PHYSIOLOGY AND ENDOCRINOLOGY: INTERRELATIONSHIPS BETWEEN ENVIRONMENTAL, METABOLIC, AND PHYSIOLOGICAL PROCESSES I

0498 Insulin sensitivity of the lipid metabolism of precalving dairy cows across a range of body condition scores. J. De Koster* and G. Opsomer, *Department of Reproduction, Obstetrics and Herd Health, Faculty of Veterinary Medicine, Ghent University, Ghent, Belgium.*

Insulin plays a central role during the transition period of dairy cows by influencing glucose, lipid, and protein metabolism. At the adipose tissue, insulin stimulates lipogenesis and inhibits lipolysis, thereby regulating the circulating NEFA concentration. Overconditioning is known to induce insulin resistance of the glucose metabolism in dairy cows. In the present study, we identified if factors related to adiposity (BCS, BFT, NEFA concentration during the dry period) influenced insulin sensitivity of the lipid metabolism in 8 healthy dairy cows at the end of pregnancy across a range of BCS (2.75 to 5). Hyperinsulinemic euglycemic clamp tests were performed consisting of 4 insulin infusions: 0.1, 0.5, 2, or 5 $mU \cdot kg^{-1} \cdot min^{-1}$. At regular time intervals during the infusions, blood glucose concentration was determined using a glucometer and the speed of a concomitant glucose infusion was adapted to keep blood glucose concentration constant. At the end of each infusion, a steady state (SS) was maintained for 30 min. During the SS, minor changes of the glucose infusion were necessary to maintain normal blood glucose level. During the SS, blood samples were taken at 10 min interval to determine SS insulin (SSIC) and NEFA (SSNEFA) concentrations. The SSIC was 8.77 ± 3.04; 52.38 ± 16.11; 339.04 ± 122.01; 1411.5 ± 500.08 μU/mL and the SSNEFA was 0.62 ± 0.20; 0.26 ± 0.08; 0.14 ± 0.09; 0.11 ± 0.08 mmol/L for the insulin infusions of 0.1, 0.5, 2, and 5 $mU \cdot kg^{-1} \cdot min^{-1}$, respectively. The SSNEFA is the resultant of both the inhibitory effect of insulin on lipolysis and the stimulatory effect of insulin on lipogenesis. To correct for different basal NEFA levels, the NEFA lowering effect of insulin was calculated as % compared with basal values. Dose response curves were created using PROC NLIN in SAS (SAS Inst. Inc., Cary, NC) to determine maximal effect and insulin dose needed to elicit half-maximal effect (logED50). Maximal effect and logED50 were, respectively, 0.90 ± 0.07% and 1.24 ± 0.29 μU/mL. Effects on both parameters were analyzed using PROC MIXED in SAS, with parity as random factor and BCS, BFT, and NEFA concentration during the dry period as independent variables. Maximal effect of insulin was negatively influenced by NEFA concentrations during the dry period ($\beta = -0.3065$; $P < 0.05$) while the effect of BFT and BCS was not significant. None of the independent variables had a significant influence on logED50. It can be concluded that elevated NEFA concentrations during the dry period decrease the maximal effect of insulin on lipolysis and lipogenesis.

Key Words: insulin sensitivity, lipid metabolism, dairy cow

499 Effect of ractopamine hydrochloride and zilpaterol hydrochloride on the electrocardiogram and blood lactate in finishing steers. D. A. Frese*[1], C. Reinhardt[1], S. J. Bartle[1], D. N. Rethorst[1], B. S. Bawa[1], J. D. Thomason[1], G. H. Loneragan[2], and D. Thomson[1], *[1]Kansas State University, Manhattan, [2]Texas Tech University, Lubbock.*

Thirty Angus steers (506 ± 5.5 kg) were used to examine the effect of ractopamine hydrochloride and zilpaterol hydrochloride on the cardiac physiology and blood lactate concentration of finishing beef steers. Cattle were randomly assigned to 1 of 3 treatment groups: control (CON), ractopamine hydrochloride (300 $mg \cdot animal^{-1} \cdot d^{-1}$; RAC), and zilpaterol hydrochloride (8.3 mg/kg DM basis; ZIL). Cattle were allowed to acclimate to pens and Calan Gate feeders for 43 d before trial initiation. Steers were housed in outdoor dirt-floor pens with ad libitum access to feed and water. Holter electrocardiograph (ECG) monitors were placed on cattle on d -2, 6, 13, and 24 of the trial and recorded continuously for 72, 24, 24, and 96 h, respectively; d 0 was the first day of β agonist feeding. Blood samples were obtained via jugular venipuncture for complete blood count, serum chemistry, and blood lactate (BL) analysis at the time of ECG monitor application. Electrocardiogram recordings were evaluated for mean heart rate (MHR) in beats per minute (bpm), ventricular (VPB), and supraventricular arrhythmia events per day (SVPB). Cattle fed ZIL (77.6 bpm ± 1.19) and RAC (78.4 bpm ± 1.18) had greater MHR than CON (74.2 bpm ± 1.27). No differences were observed in VPB, or SVPB in the CON, RAC, or ZIL treated cattle. No differences were found among treatments in arrythmia rate when classified as single beat, paired beat, or > 2 beats per event. Single beat events represented 84% of VPB and 90% of SVPB events. No differences were observed in BL among CON (3.1 mmol/L), RAC (2.9 mmol/L), and ZIL (2.8 mmol/L). Creatinine kinase (CK) increased ($P < 0.03$) in ZIL cattle (220.3 U/L), compared with CON (111.9 U/L) and RAC cattle (120.2 U/L) at d 13. On d 24 CK was increased in ZIL (226.9 U/L), than CON (132.5 U/L) and RAC (135.4 U/L). In conclusion, RAC and ZIL increased MHR in feedlot cattle, but had no effect on arrythmia rate, arrythmia classification, or blood lactate. Also, ZIL increased CK compared with CON and RAC on d 13 and 24.

Key Words: β agonist, electrocardiogram, blood lactate, cattle

0500 Expansion and evaluation of a dynamic, mechanistic model of nutritional and reproductive processes in dairy cattle. J. P. McNamara*[1] and S. L. Shields[2], [1]*Washington State University, Pullman,* [2]*Elanco Inc, Pasco, WA.*

The effects of nutrition and genetics on fertility are multiple, and although we do have a large knowledge base and good management practices, reproductive efficiency does not match the biological potential. In part, this is because we lack a full systems approach to managing the genetics and nutrition of cows to improve reproduction. Our objective was to expand the integration of nutritional and reproductive processes in a mechanistic, dynamic model of the dairy cow; suitable for evaluation of data, concepts, and hypotheses regarding underlying genetic, nutritional, and physiological control of reproduction. A model of metabolism (Molly, UC Davis); which describes nutrient metabolism, as well as tracking energy transactions; was integrated with a model of reproductive processes, which describes growth and decay of the follicles and corpus luteum, gonadotropin releasing hormone, follicle stimulating hormone, luteinizing hormone, progesterone, estrogen, oxytocin, and prostaglandin F2α over time. The models are integrated at specific points based on available literature data, for example: glucose and IGF-I affect rates of synthesis and release of follicle stimulating hormone, luteinizing hormone, and follicular growth according: follicular_growth = {follicular_rate_constant = hp_fsh_mod + [follicular_ rate_factor_IGF_1(0.001833) × (IGF_1– average_IGF_1)]}, where follicular_rate_constant is the rate of follicular growth, hp_fs_mod is a Hill function describing the effect of FSH on growth, and follicular_ rate_factor_IGF_1 which affects follicular growth. Degradation of estrogen and progesterone is a function of metabolic rate in visceral tissues of Molly (AtAdV), for example: progesterone degradation = 0.0005669 (deg_const_P4 = progesterone degradation factor (0.0005669) + [metab_rate_degradation_factor_P4 × (AtAdV–avg_ATADV)]. During pregnancy, cycling ceases and the model maintains progesterone concentrations and describes fetal growth. A modeling analysis that varied milk production from 25 to 55 kg/d DMI from 18.8 to 27.3 kg DMI, gave a range of metabolic rate from 1090 to 1426 M/d and a range of IGFI from 86.4 to 106.4 ng/L). Increasing IFGI increased follicular growth], while increasing metabolic rate increased the degradation of estrogen and progesterone. Because most reproductive systems have negative and positive effects on each other, it is the interaction of these systems which provided an interesting pattern of change in follicular growth and steroid degradation. This model should be of use in testing hypotheses about effects of genetic selection and nutritional management in dairy cattle.

Key Words: systems biology, reproduction, nutrition

0501 Metabolic, paracellular permeability, and immune gene expression in ruminal epithelium during the transition period in dairy cattle. A. Minuti*[1], S. Alqarni[2], P. