M75  Sodium salicylate reduced transcription abundance of hypoxia-associated genes in MAC-T cells. C. M. Ylioja, T. H. Swartz, L. K. Mamedova*, and B. J. Bradford, Kansas State University, Manhattan, KS.

Hypoxia is an oxygen deficiency commonly found in growing tissues and is speculated to occur in the rapidly developing mammary gland in peripartum dairy cattle. Low oxygen concentrations can activate hypoxia-inducible factor-1 (HIF-1), which increases transcription of genes involved in angiogenesis (VEGF) and glucose transport (GLUT1). The mRNA stability of these genes is positively regulated by AUF1. In our previous research, postpartum administration of sodium salicylate (SS) increased whole lactation milk yield in multiparous cows but tended to reduce milk yield in primiparous. Because rapid mammary tissue development likely occurs in cows approaching first lactation, we hypothesized that SS inhibited the activation of HIF-1α and decreased transcription of downstream targets. MAC-T cells were treated with SS (100 μM) or control media before incubation under either hypoxic (1% O₂) or normoxic conditions for 12 h. Additionally, cells were transfected with either HIF1α siRNA or a scrambled siRNA negative control 48 h before hypoxia treatments. HIF1α, GLUT1, VEGF, and AUF1 were quantified using the 2⁻ΔΔCt method and normalized to the internal control gene NENF. Transcription abundance was assessed using a linear mixed model with the fixed effects of SS, hypoxia, and siRNA and all 2- and 3-way interaction terms, and the random effect of plate nested within hypoxia. SS tended to decrease HIF1α as compared with untreated cells (P = 0.09). For GLUT1, SS treatment interacted with hypoxia (P = 0.05), as SS reduced GLUT1 when MAC-T cells were cultured in normoxic conditions (P = 0.01), however, no effect of SS was found in hypoxia-treated cells (P = 0.39). Regardless of oxygen status, SS reduced VEGF (P = 0.04) and AUF1 (P = 0.04) relative to untreated cells. Hypoxia increased GLUT1 (P = 0.01), yet no effect was identified on VEGF (P = 0.45) or AUF1 (P = 0.22). siRNA knocked down HIF1α (P < 0.01), but no effect was found on GLUT1 (P = 0.98), VEGF (P = 0.99), or AUF1 (P = 0.62). In conclusion, SS reduced transcription abundance of genes involved with mammary gland development, but generally did not interact with oxygen status.

Key Words: hypoxia, NSAID, mammary gland development

M76  Circadian PER2 gene silencing suppresses lipid synthesis partly via inhibition of PPARG and SREBF1 in bovine mammary epithelial cells. Y. J. Jing1, Y. F. Chen*, M. Z. Wang1, L. Y. Hu1, Q. Y. Xu1, Z. N. Xi1, and J. J. Loo2, Yangzhou University, Jiangsu, China, 1University of Illinois, Urbana, IL.

In non-ruminants it is well-established that biological rhythms play a profound role in coordinating whole-body metabolism. In dairy cows there is evidence that milk yield and milk fat content have rhythmic pattern thought to be regulated by circadian rhythms. The core circadian clock gene period 2 (PER2) is associated with mammary gland development and lipid synthesis in rodents, partly via regulating peroxisome proliferator-activated receptor gamma (PPARG). Whether such type of molecular link between circadian clock and lipid metabolism exists in bovine is unclear. We hypothesized that PER2 is associated with lipid metabolism in bovine mammary cells. To test this hypothesis, the bovine mammary tissue samples were obtained from 3 mid-lactation (averaged 110 d postpartum) cows and digested by collagenase to gain the primary bovine mammary epithelial cells (BMECs). Small interfering RNA (siRNA) technology was used to inhibit PER2 expression in primary BMECs. The primary BMECs were transfected with 3 siRNAs at 0, 12, 24, 36, 48, 60 h to screen out the best siRNA and its transfection time point. The lipid droplet was measured by red oil O staining, and the triacylglycerol (TAG) content of BMEC was determined with the tissue triglyceride assay kit (APPLYGEN, China). The lipid droplet and TAG content were determined at 36 h (36 h showed the greatest PER2 gene inhibitory effect of 84.7%) after the siRNA transfection. One-way ANOVA and Duncan’s multiple comparison were used to conduct statistical analysis by SPSS software version 22.0 (statistical significance set at P < 0.05). Silencing of PER2 led to lower concentration of cellular lipid droplets and TAG levels in BMECs (P < 0.05). In addition, PER2 silencing downregulated mRNA of ACACA, FASN, LPIN1 and SCD (P < 0.05), indicating an overall inhibition of lipogenesis and desaturation. The downregulation of PPARG and SREBF1 in response to PER2 silencing underscore the importance of circadian clock signaling and transcriptional regulation of lipogenesis. Therefore, data suggest that PER2 participates in the coordination of mammary lipid metabolism and may be a component of the control of lipid droplet and TAG synthesis in mammary cells.

Key Words: PER2 silencing, mammary epithelial cell, lipid metabolism

M77  Milk fatty acid profiles of beef cows in response to a short feed restriction during lactation. I. Casasús*, J. R. Bertolin, K. Orquera, J. Ferrer, and M. Blanco, Cir Invest y Tecnol Agroal Aracon (CITA), IA2 (CITA-Universidad de Zaragoza), Zaragoza, Spain.

The relationship between energy balance and the milk fatty acid (FA) profile is well established in dairy cows but has received little attention in beef cattle. We analyzed the milk fatty acid profile of 16 Parda de Montaña beef cows 2 mo post-calving in response to a 4-d (d) dietary restriction (55% of energy requirements, 6.2 kg dry matter (DM) hay/d), as compared with a previous basal and an 8-d refeeding period (100% of requirements; 7.0 kg DM/d hay + 2.7 kg DM/d concentrate). With d0 as the start of restriction, milk was sampled on days d2 (basal), d1, d3 (restriction) and d5, d6, d8 (refeeding). Individual FA were identified by gas chromatography, and sums of FA were calculated (saturated (SFA), monounsaturated (MUFA), polyunsaturated (PUFA), cis-MUFA, trans-MUFA, C4-C15 de novo synthesis FA and C16-C24 mobilization FA). These sums and the 4 major FA (C16:0, C18:1–9c, C18:0, C14:0) were analyzed using mixed models, with day as fixed and cow as random effects. All the results presented here were significant at P < 0.001. The milk FA profile responded immediately to changes in the energy balance and/or the diet. On d1 of restriction, the concentrations of SFA decreased, mainly due to a reduction in the de novo synthesis FA and C16. A concomitant increase in MUFA (associated with that of C18:1–9c, predominant in body fat) was observed. These changes, along with the increments in C16-C24 FA, indicate an enhanced fat mobilization from the adipose tissue. During the restriction, C18:0 and trans-MUFA decreased while cis-MUFA and PUFA increased, as a result of both the mobilization and the change in diet composition. The opposite occurred in the refeeding phase. On d5, MUFA decreased (due to the reduction in C18:1–9c) and SFA increased because of the rise in the de novo synthesis FAs and C16:0, reflecting the reversion of fat mobilization. At the end of refeeding (d8), the individual FA returned to basal concentrations, but the sum of C16-C24 mobilization FAs was even lower than that of C4-C15 de novo synthesis FAs was higher than basal values, indicating a possible “rebound effect” after restriction and refeeding.

Key Words: beef cows, nutritional challenge, milk fatty acid profile

M78  Effects of glucose and acetate infusion on mammary uptakes of essential amino acids by lactating dairy cows. B. Li*, R. Laforest1, L. Wright1, J. Kim1, P. Kedzierski2, V. Osborne1, J. Doelman2, and J. Cant1, 1University of Guelph, Guelph, ON, Canada, 2Trouw nutrition, Putten, the Netherlands.

Previous research suggests that glucogenic energy can stimulate milk protein yield of dairy cows while lipogenic energy does not. To explore differences in mammary essential amino acid (EAA) utilization between these types of energy, 5 rumen-fistulated cows were given additional glucose or acetic acid in a 5 × 5 Latin square design. Infusion treatments were:

Methionine (Met) supplementation increases milk, protein and fat yields in cows. We investigated whether this could be partly explained by an increasing flow of milk components in the secretory pathways of mammary epithelial cells. Multiparous Alpine goats at mid lactation (n = 48), grouped by levels of expression of the CSN1S1, were assigned to 4 treatments in a randomized complete block design. Goats were fed a fixed diet of processed grass silage (5.2% DM) and 4 levels of abomasal glucose, and 4) 2.2 kg/d (HiG) ruminal acetic acid. Acetic acid and glucose infusion rates were isocaloric at low and high levels, respectively. Milk yields were recorded daily and milk samples were collected on the last 3 d of each 7-d infusion period. Tail and mammary venous samples were collected on d 7 to estimate mammary uptakes. Plasma samples for each cow were pooled over time by period. Plasma AA concentrations for each time point were analyzed using Ultra Performance Liquid Chromatography in conjuction with Empower Chromatography Data Software (Waters Corporation, Milford, MA). Linear contrasts of glucose and acetic acid dose were estimated by ANOVA assuming fixed effects of period and treatment, and random effects of cow. Glucose infusion had no effect on DMI (P = 0.97) or milk protein yield (P = 0.15) but increased lactose yield (P = 0.03) and tended to increase milk yield (P = 0.07). Acetic acid infusion dramatically decreased DMI from 18.8 kg/d on CTL to 13.8 and 14.9 kg/d on LoA and HiA respectively. Milk yield decreased 5.4 kg/d, protein yield decreased 201 g/d and lactose yield decreased 224 g/d on HiA compared with CTL (P ≤ 0.01) due to the decrease of DMI. Glucose infusion decreased arterial concentrations of all EAA (P < 0.01) except Met and Thr, but increased mammary plasma flow (MPF) rate (P < 0.01), so that mammary uptakes of EAA were not affected (P > 0.16). In contrast, acetic acid infusion increased concentrations of Ile, Leu, and Val (P < 0.08) without affecting other EAA concentrations (P > 0.20), had no effect on MPF (P = 0.70), and decreased mammary uptakes of Arg, Ile, Leu, and Phe (P < 0.10). Findings suggest that exogenous glucose encouraged milk protein production despite reduced plasma concentrations of some EAA, while exogenous acetic acid discouraged milk protein yield thereby increasing concentrations of some EAA.

Key Words: cow, amino acid, milk protein

M80 Effect of heat stress during the dry period on estradiol and prolactin interactions in mammary gland gene expression of Holstein cows. J. A. Negrao1,2, V. Ouellet2, M. Marrero-Perez2, T. F. Fabris2, J. Laporta2, and G. E. Dahl3, 1University of Sao Paulo, Pirassununga, SP, Brazil, 2University of Florida, Gainesville, FL.

The dry period, a 6 to 8-week nonlactating state between lactations, is essential for maximal mammary development and lactation in dairy cows. Although late-gestation heat stress decreases estrogen (E) and increases prolactin (PRL) concentrations in blood, those impacts on mammary development remain unclear. The objective of this study was to determine how late gestation heat stress-induced E and PRL alterations affect the expression of their receptors and signaling in the mammary gland at different stages of the dry period. Fourteen cows were either exposed to in vivo heat stress (HT, n = 7) or active cooling by fans and soakers (CL, n = 7) for the entire dry period (-45 d). Mammary gland biopsies were performed on d 3 (i.e., involution) and 35 (i.e., proliferation) relative to dry off and equally divided in 3 explants, that were incubated in vitro for 24h in 1 of the 3 mediums: 1- Basal (Bm no PRL or E); 2- CL mimic (Cm: basal + 20ng/mL PRL + 5.8ng/mL E); and 3- HT mimic (Hm: basal + 40ng/mL PRL + 2.9ng/mL E). Gene expression of PRLR-SF, PRLR-LF, ESR1 and ESR2 were measured using Real Time qPCR. An ANOVA using the mixed procedure of SAS was performed to assess the impacts of in vivo (HT, CL), in vitro (Bm, Cm, Hm) treatments and their interaction on relative transcript expression. Dry cows subjected to HT had increased rectal temperature and respiration rate relative to cows subjected to CL (39.1 vs 38.8 ± 0.01°C and 65.2 vs 55.4 ± 1.2 breaths/min, respectively), which confirms cooling conditions are effective and necessary for the thermal equilibrium of the CL cows. In vivo HT increased the expression of PRLR-LF relative to CL. However, Hm in vitro treatment decreased the expression of PRLR-SF, ESR1 and ESR2 relative to Bm treatment. These results suggest that E and PRL alterations caused by heat stress exposure can modulate the expression of receptors in the mammary gland, with potential implications for normal mammary development during the dry period.

