

Dietary yeast culture supplementation improves meat quality and fat metabolism-related gene expression in lambs

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Abstract: This study evaluated the effects of dietary yeast culture (YC) supplementation on lamb growth performance and meat quality. After 14 days of acclimation, 20 three-month-old lambs (30.46 ± 1.77 kg) were randomly assigned to the control (CON, basal diet) or YC-supplemented group (0.625 g/kg DM) for 50 days. While YC induced no significant improvements in growth parameters (average daily gain, average daily feed intake, and feed to gain ratio; $P > 0.05$), it enhanced the *longissimus thoracis* (LT) meat quality by elevating the L^* (lightness) and a^* (redness) values ($P < 0.05$), reducing shear force ($P < 0.05$), increasing intramuscular fat (EE, $P < 0.05$), and decreasing crude protein ($P < 0.05$). YC modified fatty acid profiles by reducing atherogenic saturated fatty acids ($P < 0.05$) and elevating C16:1 ($P < 0.05$). Transcriptional analysis revealed the depot-specific regulation: YC suppressed subcutaneous adipogenesis via downregulation of *PPAR γ /SREBP-1/HSL* and upregulation of *LPL* and promoted intramuscular fat deposition in LT through the coordinated activation of *PPAR γ /SREBP-1/FAS/ACC* and inhibition of *LPL* ($P < 0.05$). These findings demonstrate the capacity of YC to optimise meat sensory attributes and lipid healthfulness through tissue-specific metabolic modulation, supporting its application as a functional feed additive in precision lamb production.

Keywords: fatty acid; growth performance; transcriptional regulation; yeast culture

The global lamb industry faces escalating demand for premium-quality meat products driven by evolving consumer preferences for nutritious and sensorially appealing animal proteins (Wang

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et al. 2021). China's ecological restoration initiatives, particularly the Grain for Green Program, have fundamentally transformed production systems from traditional pasture-based grazing to intensive indoor feeding. This transition has improved stocking efficiency and environmental sustainability but it often compromised critical meat quality attributes, including intramuscular fat (IMF) content and flavour profiles (Bravo-Lamas et al. 2018). This paradox necessitates innovative nutritional strategies to reconcile industrial productivity with meat quality optimisation in modern lamb production systems.

Nutritional additives have emerged as pivotal tools for quality enhancement in intensive livestock operations. Among these, yeast culture (YC), which is a fermentation-derived product containing bioactive metabolites, digestive cofactors, and immunomodulatory compounds, has demonstrated multifunctional benefits in ruminant nutrition (Zhao et al. 2022; Wang et al. 2023). Substantial evidence has documented the capacity of YC to modulate rumen fermentation patterns, enhance nutrient digestibility, and improve growth performance in cattle (Dias et al. 2018b). Notably, recent studies suggest YC supplementation may enhance meat quality parameters in beef cattle through IMF modulation and collagen remodelling (Geng et al. 2016). However, its effects on ovine meat quality remain poorly characterised, particularly regarding depot-specific adipogenesis and fatty acid metabolism.

Meat quality is intrinsically linked to adipose tissue dynamics, where IMF content critically determines sensory attributes like tenderness and juiciness (Park et al. 2018). Optimal IMF accumulation (3–5%) enhances palatability by lubricating muscle fibres and retaining moisture, whereas excessive deposition (>7%) negatively impacts the consumer acceptance (Gagaoua et al. 2018). Adipogenesis is governed by the *PPAR γ /SREBP-1* signalling axis, which activates lipogenic enzymes (*FAS*, *ACC*), and is counter-regulated by lipolytic factors (*HSL*, *LPL*) through triglyceride hydrolysis (Chen et al. 2013). Strategic manipulation of these pathways could enable differential fat partitioning by suppressing the subcutaneous deposition while enhancing IMF, which is a key target for value-added lamb production (Kim et al. 2015). Emerging evidence suggests microbial additives may influence adipocyte metabolism through bioactive metabolites (Dias et al.

2018a); however, their tissue-specific regulatory mechanisms in sheep remain unexplored.

This study systematically evaluated YC supplementation effects on growth performance, meat quality parameters, and adipose metabolism in fattening lambs. We hypothesised that YC would enhance IMF deposition through the transcriptional regulation of lipid metabolic genes while maintaining growth efficiency. Our investigation provides novel insights into the dual role of YC as a growth-neutral quality enhancer and depot-specific metabolic modulator, thus offering practical solutions for premium lamb production in intensive systems.

