



반추영양

Identifying critical temperature-humidity index thresholds for heat stress in growing Korean crossbred black goats

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This study aimed to characterize heat stress responses across temperature-humidity index (THI) levels in growing Korean crossbred black goats to establish breed-specific THI classifications. Following a 14-d thermoneutral adaptation period, 32 goats ($\geq 20\%$ Korean native black $\times$ Boer; 4 mo of age; initial BW 22.0 ± 2.9 kg) were assigned to one of eight 14-d heat stress groups (T70.0–T87.7; numbers indicate THI). Growth performance, physiological responses, and blood parameters were recorded throughout the experiment. Body weight did not differ among groups. During wk 1, ADG and water intake were greatest in T87.7 ($p < 0.05$). Respiration rate was higher in T79.8, T82.9, T84.1, and T87.7 than in T70.0, T71.7, T74.2, and T76.5 on d 3, 6, 9, and 12 ($p < 0.001$). Ocular mucosal temperature was higher in T79.8, T82.9, T84.1, and T87.7 than in T70.0 and T71.7 from d 3 to d 12 ($p < 0.001$), and ear base temperature was higher in T79.8, T82.9, T84.1, and T87.7 than in T71.7 from d 3 to d 12 ($p < 0.001$). Rectal temperature was higher in T87.7 than in T70.0, T71.7, and T74.2 at 1 w and 2 w ($p < 0.05$). TG was higher in T79.8 than in T71.7 and T76.5 at 1 w ($p < 0.05$). In PBMCs, *HSP70* mRNA expression was lower in the higher THI groups (T74.2–T87.7) than in T70.0 on d 7, but was highest in T82.9 on d 14 ($p < 0.05$). *CAT* mRNA expression was lower in T82.9 than in T70.0, T74.2, T76.5, and T79.8 on d 7, and *SOD1* expression was lower in T79.8 and T84.1 than in T70.0 on d 7 ($p < 0.05$). These findings indicate that a THI of approximately 79.8 represents a critical threshold above which physiological and cellular responses to heat stress are markedly altered in growing Korean crossbred black goats, providing a physiological basis for the development of breed-specific THI classifications.

Key words : Korean crossbred black goat, heat stress, critical THI, HSP70, peripheral blood mononuclear cells

Sporulation potential is associated with prophage carriage in bovine gut Bacillota

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Endospore formation is a major life-history trait in Bacillota and can promote persistence and transmission in gut-associated microbial communities. Because prophages are inherited with bacterial hosts during lysogeny, prophage persistence may be influenced by host traits that enhance long-term survival and dispersal. Although phage–sporulation relationships have been reported in model spore-forming bacteria and phage-centered gut studies, whether prophage carriage is broadly associated with host sporulation potential across complex gut microbial communities remains unclear. Here, we analyzed high-quality rumen Bacillota metagenome-assembled genomes to test whether provirus carriage is associated with host sporulation potential. Sporulation potential was quantified using *spo0A* (master regulator for sporulation) and 112 sporulation-related genes spanning major developmental stages. *Spo0A*+genomes encoded more complete sporulation repertoires than *Spo0A*– genomes and showed higher provirus prevalence. Provirus prevalence also increased across sporulation gene completeness quartiles and was observed across major Bacillota lineages. These findings suggest that prophage carriage is associated with sporulation-capable host genomic backgrounds in bovine gut Bacillota, providing community-scale evidence linking bacterial dormancy potential and temperate phage retention.

Key words : spore-forming bacteria, Bacillota, provirus

Shotgun metagenomic and genome-resolved analysis of 3-nitrooxypropanol mediated methane mitigation in Hanwoo steers during the early fattening period

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3-Nitrooxypropanol (3-NOP) is a well-known methane inhibitor that targets methyl-coenzyme M reductase. In this study, 12 Hanwoo steers in the early fattening period were assigned to a randomized 3×3 Latin square design with three dietary treatments: control (CON), 100 ppm 3-NOP, and 150 ppm 3-NOP. Shotgun metagenomic sequencing was subsequently performed to investigate the taxonomic composition and functional profiles of the rumen microbiome. In addition, metagenome-assembled genomes (MAGs) were reconstructed to characterize genome-resolved microbial responses to 3-NOP. Statistical analyses of metagenomic features were conducted using MaAsLin3, with significance defined as a *Q*-value < 0.05. With a dose-dependent methane reduction, the archaeal genera *Methanobrevibacter* and *Methanosphaera* showed linear decreases following 3-NOP supplementation. The treatment also significantly affected several bacterial genera, including *Acinetobacter*, *Bacteroides*, *Parabacteroides*, and *Segatella*, as well as the fungal species *Neocallimastix californiae* and the protozoal family Isotrichidae. Functional profiling revealed decreased cofactor biosynthesis modules, including NAD biosynthesis and thiamine/TPP biosynthesis, whereas the acetyl-CoA pathway was increased. Among 1,310 reconstructed MAGs, 128 were significantly differed in response to 3-NOP. Pangenome analysis of these 3-NOP-responsive MAGs identified 7,672 gene clusters, including 2,087 clusters specific to increased MAGs and 1,394 specific to decreased MAGs. These results indicate that 3-NOP supplementation differs the rumen microbiome not only through taxonomic and functional shifts but also through distinct genome-resolved changes.

Key words : methane mitigation, 3-nitrooxypropanol, metagenome assembled genome, shotgun metagenome

Comparison of growth performance, rumen fermentation characteristics, blood profiles, and carcass traits in finishing Hanwoo heifers divergent in genomic estimated breeding value for marbling score

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This study compared growth performance, rumen fermentation characteristics, blood profiles, and carcass traits in finishing Hanwoo heifers with divergent genomic estimated breeding values (GEBV) for marbling score. Eighteen Hanwoo heifers were classified into high (HGMS, $n = 9$) and low (LGMS, $n = 9$) marbling score GEBV groups. GEBV for carcass weight and eye muscle area were similar between groups, allowing the comparison to focus on marbling potential. Growth performance, dry matter intake (DMI), rumen fermentation parameters, serum biochemical profiles, hematological parameters, and carcass traits were evaluated. Repeated measures data were analyzed using a mixed model with treatment, week, and their interaction as fixed effects, and animal within treatment as a random effect. Initial body weight did not differ between groups, whereas average daily gain was greater in HGMS than in LGMS (0.64 vs. 0.52 kg/d, $p = 0.0456$). Total and concentrate DMI tended to be higher in HGMS ($p < 0.10$). In the HGMS group, total volatile fatty acid concentration was lower ($p < 0.05$), whereas ruminal pH tended to be higher ($p < 0.10$). Blood parameters and carcass traits did not differ between groups, except for lower creatinine in HGMS ($p < 0.05$). These results suggest that GEBV for marbling score may be associated with growth performance and metabolic status, although carcass traits were not clearly differentiated under the present finishing conditions.

Key words : genomic estimated breeding value, Hanwoo heifers, growth performance, rumen fermentation characteristics, carcass traits

Effects of total mixed ration with methane-mitigating microbes on growth performance, rumen fermentation, methane emissions, and rumen microbiota in Hanwoo steers

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This study aimed to evaluate the effects of a total mixed ration (TMR) with methane-mitigating microbial strains (MMM) on growth performance, rumen fermentation characteristics, methane (CH₄) emissions, and rumen microbiota in Hanwoo steers. Eight steers (277 ± 22 kg) were used in a 2-period crossover design and assigned to one of two experimental groups: (1) CON (control; commercial TMR) or (2) TMR + MMM (TMR with methane-mitigating microbes). Rumen fermentation parameters (pH, ammonia-nitrogen, and volatile fatty acids) were analyzed. Total weight gain, average daily gain, dry matter intake (DMI), and feed efficiency were calculated. Enteric CH₄ emissions were measured using the GreenFeed system and expressed as daily production (g/d), yield (g/kg DMI), and intensity (g/kg BW^{0.75}). The 16S rRNA amplicon sequencing was employed to characterize the rumen microbial composition. Feeding of TMR with methane-mitigating microbes (MMM) did not influence growth performance and rumen fermentation parameters of Hanwoo steers ($p > 0.05$). Steers fed TMR + MMM showed numerically reduced CH₄ production (5.0%), yield (2.7%), and intensity (5.1%) compared with the CON group ($p > 0.05$). Taxonomic analysis revealed that Bacteroidota and Bacillota were the most dominant phyla. The TMR + MMM group exhibited a lower relative abundance of Bacteroidota and a higher Bacillota compared to the CON group. Relative abundance of *Methanobrevibacter* was lower in TMR + MMM compared to the CON group (97.5% vs. 99.1%). These findings suggest that feeding TMR with methane-mitigating microbes did not negatively affect growth performance or rumen fermentation in Hanwoo steers, while showing potential to reduce methane emissions. Further studies are warranted to enhance the methane-mitigation efficacy of this TMR diet.

