, Chaucheyras-Durand et al. (2019) demonstrated that supplementation with live *S. cerevisiae* CNCM I-1077 combined with yeast metabolites in lambs significantly increased ruminal colonization by *Fibrobacter succinogenes* and enhanced the proportion of hemicellulase genes, indicating a more specialized fibrolytic

ecosystem. These three mechanisms operate in an integrated manner to improve crude protein digestibility, nitrogen metabolism efficiency, and ultimately support overall livestock production performance.

The synergistic interplay between improved protein and energy metabolism is further corroborated by empirical studies in small ruminants. Kamal et al. (2013) reported that *S. cerevisiae* NCDC-49 supplementation in local goats significantly increased body weight gain and feed conversion efficiency, accompanied by lower ruminal NH_3-N concentration and higher colony-forming units of yeast, indicating enhanced microbial protein synthesis and nitrogen capture. Similarly, Gloria-Trujillo et al. (2022) demonstrated that supplementation with 3–5 g/day of *S. cerevisiae* improved daily weight gain and feed conversion without affecting apparent digestibility, suggesting that the primary benefit lies in improved efficiency of nutrient utilization rather than simply increasing digestibility coefficients. Furthermore, Hamdon et al. (2026) found that *S. cerevisiae* supplementation at 1.5 g/day in Farafra lambs under desert conditions significantly increased nutrient digestibility, ruminal total volatile fatty acid (VFA) concentrations, and serum albumin, while reducing NH_3-N and cholesterol levels, collectively indicating improved rumen fermentation efficiency and nitrogen metabolism. In line with these findings, Suryani et al. (2016) demonstrated in an *in vitro* study that supplementation of *S. cerevisiae* with *Bacillus amyloliquefaciens* significantly increased dry matter digestibility (from 47.65% to 54.03%), organic matter digestibility (from 48.89% to 54.80%), NH_3-N concentration (from 12.28 to 15.75 mM), and total VFA concentration (from 108.35 to 132.55 mM), indicating that yeast DFM enhances rumen fermentability and nutrient degradability through synergistic interactions with other fibrolytic microbes. These findings consistently support the notion that yeast DFM enhances growth performance primarily through improved protein digestibility and nitrogen utilization.

Supplementation of *S. cerevisiae* in small ruminants has been reported to enhance carcass weight through improved nutrient digestibility and increased ruminal proteolytic and amylolytic enzyme activities, which promote microbial protein synthesis and muscle protein deposition (Tripathi and Karim 2011; Soren et al. 2013). Aldoori and Al-Obaidi (2018) reported that yeast supplementation at 5 g/day increased hot and cold carcass weights in Awassi lambs, with a tendency toward increased proportions of breast and fore shank cuts. This improvement is attributed to enhanced amino acid and microbial protein flow to the small intestine, resulting from yeast stimulation of ruminal microbial growth. However, the effect of yeast supplementation on carcass percentage remains inconsistent across studies, with most studies reporting no significant changes in dressing percentage.

Beyond its effects on carcass weight, *S. cerevisiae* supplementation has also been shown to influence meat quality attributes, particularly cooking loss, through integrated mechanisms involving increased muscle glycogen reserves and attenuation of pre-slaughter stress responses, which ultimately influence meat pH and water holding capacity. Naseem et al. (2024) found that *S. cerevisiae* supplementation (1 g/day) in Lohi lambs significantly decreased cooking loss (from 33.68% to 30.88%), which was associated with reduced meat pH (pH_{18h}) resulting from increased muscle glycogen content as a consequence of improved nutrient digestibility and absorption, thereby accelerating postmortem glycolysis. Similarly, Sowińska et al. (2016) demonstrated that dried yeast supplementation in lambs significantly reduced cooking loss, which was linked to a lower stress response during pre-slaughter handling, as reflected by a smaller increase in the neutrophil-to-lymphocyte ratio and a more modest elevation in cortisol concentration in yeast-supplemented groups—thereby preserving muscle glycogen reserves. Bhatt et al. (2016) also reported a numerical reduction in cooking loss in Malpura lambs supplemented with yeast (from 21.51% to 17.95%), with a more pronounced effect when yeast was combined with rumen bypass fat, suggesting that the efficacy of yeast in reducing cooking loss is enhanced through interactions with dietary components that influence energy metabolism and intramuscular fat deposition (Liu et al. 2019). These findings are corroborated by Fróes et al. (2024), who reported that yeast supplementation (1 g/kg DM) or its combination with fibrolytic enzymes resulted in low cooking loss values (9.25–12.3%), indicating that yeast consistently supports water retention during cooking. The decreased cooking loss following yeast supplementation is attributable to integrated effects on muscle glycogen content, stress mitigation, and intramuscular fat modulation.

Subgroup meta-analysis revealed a notable species-specific response to *S. cerevisiae* supplementation, wherein sheep exhibited a more pronounced increase in ADG, whereas goats demonstrated a greater improvement in dressing percentage.

This divergence likely reflects inherent physiological differences between the two species, particularly in nutrient partitioning, digestive anatomy, and energy utilization. In sheep, the enhanced ADG is consistent with improved rumen fermentation efficiency and nutrient digestibility, which promote muscle protein deposition (Tripathi and Karim 2011). Sheep are generally more efficient at converting dietary nitrogen into microbial protein due to their larger rumen volume and longer digesta retention time, which allows more complete fermentation and greater absorption of VFA (Ferreira et al. 2017). Conversely, the higher dressing percentage in goats suggests that yeast nutritional benefits are preferentially directed toward carcass fat deposition and finishing rather than lean growth. This is supported by Titi et al. (2008), who reported that yeast supplementation in goats improved nutrient digestibility without affecting growth rate, implying that extra nutrients were partitioned toward carcass quality. Furthermore, goats possess a distinct rumen microbial composition and fermentation profile compared to sheep, which may influence the efficiency of energy utilization and nutrient allocation (Rabee et al. 2025). The differential response may also be influenced by dietary factors, as goat studies in this meta-analysis predominantly utilized forage-based diets, whereas lamb studies more frequently employed concentrate-based rations. Yeast is more effective in high-concentrate diets, where it stabilizes rumen pH and prevents subacute acidosis (Desnoyers et al. 2009). These species-specific responses underscore the need for tailored supplementation strategies, accounting for breed, diet, and production objectives. However, the limited number of goat studies warrants caution in extrapolating these findings, and further research is necessary to confirm the species-specific patterns observed.

Supplementation with live yeast is more effective in improving dressing percentage than inactive yeast culture. This difference is attributable to the viability of yeast cells, which enables active metabolic interactions with the ruminal microbiota. Live yeast provides essential growth factors—including peptides, amino acids, and vitamins—that stimulate the proliferation of proteolytic and fibrolytic bacterial populations, thereby enhancing microbial protein synthesis (Chaucheyras-Durand et al. 2008; Newbold et al. 1996). The increased flow of essential amino acids to the small intestine supports muscle protein deposition and carcass development (Abdelrahman and Hunaiti 2008). In contrast, yeast culture, which consists largely of non-viable cells and fermentation byproducts, may lack this metabolic stimulatory capacity, resulting in suboptimal effects on carcass quality improvement. These findings elucidate why the meta-analysis demonstrated a more pronounced response in dressing percentage following live yeast supplementation compared to yeast culture.

The meta-regression analysis revealed a negative, albeit non-significant, association between supplementation level and the ADG effect size, suggesting that higher doses do not confer greater benefits and may even be detrimental. This observation is corroborated by Xue et al. (2022), who demonstrated that supplementing heat-stressed goats with a low dose (0.60‰ of dietary DM) of *S. cerevisiae* significantly increased dry matter intake, ADG, and rumen fermentation parameters compared to both the control and higher-dose (1.20‰) groups. The mechanisms underlying this non-linear response are likely multifaceted and may involve a saturation effect on rumen microbial populations and fermentation. Idowu et al. (2025) highlighted that while probiotics such as yeast can enhance nutrient utilization, microbial balance, and overall growth performance, excessive supplementation levels may disrupt microbial ecosystem and lead to inconsistent responses. Yeast supplementation modifies the composition of ruminal fungal communities. Ge et al. (2025) demonstrated that yeast culture significantly altered the ruminal fungal community structure, upregulating 13 genera while downregulating 11 others. This finding indicates that yeast plays an active role in modulating the population dynamics of ruminal fungi.

Further analysis showed no significant linear association between supplementation duration and the ADG effect size, nor a significant moderating effect of ruminant type. These findings align with a previous meta-analysis in sheep, which also found that study duration did not effectively explain the substantial between-study variability in growth responses to *S. cerevisiae* supplementation (Sales 2011). Similarly, a meta-analysis in beef cattle identified the experimental period as a key factor influencing final body weight, but not ADG, suggesting that the effects of yeast on growth may be more related to the inclusion level or duration for specific outcomes such as final weight (Torres et al. 2022). The non-significant coefficient for ruminant type further indicates that the ADG response to yeast DFM did not differ between lambs and goats after accounting for duration, which is consistent with the overlapping confidence intervals observed in the subgroup analysis for ADG. These results suggest that the positive effect of yeast DFM on ADG is not linearly dependent on the length of the

supplementation period, nor is it strongly moderated by species, implying that other factors—such as yeast strain, dosage, or dietary composition—may play a more critical role in driving the observed responses (Xu et al. 2025).

This notion is further supported by the findings of Zhang et al. (2023) and Gunun et al. (2022), which illustrate that improvements in rumen fermentation and nutrient digestibility do not always translate into a linear increase in ADG over time. In Gunun et al. (2022), supplementation with hydrolyzed yeast enhanced crude protein digestibility and VFA production over a 90-day period, yet ADG remained unchanged, suggesting that the relationship between enhanced rumen metabolism and growth performance is not straightforward. The wide scattering of data points and the near-horizontal regression line in the bubble plot further support the notion that the relationship between duration and effect size is weak and highly variable across studies. These findings indicate that the efficacy of yeast DFM supplementation is not determined by a straightforward linear dose-response or duration-dependent relationship. Instead, it is shaped by a complex interaction among multiple factors, including dosage, duration, host species, and basal diet composition. The absence of significant associations for both level and duration, coupled with the substantial heterogeneity observed across studies, highlights the need for more standardized experimental protocols and further investigation into the mechanisms underlying the non-linear responses to yeast DFM supplementation in small ruminants.

This meta-analysis reveals a high degree of heterogeneity in key parameters, especially in growth performance indicators such as ADG and dry matter intake. This substantial variability stems from differences in yeast type, supplementation dosage, ruminant species (predominantly lamb), basal diet, production phase, supplementation duration, and the wide range of yeast concentrations used, particularly in lamb studies. Desnoyers et al. (2009) demonstrated that the effects of *S. cerevisiae* on rumen fermentation and milk production are modulated by interfering factors such as dietary concentrate percentage, dry matter intake, and neutral detergent fiber levels, which may similarly explain the variability observed in growth performance responses. While subgroup and meta-regression analyses showed that stratifying by species, dosage, and yeast status can reduce heterogeneity for certain outcomes, overall responses to yeast DFM supplementation were not linear with respect to dosage or duration, but were strongly influenced by experimental context and population characteristics.

Several limitations must be acknowledged in this study. High heterogeneity in both methodology and animal populations limits the generalizability of the findings. Variations in experimental design, breed, age, initial body weight, and inconsistent data reporting increase the risk of bias. Some parameters, such as drip loss and water holding capacity, were assessed in only a few studies, reducing statistical power. Although no significant publication bias was detected overall, potential bias for feed efficiency remains. Furthermore, the dominance of lamb studies from developing countries may limit applicability to goats and production systems in developed regions.

Future studies should focus on standardizing experimental protocols, particularly regarding animal selection, diet composition, and yeast DFM dosage, to minimize variability and enhance the reliability of results. Mechanistic studies employing advanced molecular approaches are recommended to clarify how yeast DFM modulates rumen microbiota and animal metabolism. Importantly, large-scale and long-term field trials are needed to confirm the practical benefits and economic viability of yeast DFM supplementation under real farming conditions. Investigating the interactions between yeast DFM and different dietary components will help optimize feeding strategies for various production goals. Expanding research to include goats, local breeds, and diverse environments will also improve the relevance and applicability of future findings. Practically, these efforts will enable the development of more precise, cost-effective supplementation guidelines, allowing producers to maximize animal performance and feed efficiency while minimizing unnecessary input costs.

This meta-analysis of 27 studies provides robust evidence that yeast DFM supplementation, particularly *S. cerevisiae*, consistently improves growth performance, crude protein digestibility, carcass traits, and meat quality in small ruminants, especially lambs. The most robust finding was the significant increase in crude protein digestibility, suggesting that enhanced protein utilization serves as the primary mechanism underlying the observed growth responses. Significant improvements were also observed in hot and cold carcass weight, as well as reduced cooking loss, which have direct

implications for enhanced productivity and meat quality. Notably, species-specific responses were observed, with lambs showing numerically higher ADG responses, whereas goats exhibited significant improvements in dressing percentage, and live yeast supplementation demonstrated a more favorable effect on dressing percentage compared to yeast culture, underscoring the importance of yeast viability and metabolic activity for optimizing carcass traits. A non-linear dose-response relationship was observed, with low supplementation levels (≤ 4 g/head/day) yielding the largest effect size for ADG, while higher doses showed diminishing or negative effects, suggesting that optimal benefits are achievable at relatively low doses (2–4 g/head/day), which has important economic implications for commercial application. Despite substantial heterogeneity across studies, the consistent positive effects on crude protein digestibility and carcass traits suggest that yeast DFM supplementation is broadly effective across diverse experimental conditions. From a practical standpoint, these findings support the use of live yeast DFM at low doses as a cost-effective nutritional strategy to improve feed efficiency, growth performance, and carcass quality in small ruminant production systems while also supporting animal protein-based food security. However, the observed substantial heterogeneity highlights the need for dose optimization, selection of appropriate yeast formulations, and standardization of on-farm application protocols to ensure consistent realization of maximum benefits across diverse production conditions. Future research should prioritize dose-response studies with standardized protocols, comprehensive characterization of yeast strains and viability, and detailed reporting of basal diet composition and animal characteristics to further elucidate the conditions under which yeast DFM supplementation consistently improves growth performance.

Declarations

Author contributions HS and MM contributed equally to this work. Conceptualization: HS; Methodology: MM; Formal analysis and investigation: MM; Data curation: MM; Writing – original draft preparation: HS, MM, GGM, and MWF; Writing – review and editing: HS, MM, GGM, and MWF; Supervision: HS; Funding acquisition: HS. All authors read and approved the final manuscript.

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Data availability The datasets generated and/or analysed during the current study are available from the corresponding author on reasonable request.

Declaration of generative AI and AI-assisted technologies The authors used AI-assisted tools for language editing and proofreading purposes only. No generative AI was used for content creation, data analysis, or scientific decision-making. The authors assume full responsibility for the final manuscript.

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Figures

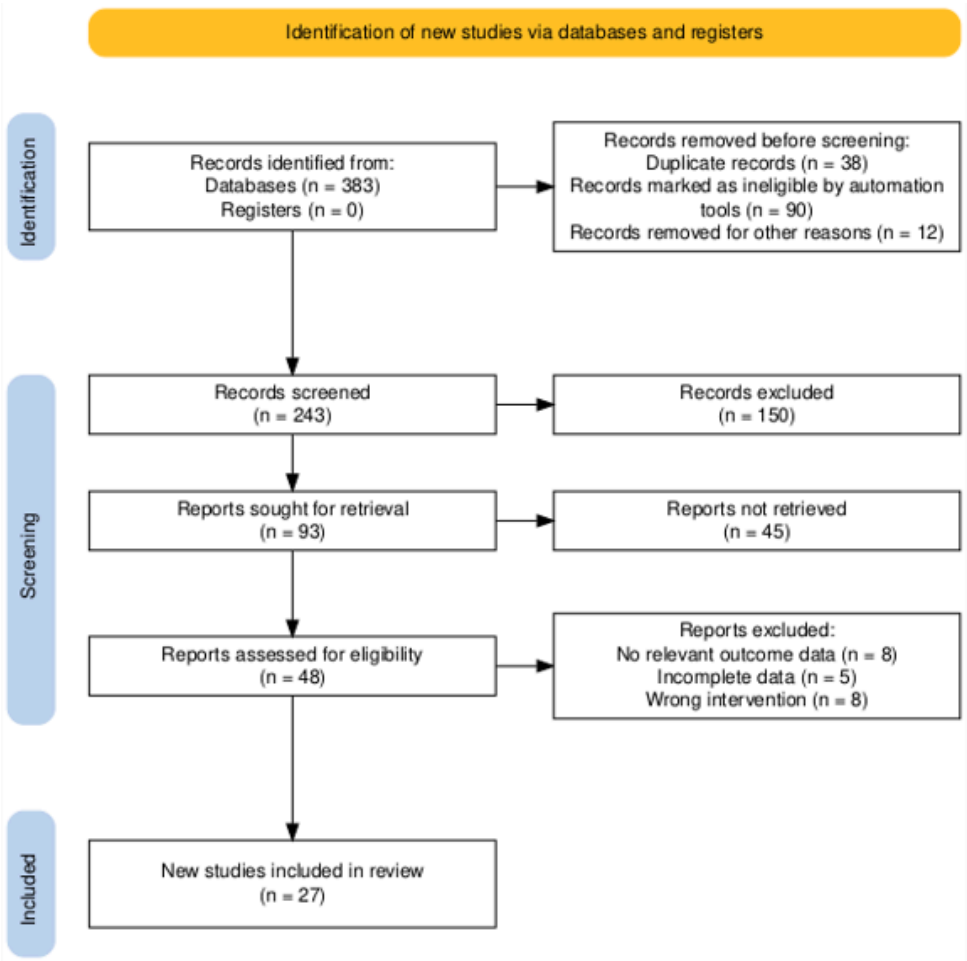


Figure 1

PRISMA flow diagram of selection studies.

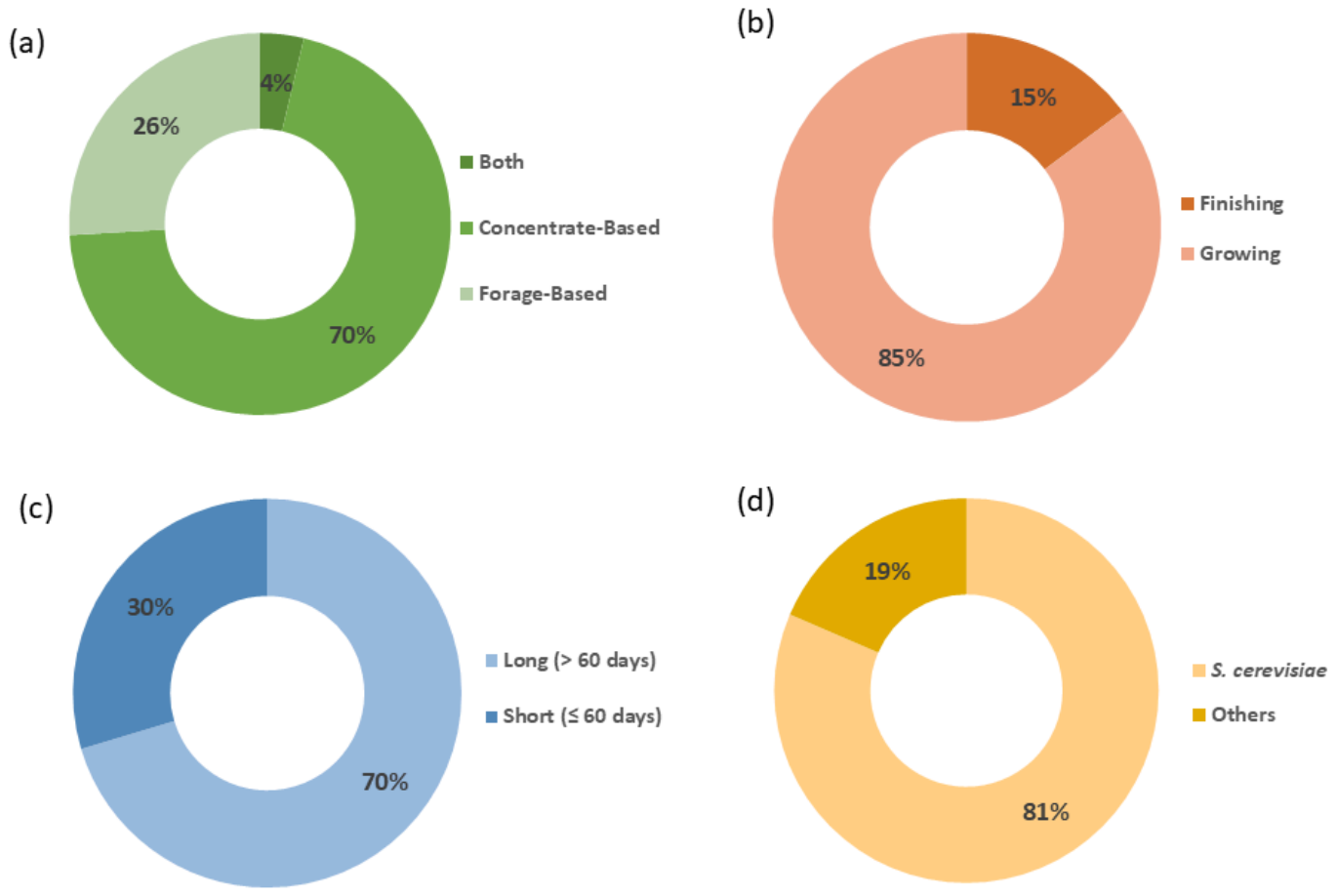


Figure 2

Distribution of studies according to (a) basal diets (b) production stage, (c) supplementation duration, and (d) yeast DFM type. Percentages indicate the proportion of studies within each category.

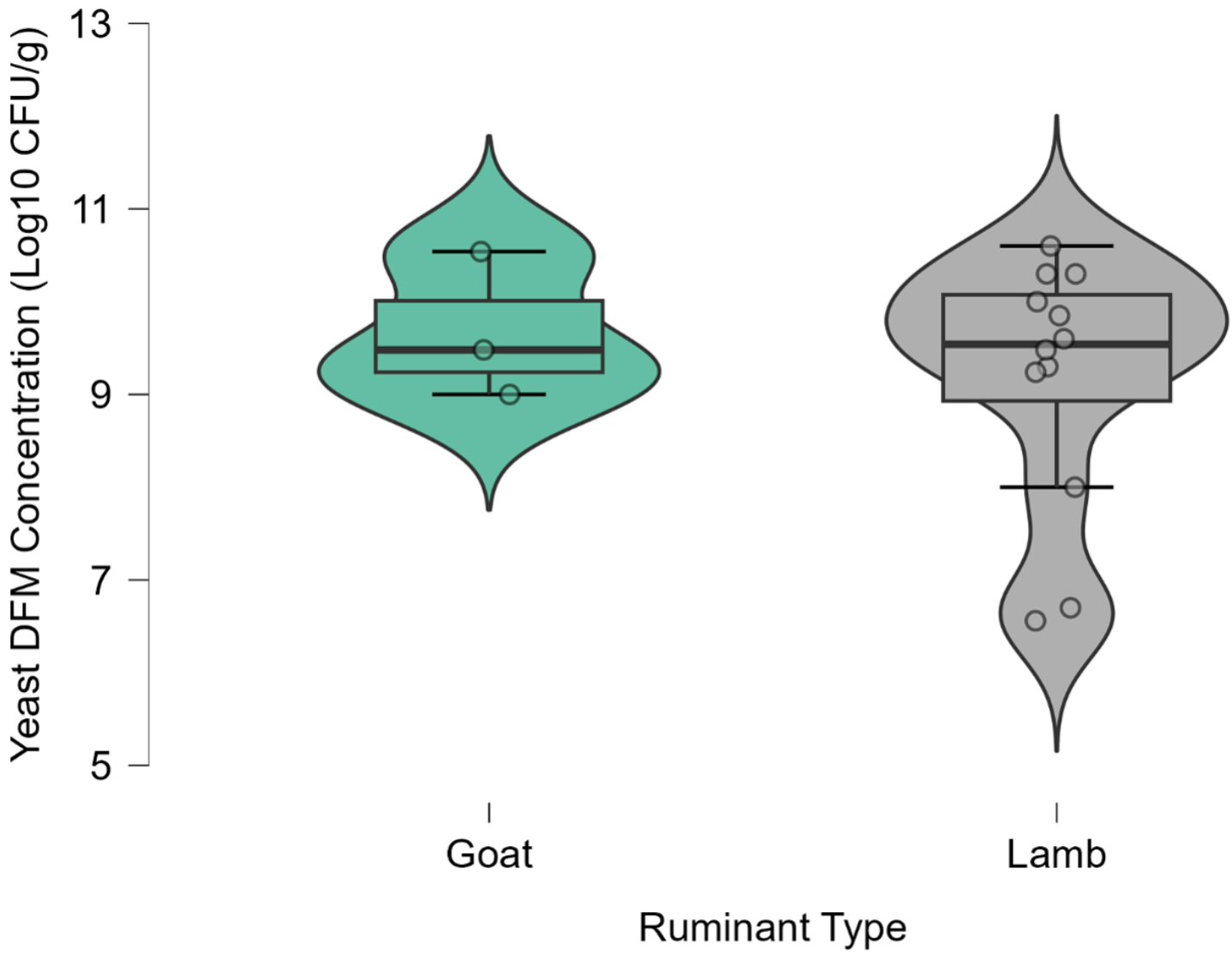


Figure 3

Boxplot of yeast concentration (Log_{10} CFU/g) reported in the included studies, stratified by ruminant type.

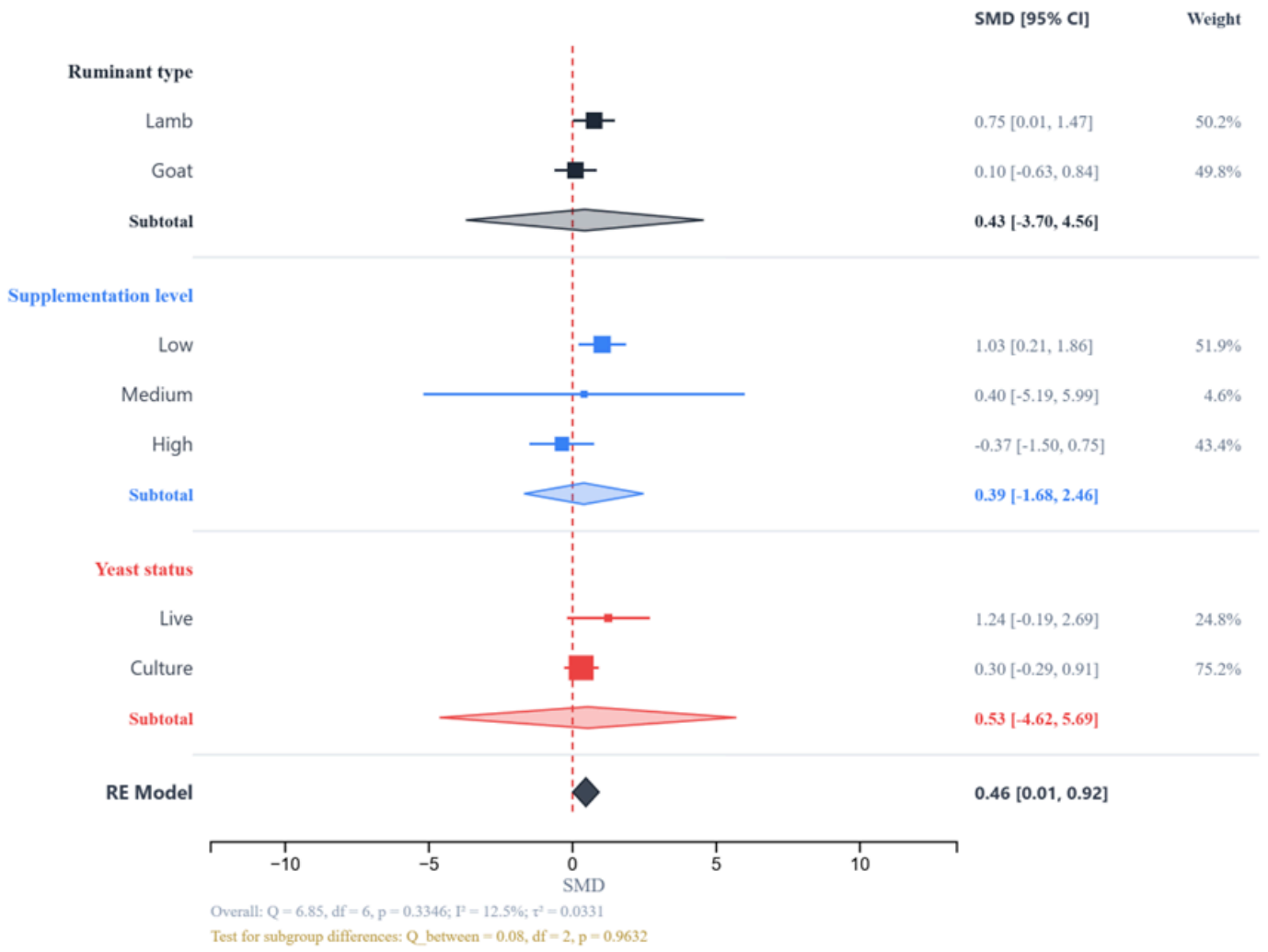


Figure 4

Forest plot of subgroup meta-analysis for the effect of yeast DFM on ADG in small ruminants.

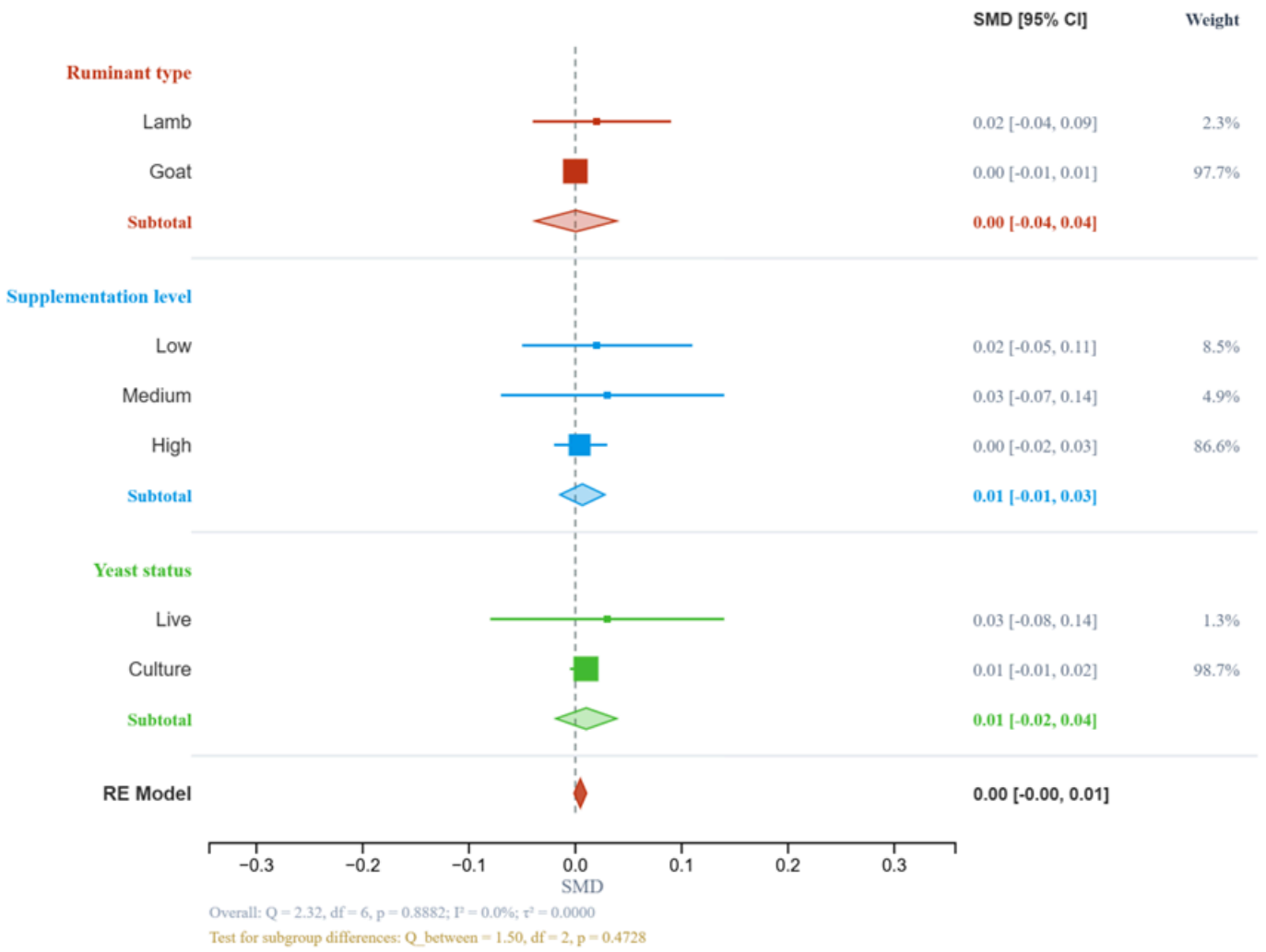


Figure 5

Forest plot of subgroup meta-analysis for the effect of yeast DFM on feed efficiency in small ruminants.

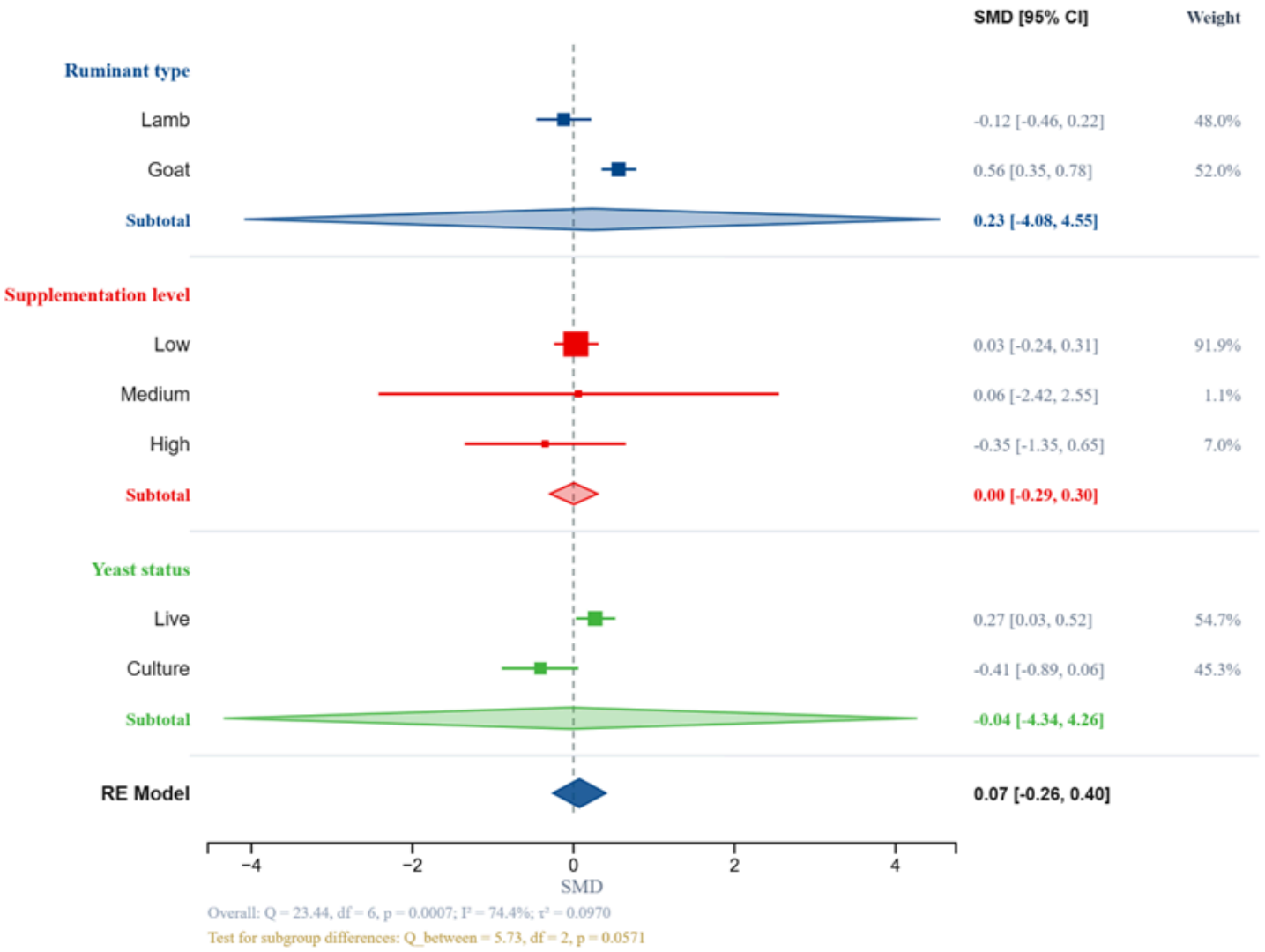


Figure 6

Forest plot of subgroup meta-analysis for the effect of yeast DFM on dressing percentage in small ruminants.

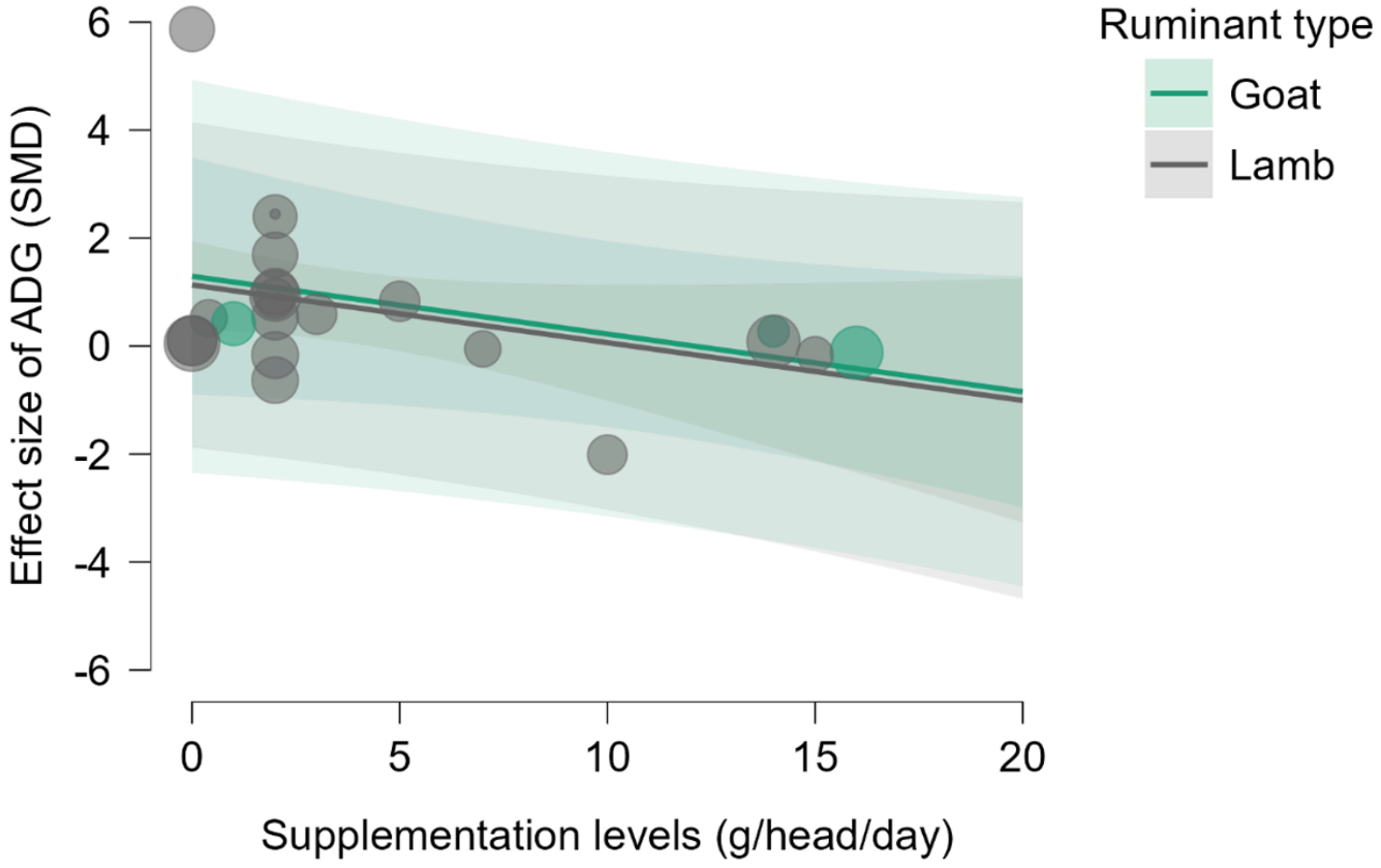


Figure 7

Meta-regression bubble plot of supplementation levels (g/head/day) versus ADG effect size (SMD) in small ruminants, adjusted for ruminant type. Bubble size represents study weight. The analysis showed no significant association for levels (slope = -0.107; p = 0.106) or ruminant type (slope = -0.160; p = 0.872).