MATERIAL AND METHODS

Experimental design. The research subjects were 20 lambs aged approximately 3 months (all males), with an average weight of 30.46 ± 1.77 kg. The lambs were randomly allocated into two experimental groups (10 animals per group): control (CON) group, which received a basal diet without additives; and YC group, which was fed the same basal diet supplemented with 0.625 g/kg YC (dry matter basis). For the YC group, the yeast culture was first pre-mixed with a small portion of the basal diet and then thoroughly blended into the complete ration. Animals were housed under natural photoperiod. Dietary formulations and nutritional compositions are detailed in Table 1.

The experiment consisted of a 14-day acclimation period (deworming with ivermectin and vaccination against orf, capripox, and clostridial diseases), followed by a 50-day formal trial. Animals were individually housed in metabolic crates under controlled environmental conditions with *ad libitum* access to water and feed (pelleted diet administered twice daily at 08:00 and 17:00). Body weights were recorded after a 12 h fasting period on days 1 and 50 of the formal trial. Daily feed intake was measured gravimetrically, and growth performance parameters, including average daily gain (ADG), average daily feed intake (ADFI), and feed to gain ratio (F/G), were calculated. Husbandry protocols included daily sanitisation of enclosures, standardised biosecurity measures, and continuous health monitoring. All procedures adhered to the Guidelines for the Care and Use of Laboratory Animals (Jilin Agricultural University, P.R. China; Ethics Approval JLAU-ACUC2021-014).

Table 1. Ingredients and nutritional composition of the experimental diet

Ingredients (%)	
Corn	35.00
Soybean meal	13.00
Corn germ meal	6.00
Corn bran	10.00
Peanut hull	23.00
Bentonite	4.00
Sucrose	4.00
Premix ¹	5.00
Total	100.00
Nutritional components (%DM)	
Dry matter	90.6
Crude protein (CP)	14.27
Neutral detergent fibre (NDF)	28.17
Acid detergent fibre (ADF)	18.35
Starch	25.87
Ether extract (EE)	3.94

¹Premix nutrient content (per kg): 110 g Ca²⁺; 140 mg Cu²⁺; 930 mg Zn²⁺; 600 mg Mn²⁺; 13 mg Co²⁺; 20 mg I⁻; 13 mg Se⁴⁺; 340 KIU vitamin A; 120 KIU vitamin D3; 1 700 IU vitamin E

Slaughter procedures and sample collection.

Following a 12-hour fasting period on the last day of the experiment (day 50), all subjects were humanely euthanised through carotid artery exsanguination in compliance with Chinese Standard NY/T 3469-2019. Carcass characteristics and meat quality parameters were systematically evaluated postmortem. Muscle tissue sampling protocols were initiated within 30 min of expiration. From the LT (*longissimus thoracis*) muscle, six 500 g sub-samples were aseptically excised, vacuum-sealed in sterile barrier pouches, and stored at -40 °C for a subsequent proximate composition analysis.

Concurrently, 100 g LT specimens were collected from the left carcass quarter between the 12th and 13th thoracic vertebra, flash-frozen in liquid nitrogen, and archived at -80 °C for fatty acid profiling and qRT-PCR quantification of lipid metabolism-associated genes. Adipose tissue depots, including subcutaneous caudal fat, abdominal visceral fat, and biceps femoris-associated intermuscular fat (2 g aliquots per depot), were surgically dissected using sterile instruments. All adipocyte samples were immediately transferred to pre-chilled 2 ml cryovials, immersed in liquid nitrogen for vitri-

fication, and maintained at -80 °C until RNA extraction.

Fatty acid analysis. The samples were crushed using a food grinder at medium speed for 30 s (FW100; Taisite Instrument). The proximate composition was determined using the AOAC (2002). Lipids were extracted from the LT samples with a chloroform-methanol (2 : 1 v/v) solution. After methyl esterification, the fatty acid profiles were determined using a gas chromatography system (7890A; Agilent Technologies) with a 100 m (internal diameter, 0.25 mm) fused silica capillary *cis/trans* column (SP2560; Supelco).

Measurement of mRNA expression of genes related to fat metabolism. Total RNA isolation from LT muscle and adipose tissues was performed using TRIzolTM Reagent (TaKaRa Bio, Dalian, P.R. China; Cat# 9109) following the manufacturer's protocols. RNA integrity was verified through 1% agarose gel electrophoresis, and purity was quantified using a NanoDropTM OneC spectrophotometer (Thermo Fisher Scientific, MA, USA), with absorbance ratios (A260/A280) between 1.8 and 2.0. First-strand cDNA synthesis was conducted with 1 µg total RNA using the HiScript III Reverse Transcriptase kit (Vazyme, Nanjing, P.R. China; Cat# R323-01), incorporating oligo(dT)18 primers and random hexamers. Quantitative real-time PCR (qPCR) was performed using TB GreenTM Premix Ex TaqTM II (Tli RNaseH Plus) (TaKaRa Bio; Cat# RR820A) on a QuantStudioTM 5 Real-Time PCR System (Applied Biosystems, CA, USA). Each 20 µl reaction mixture contained 10 µl 2× Premix Ex Taq II, 0.8 µl each of forward/reverse primers (10 µM), 0.4 µl ROX Reference Dye II (50×), 2 µl cDNA template (diluted 1 : 10), and 6 µl nuclease-free water. Thermal cycling conditions were as follows: initial denaturation at 95 °C for 30 s; 40 cycles of 95 °C for 5 s and 60 °C for 30 s; followed by the melt curve analysis (95 °C for 15 s, 60 °C for 60 s, 15 °C for 15 seconds). Target genes included *PPAR γ* , *SREBP-1*, *FAS*, *ACC*, *HSL* (hormone-sensitive lipase), *LPL*, *FABP3* (fatty acid-binding protein 3), and *CPT1B* (carnitine palmitoyltransferase 1B), with *ACTB* (β -actin) serving as the housekeeping gene. All primers (Table 2) were designed using Primer-BLAST (NCBI) and synthesised by Sangon Biotech (Shanghai, P.R. China), with validation of amplification efficiency (90–110%) and specificity confirmed through the meltcurve analysis. Relative gene expression was calculated via the $2^{-\Delta\Delta C_t}$ method (Livak and Schmittgen 2001).

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Table 2. Primer sequence

Gene name	Direction	Primer sequence (5'-3')	Product length (bp)
<i>ACTB</i>	F	CAGAGCAAGCGTGGCATCCTAAC	81
	R	GATCTTCTCCATGTCGTCCCAGTTG	81
<i>PPARγ</i>	F	CTTACCACCGTTGACTTCTCCAG	144
	R	CAGGCTCCACTTTGATTGCACTTTG	144
<i>SREBP-1</i>	F	CTCCGACACCACCAGCATCAAC	122
	R	GCAGCCCATTTCATCAGCCAGAC	122
<i>ACC</i>	F	CTTCCACGAACTCATTGTCCTCCAG	111
	R	CATTTCGTCAGGAAGAGGCGGATG	111
<i>FAS</i>	F	CTCGGTGCCCGTTGTCTA	188
	R	GGAGGTATGCCCGCTTTT	188
<i>LPL</i>	F	GCCGCCGACAGGATTACAAGAG	129
	R	GTTAGCCACAGATTCCGTCCTCC	129
<i>HSL</i>	F	TTCGCACCAGCCACAAC	136
	R	TCTCGTCGCCCTCAAAGAA	136
<i>FABP-3</i>	F	CAGAACGGAGCTGTCCTTGA	126
	R	ATGGTGAAGCTGGGCTGTG	126
<i>CPT-1</i>	F	GGCGCCGGGTGCATT	126
	R	ATGTCAGCGAGCTCCGAGT	126

Data and statistical analysis. Statistical analyses were conducted using Microsoft Excel 2016 for data processing and SPSS v23.0 for hypothesis testing. Intergroup comparisons were evaluated through two-sample *t*-tests, with statistical significance defined as $P < 0.05$.

RESULTS

Growth performance. Table 3 presents the comparative growth performance outcomes following dietary YC supplementation in fattening lambs. Although the statistical analysis revealed no significant intergroup differences ($P > 0.05$) in key nutritional efficiency indices, including the average ADFI, ADG, and F/G, between the CON and YC-supplemented groups, the YC group consistently

displayed marginally enhanced growth parameter values across all measured metrics.

Meat quality. As summarised in Figure 1, dietary YC supplementation significantly improved specific meat quality parameters of LT in fattening lambs. The YC group demonstrated higher ($P < 0.05$) L^* (lightness) and a^* (redness) values in the fresh LT muscle compared to the CON group. Shear force measurements revealed significantly lower values ($P < 0.05$) in YC-supplemented lambs relative to the CON group. No statistically significant differences were observed between the groups for the b^* (yellowness) value of meat colour ($P > 0.05$) and cooking loss percentage ($P > 0.05$) (Figure 1A). Regarding chemical composition, the CP content was reduced in the YC group ($P < 0.05$) while the EE content showed a significant increase compared to the CON group ($P < 0.05$). The crude ash (Ash)

Table 3. Effects of dietary YC on the growth performance of fattening lambs

Item	CON	YC	<i>P</i> -value
ADFI/kg	1.68 ± 0.17	1.82 ± 0.20	0.140
ADG/kg	0.27 ± 0.04	0.30 ± 0.06	0.194
Ratio of feed to gain (F/G)	6.31 ± 0.72	6.12 ± 0.58	0.529

Data are shown as the mean ± SEM, $n = 10$, not significant (two-tailed test)

ADFI = average daily feed intake; ADG = average daily gain; CON = control group; YC = yeast culture group

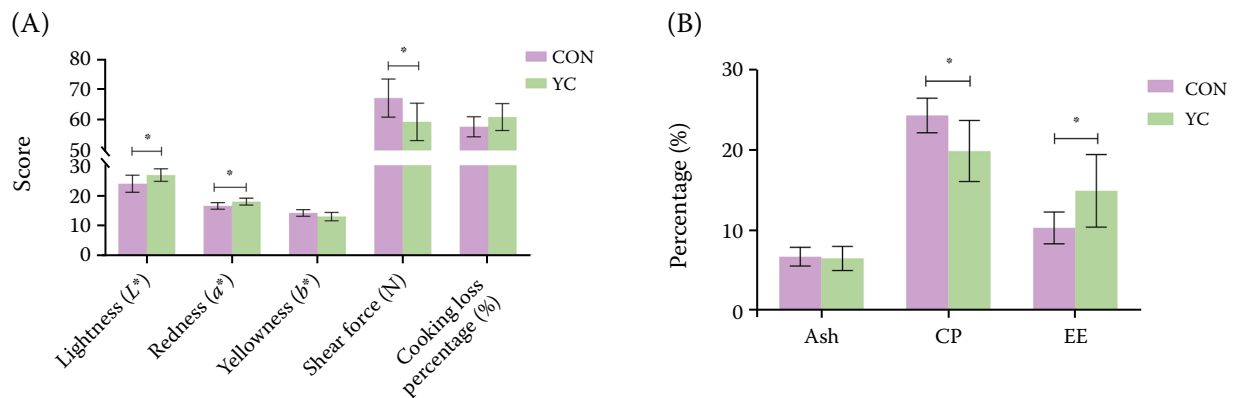


Figure 1. Effects of YC on quality-related indices of finishing lambs

The same line with * indicates a significant difference ($P < 0.05$); Data are shown as the mean \pm SEM, $n = 10$, not significant, * $P < 0.05$ (two-tailed test)

CON = control group; YC = yeast culture group

content analysis indicated no treatment-induced alterations ($P > 0.05$) (Figure 1B).

Fatty acid content and composition. Dietary YC supplementation induced specific modifications in the fatty acid profile of the LT muscle, as detailed in Figure 2. The saturated fatty acid (SFA) composition showed differential responses relative to the CON group, with myristic acid (C14:0) and palmitic acid (C16:0) exhibiting non-significant increases (7.71% and 5.74% respectively, $P > 0.05$) and heptadecanoic acid (C17:0) and stearic acid (C18:0) showing significant reductions (23.19% and 6.92%, $P < 0.05$). Regarding monounsaturated

fatty acids (MUFAs), palmitoleic acid (C16:1) increased significantly (14.70%, $P < 0.05$) while oleic acid (C18:1n-9c) and its *trans* isomer (C18:1n-9t) showed non-significant elevations (1.94–2.76%, $P > 0.05$) with YC supplementation. No treatment effects ($P > 0.05$) were observed for polyunsaturated fatty acids (PUFAs), including linoleic acid (C18:2n-6c) and arachidonic acid (C20:4n-6). Although total *trans* fatty acids (TFAs) displayed an increase in the YC group, the difference did not reach statistical significance.

mRNA expression of fat metabolism-related genes. The transcriptional analysis revealed depot-

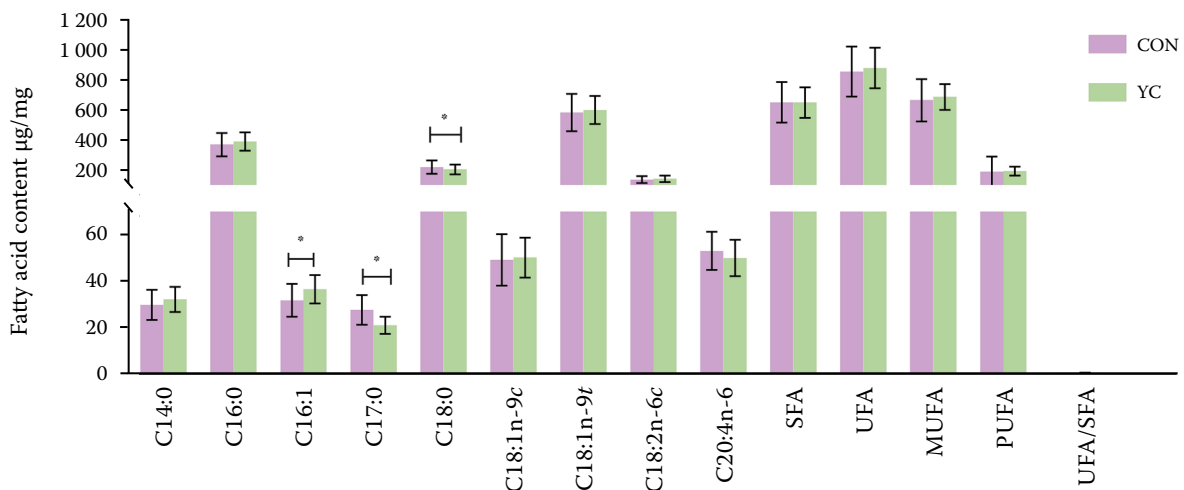


Figure 2. Effects of dietary YC on fatty acid content and composition in the LT of finishing lambs

The same line with * indicates a significant difference ($P < 0.05$); Data are shown as the mean \pm SEM, $n = 10$, not significant, * $P < 0.05$ (two-tailed test)

CON = control group; MUFA = monounsaturated fatty acid; PUFA = polyunsaturated fatty acid; SFA = saturated fatty acid; YC = yeast culture group

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specific modulation of lipid metabolic regulators in YC-supplemented lambs ($P < 0.05$). In subcutaneous adipose tissue, YC-fed lambs exhibited significant downregulation of lipogenic transcription factors (*PPAR γ* , *SREBP-1*) and lipolytic enzyme *HSL* concurrent with upregulated *LPL* expression compared to the CON group ($P < 0.05$) (Figure 3A). Conversely, the *biceps femoris* intermuscular fat demonstrated elevated adipogenic drivers (*PPAR γ*) but suppressed *LPL* expression in the YC group ($P < 0.05$) (Figure 3B). Most notably, the LT muscle

in the YC group displayed coordinated upregulation of lipogenic enzymes (*PPAR γ* , *SREBP-1*, *FAS*, *ACC*) with concomitant *LPL* downregulation ($P < 0.05$) (Figure 3C).

DISCUSSION

Studies have shown that YC supplementation modulates the animal growth performance (Hoque et al. 2021), although paradoxical outcomes have been observed across lamb experiments. Haddad and Goussous (2005) revealed that YC administration significantly enhanced ADFI and feed conversion in lambs, while Soren et al. (2013) and Abu El-Kassim et al. (2021) reported that ADG was not significantly influenced by YC supplementation in lambs, which is consistent with the present study. The lack of significant differences in growth performance in the present study was likely because the fattening cycle was short, which did not produce any obvious growth differences between fattening lambs.

Meat colour serves as a critical quality attribute that influences consumer purchasing decisions, and it is primarily determined by the myoglobin and haemoglobin concentrations in muscle tissue (Kerry et al. 2006). Elevated myoglobin levels correlate with darker meat coloration, while higher a^* values (redness intensity) indicate superior freshness and visual appeal (Carlez et al. 1995). Our findings align with previous investigations demonstrating YC supplementation enhances meat colour parameters. Consistently with Li et al. (2024), we observed a significant elevation of muscle a^* values following YC administration. This chromatic improvement corroborates reports by Lin et al. (2022) in pig models, though our study detected no significant alteration in b^* values (yellowness). This discrepancy may be attributable to interspecies variations in pigment metabolism. Notably, Wang et al. (2021) associated elevated L^* values (lightness) with improved mutton sensory quality, which was replicated in our fattening lamb trials. Tenderness, another essential quality parameter, relates to muscle fibre morphology and structural integrity, with shear force measurements inversely reflecting tenderness. Mechanical tenderness indicators further demonstrated YC efficacy, with reduced shear force values and diminished cooking loss rates mirroring results from Geng et al. (2016).

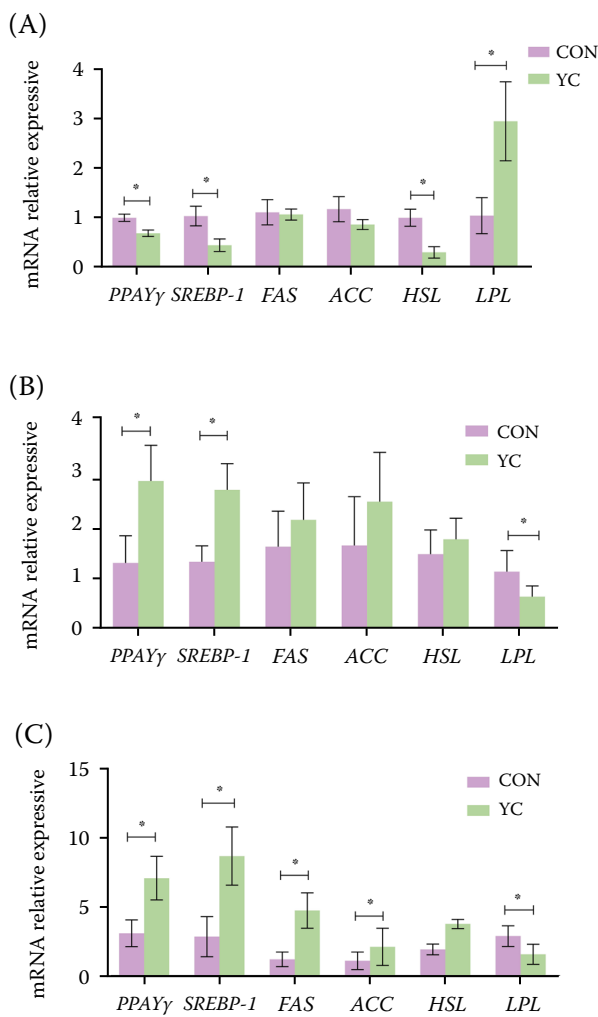


Figure 3. Effects of YC supplementation on lipid metabolism-related gene expression in adipose depots of lambs. Statistical significance was determined by two-tailed Student's t -test ($*P < 0.05$)

Gene symbols: *PPAR γ* (peroxisome proliferator-activated receptor gamma), *SREBP-1* (sterol regulatory element-binding protein 1), *HSL* (hormone-sensitive lipase), *LPL* (lipoprotein lipase), *FAS* (fatty acid synthase), *ACC* (acetyl-CoA carboxylase alpha)

These improvements likely stem from the YC-induced modulation of muscle ultrastructure and protein hydration capacity. While breed-specific responses may account for a partial variance in chromatic parameter responses (particularly b^* values), the consistent enhancement of key quality indices (a^* , L^* , shear force, and cooking loss) across species substantiates the YC role as a multifunctional feed additive for meat quality optimisation.

The nutritional and sensory characteristics of mutton are intrinsically linked to its biochemical composition, particularly protein and fat content. While the protein concentration remains a primary nutritional quality indicator, emerging evidence suggests an inverse relationship between crude protein levels and tenderness, with elevated protein content potentially enhancing collagen fibre cross-linking and increasing muscle stiffness (Piao et al. 2017). Our findings demonstrate that YC supplementation significantly reduced the muscle protein content in fattening lambs, potentially attributable to its concurrent enhancement of IMF deposition. Optimal fat deposition modulates muscle texture, tenderness, and flavour profiles. As observed in pig models (Aurousseau et al. 2004; Nuernberg et al. 2005), we confirmed that YC-induced feed intake elevation correlated with significantly increased IMF content. This aligns with established positive correlations between IMF levels and meat palatability, where higher IMF content improves tenderness and juiciness (Piao et al. 2017). Notably, while excessive fat consumption poses health risks, consumer preference consistently favours lamb with moderate IMF enrichment due to its enhanced flavour and mouthfeel. The YC-mediated protein reduction observed in our study presents the paradoxical quality dynamics. Although decreased protein content might theoretically diminish nutritional valuation, this metabolic shift potentially improves sensory attributes through two mechanisms: *i*) Reduced collagen cross-linking from lower protein availability, and *ii*) IMF-associated texture optimisation. Importantly, our results corroborate previous findings where concentrate-rich diets enhanced IMF deposition in ruminants (Aurousseau et al. 2004; Nuernberg et al. 2005), suggesting that YC acts as a functional feed additive mimicking high-energy dietary effects.

Fatty acid composition in ruminant muscles is a critical determinant of meat quality and human health implications that is modulated by dietary in-

puts, rumen microbial activity, and lipid metabolic pathways (Jiang et al. 2017). Our analysis revealed trace short-chain fatty acids in LT, which is consistent with their preferential gastrointestinal absorption and hepatic metabolism rather than adipose deposition (Demirel et al. 2006). The LT profile was dominated by oleic acid (C18:1n-9c) and stearic acid (C18:0), aligning with ovine fatty acid patterns reported by Liu et al. (2019). Notably, elevated SFA intake, particularly of C18:0 and heptadecanoic acid (C17:0), correlates with increased cardiovascular risks through cholesterol elevation (Givens 2005), while MUFAs and PUFAs demonstrate cardioprotective and metabolic benefits (Scerra et al. 2007). YC supplementation significantly altered the LT fatty acid dynamics. Contrary to Liu et al. (2019), who observed increases in C18:0 under 2.3 g/kg YC supplementation in high-energy diets, our study demonstrated reduced C18:0 levels, which is a paradoxical outcome suggesting dose-dependent or diet-contextual modulation of stearic acid synthesis. This reduction holds dual significance by *i*) mitigating the C18:0-associated mutton odour through lipid enzyme regulation (Ding et al. 2021) and *ii*) reducing a potential cardiovascular risk. Concurrently, YC enhanced palmitoleic acid (C16:1), a modulator of glucose metabolism and insulin regulation, while suppressing linoleic acid (C18:2n-6c) irrespective of dietary structure. These compositional shifts suggest that YC influences lipid metabolism may through multiple mechanisms: *i*) antioxidant-mediated protection of PUFAs from ruminal biohydrogenation, *ii*) microbial modulation favouring MUFA synthesis, and *iii*) enzymatic regulation of SFA elongation. The net effect of reduced SFAs (C18:0/C17:0) with elevated beneficial C16:1 indicates the YC capacity to improve both nutritional value and sensory attributes of mutton. While the observed PUFA reduction warrants further investigation, the overall profile aligns with health-conscious meat optimisation strategies that prioritise MUFA enrichment over PUFA maximisation (Buckley et al. 2017).

Adipogenesis in ruminants involves the complex transcriptional regulation through interconnected signalling pathways and metabolic genes (Chen et al. 2013). The dynamic balance between lipid synthesis and catabolism determines IMF deposition, which is governed by anabolic regulators (*PPARY*, *SREBP-1*, *FAS*, *ACC*) and catabolic factors (*HSL*, *LPL*, *CPTB*) (Pols et al. 2008; Mir

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et al. 2020). *PPAR γ* and *SREBP-1* serve as master transcriptional activators of adipocyte differentiation, directly upregulating *FAS* and *ACC* expression to drive the fatty acid biosynthesis (Nadeau et al. 2006). *FAS* catalyses the terminal steps of palmitate synthesis from acetyl-CoA and malonyl-CoA precursors, while *ACC* regulates the rate-limiting carboxylation of acetyl-CoA to malonyl-CoA. Conversely, *HSL* mediates triglyceride hydrolysis into free fatty acids, and *LPL* facilitates lipoprotein-derived lipid uptake (Raben and Baldassare 2005). Our experimental findings demonstrate that YC exerts the depot-specific modulation of adipogenic programming. In subcutaneous adipose tissue, YC supplementation (50 days) suppressed *PPAR γ* and *SREBP-1* expression while enhancing *LPL* activity, indicating attenuated lipogenesis and promoted lipid mobilisation. In contrast, in *biceps femoris* IMF, YC upregulated *PPAR γ* /*SREBP-1* while down-regulating *LPL*, suggesting enhanced lipid accumulation through coordinated stimulation of synthesis pathways and inhibition of catabolism. This depot-specific regulation extended to the LT, where YC simultaneously activated the *PPAR γ* /*SREBP-1*/*FAS*/*ACC* axis and inhibited *LPL*, thereby promoting IMF deposition through dual mechanisms: *i*) Enhanced *de novo* lipogenesis via *FAS*/*ACC* activation and *ii*) reduced lipid clearance through *LPL* suppression. These spatial regulatory patterns align

with previous observations in pig models. Renaville et al. (2015) identified *FAS* as a critical determinant of porcine meat quality, while Gallardo et al. (2009) established the role of *ACC* in modulating the porcine IMF content. Our results extend these findings to ovine systems, revealing the YC capacity to differentially reprogram adipogenic networks across fat depots. The enhanced IMF accumulation in LT correlates with improved meat sensory attributes, as increased IMF typically enhances tenderness and flavour (Piao et al. 2017). Conversely, reduced subcutaneous adipogenesis may improve carcass leanness, which is a desirable trait in commercial lamb production. Collectively, these depot-specific regulatory effects are summarised in Figure 4, which illustrates the mechanism of action of yeast culture.

CONCLUSION

Dietary YC supplementation improved meat quality in fattening lambs without affecting the growth performance. YC enhanced LT lightness (L^*) and redness (a^*), reduced shear force, and increased intramuscular fat content while decreasing crude protein. Fatty acid profiles showed reduced atherogenic SFAs (C17:0: -23.19%; C18:0: -6.92%) and elevated C16:1. Transcriptional regulation

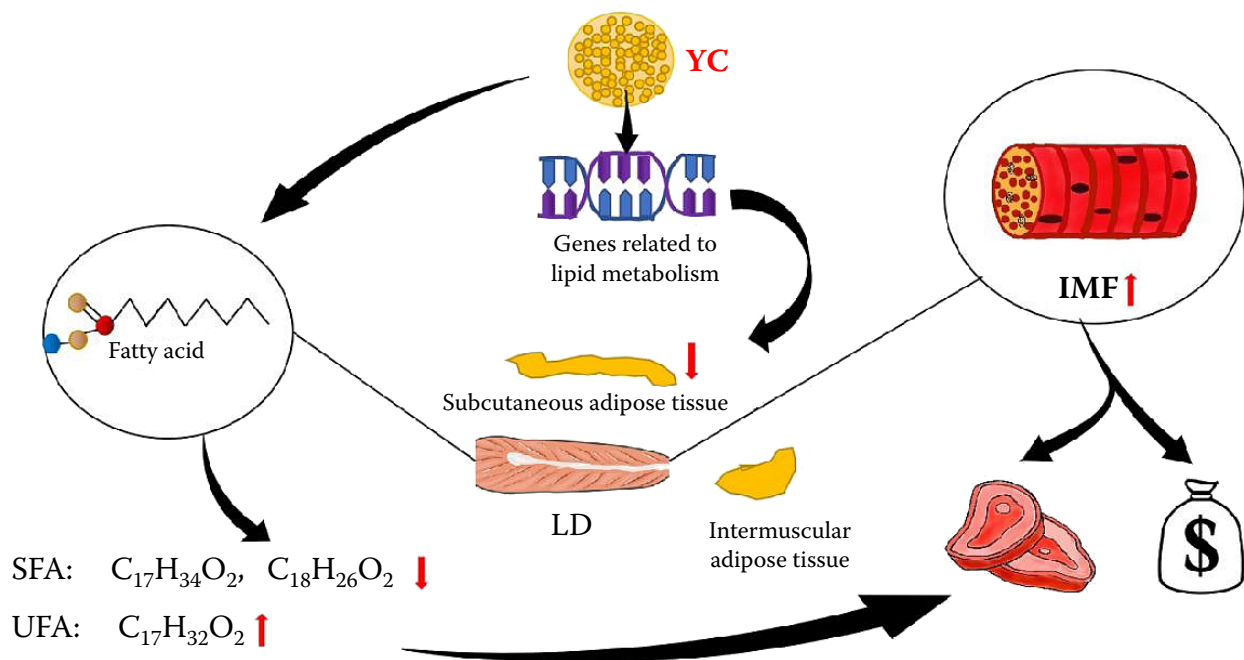


Figure 4. Mechanism of action of YC

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demonstrated the depot-specific effects of YC, namely, suppressing subcutaneous fat synthesis via downregulated *PPAR γ /SREBP-1/HSL*, upregulating *LPL*, and promoting IMF in LT through the coordinated activation of *PPAR γ /SREBP-1/FAS/ACC* and *LPL* inhibition. These results position YC as an effective feed additive for optimising lamb meat quality and lipid healthfulness through targeted metabolic modulation.

Conflict of interest

The authors declare no conflict of interest.

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