Key words : Hanwoo, methane, methane-mitigating microbes, rumen, TMR

Effects of Methastop[®] supplementation on enteric methane emissions in Hanwoo cattle

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This study aimed to evaluate the potential of Methastop[®] as a feed additive for reducing methane emissions in Hanwoo cattle. Four Hanwoo steers (687 ± 71.4 kg BW; 33 months of age) and five Hanwoo heifers (565 ± 68.9 kg BW; 32 months of age) were assigned to a 3×3 Latin square design. Each experimental period lasted 21 d, consisting of a 14-d adaptation, a 2-d sampling, and a 5-d washout phase. Animals were allocated to one of three dietary treatments: 1) no additive (CON) as the negative control, 2) Bovaer[®] (NOP) as the positive control, and 3) Methastop[®] (MES). Each additive was supplemented at 0.2% of the offered concentrate mix. Diets were offered twice daily (0800 and 1800 h); the concentrate mix was offered at a fixed rate of 0.5% of BW per feeding, whereas forage was offered *ad libitum*. Individual concentrate intake was determined daily by the difference between the amount offered and theorts, whereas individual forage intake was automatically recorded daily using a forage intake monitoring system. Methane emissions were measured using the laser methane detector technique. Dry matter intake (DMI) and methane emissions did not differ among treatments ($p > 0.05$). However, methane yield (MY; ppm/kg of DMI) differed among treatments during respiration ($p < 0.05$) and tended to differ during eructation ($p = 0.1$). Compared with CON, NOP reduced MY by 23% during respiration and by 21% during eructation, while MES reduced MY by 24% and 15%, respectively. In conclusion, supplementation with Methastop[®] has the potential to mitigate methane yield in Hanwoo cattle without adverse effects on feed intake.

Key words: methane yield, laser methane detector, Methastop[®], Bovaer[®], Hanwoo

TMR의 발효 기간에 따른 반추위 소화율 및 메탄 발생량 평가

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본 연구는 TMR의 발효 기간이 *in vitro* 반추위 소화율, 가스 및 메탄 발생량에 미치는 영향을 평가하고자 수행되었다. 공시 시료로 상업용 한우 비육기 TMR을 사용하였으며, TMR의 발효 기간에 따라 0일(D0), 7일(D7), 14일(D14) 처리구로 구분하였다. D7 및 D14 처리구는 1L 플라스크에 250g의 시료를 충전하여 상온(20°C) 조건에서 각 기간 동안 밀폐 발효하였다. 발효 후 각 처리구의 TMR은 동결건조한 후 분쇄하였다. 분쇄한 각 처리구별 시료는 *in vitro* 반추위 배양 시스템을 이용하여 반추위 발효 및 소화율을 평가하였다. 총 가스 및 메탄 발생량은 배양 2, 4, 6, 24시간 후에 측정하였다. 진정 건물 소화율(TDMD)은 배양 6시간 및 24시간 후에, 중성세제섬유소 소화율(NDFD)은 배양 24시간 배양 후에 분석하였다. 총 가스 발생량은 2, 4, 6시간에 처리구 간 유의적인 차이가 없었으나($p > 0.05$), 24시간에는 D0에 비해 D14의 가스 발생량이 7.4% 낮았다($p = 0.023$). 메탄 발생량은 배양 시간에 상관없이 발효 기간에 따른 유의적인 차이가 없었다($p > 0.05$). 24시간 TDMD는 발효 기간이 증가함에 따라 증가하는 경향을 보였다($p = 0.062$). 24시간 NDFD는 D14가 D0과 D7에 비해 각각 17.3%, 22.8% 높았다($p = 0.006$). 결론적으로, TMR의 발효 기간의 증가는 반추위 가스 발생량은 줄이나 섬유소 소화율은 증가시켰고, 반추위 메탄 발생량에는 영향을 미치지 않았다.