Key Words: heat stress, mammary explants, culture

M82 Evaluation of breed and udder characteristics on somatic cell count and udder pathogens in lactating Holstein and Jersey cows. B. M. Brown, M. W. Hollis*, and J. G. Carter, Middle Tennessee State University, Murfreesboro, TN.

The objective of this study was to evaluate the impact of physical udder characteristics and breed on hygiene scores (HS), milk yield (MY), conductivity (COND), SCC, and bacterial cultures (BC) in lactating Holstein and Jersey dairy cows housed in a compost-bedded pack barn. Lactating Holstein and Jersey (n = 10 each) cows were evaluated during a 6-wk period. Milk samples were collected as a sterile composite from all 4 quarters during one milking/wk and SCC was determined using the DeLaval Cell Counter DCC. If SCC ≥350,000 cells/mL, the sample was cultured to determine bacterial species. Milk samples were cultured using a Tri-plate agar including Factor, MacConkey, and Focus media (University of Minnesota Easy Culture). Cows were evaluated once/wk using a multi-zone hygiene scoring system for udder cleanliness (1 = very clean to 4 = very dirty; Cook, 2002). Udder measurements were taken during wk 1 and included udder depth and circumference, and teat length. Milk yield and COND were measured daily and averaged by wk using the AfilmMilk parlor system (Afimilk, Kibbutz Afikim, Israel). Statistical analysis of MY, COND, and udder measurements were conducted using the MIXED procedure in SAS (v9.4). Analysis of HS incidence and BC species counts were evaluated using the FREQ procedure in SAS (v9.4). No differences in BC, SCC, or physical udder characteristics were observed among breeds. Holstein
cows produced more milk than Jerseys (37.6 and 26.5 ± 3.01 kg/d, respectively; \(P = 0.0181\)) and had greater COND (9.70 and 8.81 ± 0.15 mS/cm, respectively; \(P = 0.0005\)). Jerseys exhibited improved udder (64.4% vs. 25.4% score 1 and 28.8 vs. 64.4% score 2, respectively; \(P = 0.0003\)) and flank (61.0 vs. 22.0% score 1; 35.6 vs. 57.6% score 2; and 3.4 vs. 18.6% score 3, respectively; \(P = 0.0001\)). HS more frequently than Holsteins, indicating that Jersey udders and flanks were overall cleaner than Holsteins. Jerseys may be better suited for compost-bedded pack barns than Holsteins based on the observed improvements in conductivity and hygiene scores.

**Key Words:** udder measurements, breed, SCC

### M83 Relationships of somatic cell count with milk lactose and protein over the first 10 days postpartum in dairy cows

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There is little research examining the relationships of somatic cell count (SCC) with lactose and protein concentrations in bovine milk. Understanding these relationships may provide insight into how animal health is related to milk composition and quality. The objective of this study was to examine the relationships of SCC and lactose and protein in bovine milk in the first 10 d postpartum. Quarter-milk samples were collected daily from 107 cows on 4 dairies and milk components assessed by near-infrared analysis. Data were analyzed using a mixed linear regression model with SCC (log-transformed) and day postpartum as independent variables and dairy as a random variable while assuming a compound symmetric correlation structure for the repeated measures of day within quarter of each cow. Milk type was characterized ascolostrum (d0; C), transitional milk (d1-d4; TM), and mature milk (d5-d10; MM). Lactose concentrations were 3.16 ± 0.03%, 4.08 ± 0.01%, and 4.52 ± 0.01% in C, TM, and MM, respectively; protein concentrations were 9.40 ± 0.10%, 3.94 ± 0.03%, and 3.03 ± 0.01% in C, TM, and MM, respectively. The range of SCC across all samples was 1,000 to 9,999,000 cells/mL. In C, there was no relationship between SCC and lactose, but there was a negative relationship between SCC and protein (\(P = 0.0004\)). For TM and MM, there was a negative relationship between SCC and lactose that became more negative as days postpartum progressed. There was a positive relationship between SCC and protein in TM; conversely, there was a negative relationship between these variables in MM. For both TM and MM, protein decreased with increasing days postpartum. These results suggest relationships of SCC with lactose and protein exist; however, they are not consistent over time.