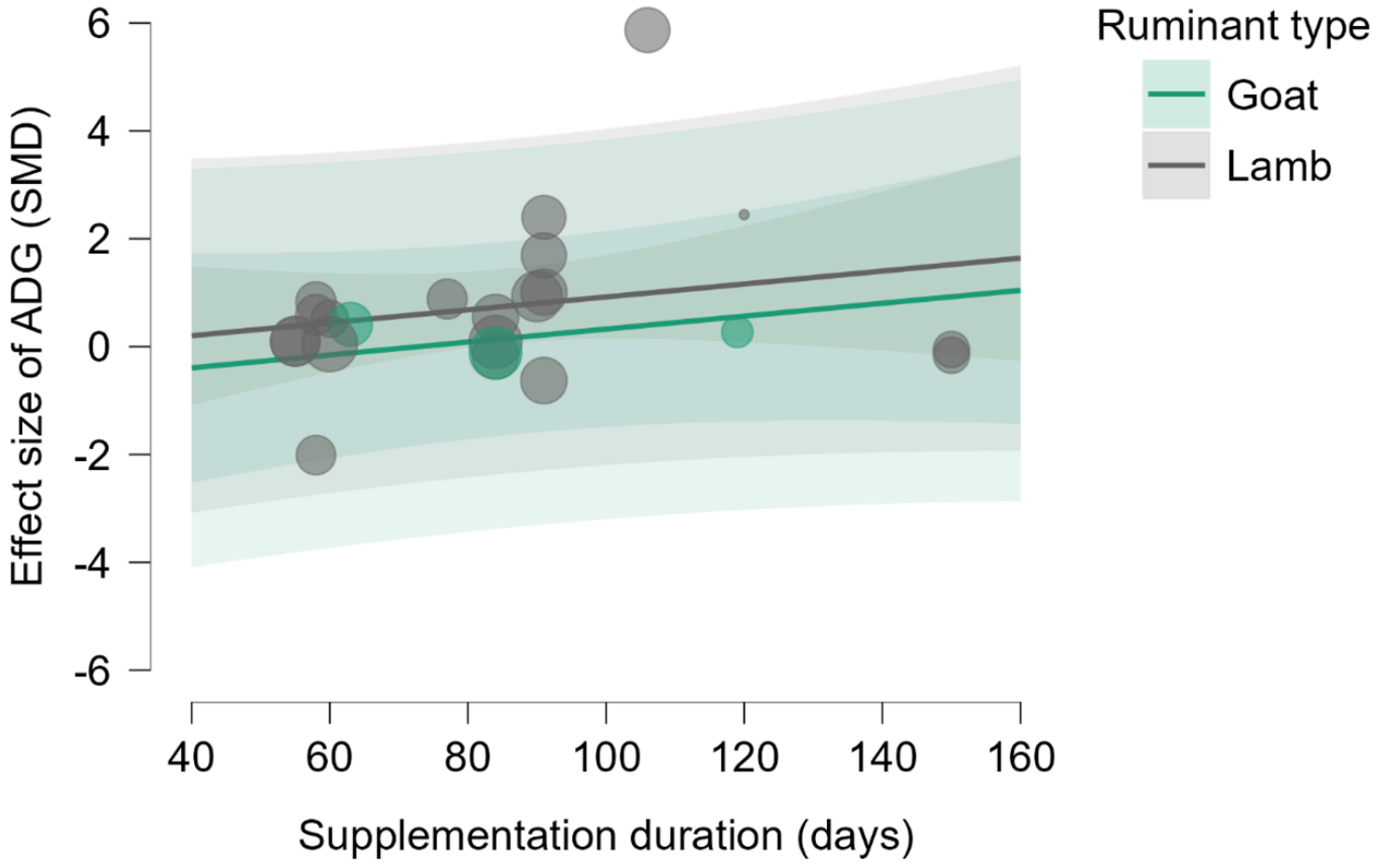


Figure 8

Meta-regression bubble plot of supplementation duration (days) versus ADG effect size (SMD) in small ruminants, adjusted for ruminant type. Bubble size represents study weight. The analysis showed no significant association for duration (slope = 0.012; p = 0.306) or ruminant type (slope = 0.596; p = 0.525).

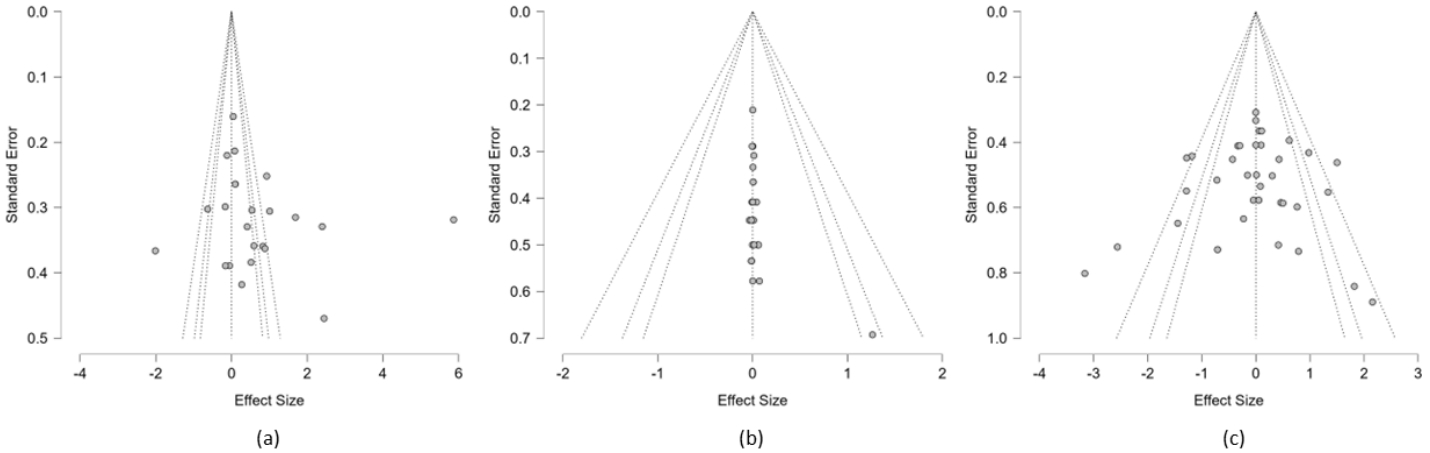


Figure 9

Funnel plot for (a) ADG, (b) feed efficiency, and (c) dressing percentage.

Supplementary Files

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