Key words : TMR, *In vitro*, 반추위 소화율, 메탄, 가스 발생량

Effect of cashew nut meal replacement on enteric methane emissions in Holstein heifers

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Methane emissions from ruminants, produced during rumen fermentation, are a major source of greenhouse gases and represent a loss of dietary energy. This study evaluated the effects of cashew nut meal (CNM) supplementation on methane emissions in Holstein heifers. Nine Holstein heifers (average age: 10.3 months) were assigned to a 3 × 3 Latin square design with three dietary treatments: control (CON), 10% CNM replacement (Trt-1), and 15% CNM replacement (Trt-2). Methane concentrations were measured twice daily (08:00 and 16:00) for 3 days using a Microportable Greenhouse Gas Analyzer (GLA131-GGA; ABB Inc., Quebec, Canada), and daily methane emissions were estimated using a previously validated regression equation based on body weight, DMI, and TDN. Compared with CON, Trt-1 reduced CH₄ emissions, CH₄ yield, and CH₄ intensity by 7.9%, 7.9%, and 8.2%, respectively, whereas Trt-2 reduced these parameters by 21.8%, 20.5%, and 22.4%, respectively ($p < 0.01$). Trt-2 exhibited greater methane mitigation effects than Trt-1 across all measured parameters. Although DMI was reduced by approximately 2.2% in Trt-2 compared with CON ($p < 0.01$), CNM supplementation did not adversely affect ADG, FCR or hematological parameters, suggesting that methane reduction was not solely attributable to reduced feed intake. These findings indicate that 15% CNM replacement may serve as a promising functional feed ingredient for enteric methane mitigation in ruminants.

Key words : Holstein heifer, cashew nut meal, enteric methane mitigation, microportable GHG analyzer (MGGA)

A comparative study on the nutritional composition, *in vitro* rumen fermentation characteristics, and microbiome of diverse forages for goats

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This study was conducted to evaluate the nutritional composition, including amino acid and fatty acid profiles, and *in vitro* rumen fermentation (24 h, 48 h) and microbiome after 48 h fermentation of forages commonly used in domestic goat farms in Korea. Thirty-one forage samples were collected from local goat farms, which included 17 types of forages. Chemical composition varied among forages, especially between crude protein (CP) and fiber fractions — crude fiber (CF), neutral detergent fiber (NDF), acid detergent fiber (ADF) — had a negative correlation (CF, NDF: $p < 0.01$; ADF: $p < 0.05$). Also, the overall CP content of forages is lower than that reported by NRC (2007). An *in vitro* rumen fermentation study was conducted in two separate experiments using different forage groups ($n = 16$); timothy hay was included as a standard forage in each experiment. Rumen fluid used in this study was obtained from three goats slaughtered at a local abattoir per experiment, resulting in donor-driven variability of rumen fluid activity between experiments 1 and 2. Accordingly, gas production and dry matter digestibility (DMD) of the standard forage were different between the two experiments. Corn silage and oat hay samples, even among the same forage type, showed differences in rumen fermentation traits; CP and DMD were significantly different. These findings provide a comprehensive understanding of forages utilized in goats, contributing to the establishment of standardized nutritional guidelines and improved feed efficiency in the domestic goat industry.

Key words : forage, goats, nutritional composition, *in vitro* rumen fermentation, rumen fluid

The effects of different vitamin mixtures on the productivity and physiological responses of Hanwoo heifers under heat stress conditions