**Key Words:** dairy cow, milk, somatic cell count

### M84 Evaluation of mammary gland involution in dairy cows during the dry period using a 3-dimensional scanner


Mammary gland involution is an important process during the dry period, and it is associated with immune defenses and the capability to prevent intramammary infection that could affect subsequent lactations. Currently methods to evaluate udder involution during the dry period are limited. The objective of this research was to compare the use of a 3D scanner and a metric tape to measure mammary gland involution in dairy cows. Clinically healthy Holstein cows (n = 15) of parity 2 through 5 were included in the study if they had a SCC < 200,000 cells/mL at the end of lactation. Mammary gland dimensions were measured at the dry off (d 0), and 2, 7, and 14 d later using both a 3D Scanner (Structure Sensor, Occipital, San Francisco) and manual measurements of marked areas between the middle rear left and right quarters and the median suspensory ligament. Data was collected from November 2019 – February 2020. Files obtained from the 3D scanning were analyzed for surface area of the rear quarters using 3-Matic software (Materialise, Belgium). Percentage change was calculated between measurements obtained at d 0, and measurements taken at d 2, 7, and 14. Analysis of variance was performed to analyze data. When measured manually using a metric tape, the width of the quarters increased and then decreased and were 116%, 101%, and 93% on d 2, 7, and 14, respectively. When measured using a 3D scanner, the surface area of the rear quarters was 125%, 100%, and 89% on d 2, 7 and 14 respectively. No significant difference in measurements was found based on method (\(P = 0.88\)). When width was measured manually, an increase in 16% and a decrease in 24% was observed from d 2 to 7 and d 2 to 14 (\(P < 0.01\)). When surface area was measured using the 3D scanner, it increased 25% and decreased 36% between d 2 to 7 and d 2 to 14, respectively (\(P < 0.001\)). No significant change in mammary gland dimensions was observed from d 7 to 14 (\(P > 0.08\)). Changes in mammary gland dimensions during the dry period were quantifiable using either manual measurements or 3-D scanning.

**Key Words:** dry period, udder involution, 3-dimensional scanner

### M85 Potential of nanoparticles containing matrix metalloproteinase-9 (MMP-9) as a dry-off enhancer: Pulling apart the effects of MMP-9 and nanoparticles

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The dry period is a non-milking interval when the mammary gland involutes and regenerates to guarantee an optimal milk production in the subsequent lactation. Several bottlenecks such as the high risk of intramammary infections may hamper this process. Antibiotics have been routinely used as a preventative treatment, but the concerns about potential antibiotic resistance calls for alternative preventive strategies. Matrix metalloproteinase-9 (MMP-9) is an enzyme able to degrade the extracellular matrix, triggering the involution and immune function of the mammary gland. Thus, the objective of this study was to determine in vivo whether the involution and immune function enhancement previously observed after the administration of inclusion bodies (IB) containing MMP-9 was due to the nanoparticle format or to the inherent properties of the MMP-9 comprised in IB. Eight cows were enrolled in this study and 30 quarters of these cows were considered the experimental unit (4 quarters per cow in 7 cows, and 2 quarters in 1 cow). A dose of 1.2 mg of both active and inactive MMP-9 IB and 10 mL of saline solution were infused into 10 quarters per treatment at dry-off. At 1, 3, 6, and 9 d after protein infusions, mammary gland secretions (MGS) were obtained and analyzed for SCC, immune cell populations, BSA, lactoferrin, Na+/K+, and endogenous MMP-9. Data were analyzed using a fixed-effects model. There were only minor differences in the parameters monitored between the infusion of active or inactive rMMP-9 IB. Briefly, concentration of BSA in MGS were greater at 1 and 6 d in quarters treated with active rMMP-9 IB (\(P < 0.01\)) than those treated with inactive IB. Similarly, the Na+/K+ ratio in MGS increased at d 6 and was sustained at d 9 (\(P < 0.01\)) with the active MMP-9 IB compared with the inactive IB. Thus, the minor differences triggered by the administration of an active or an inactive form of MMP-9 led to conclude that the response observed in the bovine mammary gland was mainly due to the protein format (nanoparticle or soluble) but not to the biological activity of the MMP-9 embedded in the IB. This study provides relevant information on the future use of protein IB in the mammary gland of cows and the role of MMP-9 at dry-off.

**Key Words:** dry period, inclusion body, mammary gland
Mitochondrial function in the liver and skeletal muscle of mid-lactation dairy cattle. V. R. Favorit\textsuperscript{1,}\ A. N. Kavazis\textsuperscript{2}, W. R. Hood\textsuperscript{2}, P. Villamediana\textsuperscript{1}, and A. L. Skibiel\textsuperscript{1}, \textsuperscript{1}University of Idaho, Moscow, ID, \textsuperscript{2}Auburn University, Auburn, AL.

Most energy produced in the cell is through oxidative phosphorylation (OXPHOS) and mitochondrial activity changes according to cellular energy demand. At peak lactation, mammary OXPHOS machinery and ATP production are upregulated in association with increased mammary energy requirement and milk output. It is unclear if concurrent shifts occur in tissues with supporting roles in milk synthesis, such as skeletal muscle and liver. We assessed relationships between milk production and measures of mitochondrial function in these tissues at mid-lactation. Liver and skeletal muscle biopsies were taken from multiparous Holstein cows (n = 11) in mid-lactation (75 ± 4 d). Milk yield was recorded daily to 80 d in milk (DIM) and milk samples collected for composition analysis (fat, protein, lactose) at 74 DIM. Mitochondria were isolated and oxygen consumption measured in a respiration chamber. Respiratory control ratio (RCR) was used as a measure of the functional and coupled state of mitochondria and calculated as the ratio of maximal ADP-stimulated respiration to basal respiration following ADP phosphorylation using either complex I (NADH-linked) or II (FADH\textsubscript{2}-linked) substrates. Mitochondrial emission of reactive oxygen species (ROS) was also measured. Correlation analysis was used to examine relationships between mitochondrial measures and average milk yield from 40 to 80 DIM (mid-lactation) only and from 5 to 80 DIM (i.e., early-to-mid). Liver complex II RCR at mid-lactation was positively correlated with early-to-mid milk yield, signifying increased fat substrate utilization to produce ATP and minimal proton leak (r = 0.74, P = 0.01). No association was observed between milk components and mitochondrial RCR or ROS. Mid-lactation milk yield was positively correlated with skeletal muscle mitochondrial ROS production (r = 0.66, P = 0.05) and tended to correlate with liver mitochondrial ROS production (r = 0.63, P = 0.1). Our results suggest that elevated energy demands associated with milk production are met with an increased efficiency of mitochondrial ATP production in liver but result in greater oxidant emission in skeletal muscle and liver.

Key Words: oxidative phosphorylation, lactation, metabolism

Laser capture microdissection (LCM) is one popular technique for isolating specific cell types from tissues. However, RNA quality, quantity and integrity in LCM samples can be greatly affected by tissue treatment, length of dissection and the total areas of cells dissected. In this study, we optimized methodology to obtain high quality RNA from mammary epithelial cells collected from bovine mammary glands treated with lipopolysaccharide (LPS) and determined if LPS affected the quality, quantity and integrity of RNA. Ten multiparous cows were used. Five treatment (T) cows received one intramammary dose of LPS (50 µg in 10 mL saline; TL) in each of 2 ipsilateral glands while the contralateral glands received saline (10 mL; TS). Likewise, in 5 control (C) cows, saline (CS) was infused into 2 ipsilateral glands and the other glands remained uninfused (CU). Mammary tissues were collected at 0, 3 and 12 h, relative to infusions and processed for LCM. After staining, tissue sections were visualized using an epifluorescence microscope with attached computer and manually selected areas of epithelial cells were dissected using LCM. Time of dissection was kept minimal (13.6 ± 0.52 min; mean + SE) to avoid RNA degradation, and areas of dissected cells were consistent across treatment groups and times. Results showed that fixation of tissue sections with chilled 70% ethanol, histogene staining (with RNase inhibitor), dehydration in absolute ethanol, and final clearing in xylene was able to preserve quality of RNA isolated from microdissected cells. Analysis of total RNA from mammary epithelial cells harvested by LCM showed RNA yield per unit area was affected by treatment, time and interaction of treatment x time, suggesting that LPS increased transcription or reduced RNA degradation in epithelial cells. In addition, RNA integrity number (RIN) was affected by treatment and time x treatment interaction (P ≤ 0.01). In summary, we developed an optimized LCM protocol to reproducibly obtain high-quality RNA and suggest that LPS treatment may affect RNA yield of mammary epithelial cells.

Key Words: mastitis, RNA quality, transcription