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Rapid temperature increases associated with climate change reduce livestock productivity by inducing endocrine and metabolic imbalances and decreasing feed intake, highlighting the need for nutritional strategies to improve animal resilience. Therefore, this study evaluated the effects of complex functional feed additives on growth performance, rumen fermentation, blood metabolic profiles, and heat stress biomarkers in Hanwoo heifers under summer heat stress conditions. Fifteen Hanwoo heifers were assigned to a 3 × 3 Latin square design over 11 weeks. The treatments were as follows: i) control, no additive; ii) Mix A, containing vitamin B₆ and choline chloride; and iii) Mix B, containing niacin and vitamin E. The average temperature–humidity index during the experimental period was 78.5, indicating severe heat stress. Mix A significantly increased forage dry matter intake compared with the control and tended to maintain higher blood hemoglobin concentrations, suggesting a potential role in supporting feed intake and hematological stability under heat stress. Mix B tended to improve average daily gain and feed efficiency and significantly decreased serum cortisol concentration compared with the control, indicating reduced endocrine stress. Rumen fermentation characteristics were largely unaffected by treatment, except for a lower isobutyrate proportion in Mix B. In blood biochemical profiles, Mix B significantly decreased serum total protein concentration and tended to decrease albumin concentration, whereas Mix A tended to increase alanine aminotransferase activity. Serum HSP70 and HSP90 concentrations were not affected by treatment. In conclusion, under summer heat stress conditions, the choline- and vitamin B₆-based additive improved forage intake and may support hematological stability, whereas the niacin- and vitamin E-based additive reduced cortisol concentration and showed potential to improve growth performance and feed efficiency. These findings suggest that complex functional feed additives may provide distinct physiological and metabolic benefits depending on their active components in heat-stressed Hanwoo heifers.

Key words : Hanwoo heifers, heat stress, feed additives, productivity, metabolic parameter

Effects of L-citrulline supplementation on lactational performance and blood responses in lactating Holstein cows with A1 and A2 β -casein genotypes under heat stress condition

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This study aimed to evaluate the effects of L-citrulline supplementation on lactational performance and metabolic responses of early- to mid-lactation Holstein cows under heat stress conditions. A total of 40 lactating Holstein cows were assigned to either a control group or an L-citrulline-supplemented group. The cows averaged 71.3 ± 33.8 d in milk, 32.4 ± 9.6 kg/d milk yield, and 2.8 ± 1.8 parity at the beginning of the experiment. Following a 7-day adaptation period, cows received the experimental treatment for 4 weeks. L-citrulline was supplemented at 0.5% of dry matter intake as a top-dressing. Milk yield, milk composition, dry matter intake, and blood parameters were analyzed. L-citrulline supplementation did not affect milk yield, milk composition, or dry matter intake. However, L-citrulline supplementation increased blood urea nitrogen ($p < 0.01$) and albumin ($p < 0.01$) levels, with tendencies toward increased creatinine ($p = 0.09$). In addition, A2 cows showed higher milk protein ($p < 0.05$) and hemoglobin ($p < 0.05$) levels than A1 cows under heat stress, suggesting that the A2 β -casein genotype may be associated with greater heat stress resistance. No significant interaction between L-citrulline supplementation and β -casein genotype was observed, indicating that L-citrulline responses were not genotype-dependent. In conclusion, L-citrulline supplementation modulated nitrogen metabolism without improving lactational performance under heat stress conditions. In contrast, A2 cows exhibited potentially greater physiological adaptability to heat stress than A1 cows.

Key words : L-citrulline, dairy cows, A1/A2 genotype, lactational performance, heat stress

인공지능(AI) 활용 스마트 축산을 위한 한우 사양 관리 온톨로지 개발

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인공지능(AI) 시대의 한우 사양에서는 한우의 영양, 사료 및 사양 관리에 관한 방대하고 복잡한 정보 및 지식을 AI가 이해할 수 있는 형태로 구조화하고 체계화한 모델, 즉 온톨로지(ontology)의 구축이 필수적이다. 본 연구는 생성형 AI가 농장 관리자의 질의에 응답하고, 사료 급여 전략의 평가 및 수정에 근거 기반 도구로 활용할 수 있는 한우 사양 관리 온톨로지 개발을 목적으로 수행되었다. 한우의 사육 및 고급육 생산 과정에서 영양, 사료 및 사양 관리를 관심 대상(도메인)으로 정의하였다. Ontology Development 101과 Methontology를 결합한 방법론을 채택하고, Protégé ver. 5.6.7을 개발 플랫폼으로 활용하여 웹 온톨로지 언어(OWL) 기반 온톨로지를 구축하였다. 다양한 문헌을 활용하여 지식을 분석한 후, 대규모 언어 모델인 Google Gemini 2.5를 활용하여 역량 질문(Competency Questions, CQs)을 생성하였고, 생성된 질문과 응답 과정에서 도출된 용어를 바탕으로 핵심 개념(클래스)을 추출하였다. 상향식 접근법과 하향식 접근법을 병행하여 추가의 클래스와 클래스 계층 구조를 정의하고, 클래스 간 관계를 나타내는 속성(property)을 부여하였다. 또한 클래스의 주석과 속성의 제한 조건을 설정하였다. 개발된 온톨로지는 문헌 검토와 CQs 재평가를 통해 누락된 클래스, 속성 및 제한 조건을 보완하는 과정을 거쳤으며, 구조적 지표를 활용하여 충실도를 평가하였다. 또한 Protégé에 내장된 HermiT 및 Pellet 추론기를 이용하여 논리적 일관성을 검증하였다. 결론적으로 본 연구에서 개발한 한우 사양 관리 온톨로지는 충실도 기준을 만족하였으며, 구조적 일관성과 논리적 정합성을 갖춘 것으로 나타났다.

Key words : 사양, 영양, 온톨로지, 인공지능(AI), Protégé, 한우

Characterizing rumen antimicrobial resistance gene composition across studies and its implications for microbiome-resistome integration

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Antimicrobial resistance (AMR) poses an increasing challenge to sustainable livestock production and One Health by connecting human, livestock, and environmental health. The beef cattle rumen microbiome represents a complex microbial ecosystem that may act as a reservoir of antimicrobial resistance genes (ARGs), yet cross-study characterization of rumen resistome patterns across production contexts remains limited. This study performed a cross-study meta-resistome analysis of publicly available shotgun metagenomic datasets to characterize the beef cattle rumen resistome and assess resistome variation across production settings. A systematic literature search identified 10 eligible studies comprising 225 rumen fluid metagenomes. Sequencing data underwent quality control and ARG annotation using a standardized bioinformatics workflow, generating normalized ARG and AMR class abundance profiles. Diversity analyses, ordination, PERMANOVA, and mixed-effects modeling were applied. Tetracycline-associated ARGs dominated the rumen resistome, with tet(Q), tet(W), tet(O/W), and tet(44) consistently detected across samples. Core ARGs included determinants associated with tetracycline, multidrug, macrolide-lincosamide-streptogramin, bacitracin, vancomycin, and polymyxin resistance classes. Study identity explained most resistome variation ($R^2 = 0.73$; $p = 0.001$), whereas diet, age, and country showed limited independent effects after accounting for study structure, highlighting substantial cross-study heterogeneity and metadata confounding. These findings reveal conserved resistome signatures and support harmonized metagenomic surveillance as a foundation for sustainable and resilient livestock systems.

Key words: beef cattle rumen microbiome, resistome, antimicrobial resistance genes, metagenomics, sustainable livestock

Integrated processing of soybean meal as nutritional strategy to support performance in heat-stressed Holstein dairy cows

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This study evaluated fermented soybean meal (FSBM), produced through sequential acid pre-treatment, lactic acid bacterial inoculation, and thermal processing, as a nutritional strategy for dairy cows under heat stress. *In vitro* rumen fermentation demonstrated that this integrated processing approach significantly increased the crude protein (CP) content of FSBM ($p < 0.001$). Compared with conventional soybean meal, FSBM significantly reduced total gas production and methane emissions ($p < 0.001$). No differences in volatile fatty acid (VFA) concentrations were observed at 12 h ($p > 0.05$). However, after 24 h of incubation, FSBM significantly altered fermentation characteristics, resulting in higher concentrations of total VFA ($p < 0.001$), acetate ($p < 0.001$), propionate ($p < 0.001$), and butyrate ($p < 0.01$), along with increased ammonia nitrogen (NH₃-N) levels ($p < 0.001$), while the acetate-to-propionate ratio remained unchanged ($p > 0.05$). In the *in vivo* study, supplementation with 0.1% FSBM did not affect dry matter intake or milk yield ($p > 0.05$). However, it significantly reduced milk somatic cell count ($p < 0.01$) and improved feed efficiency across lactation stages ($p < 0.01$). Overall, these findings suggest that properly processed FSBM can enhance rumen fermentation while supporting udder health and improving feed efficiency in lactating dairy cows under heat stress.

Key words : fermented soybean meal, by-pass protein, rumen, dairy cows, heat stress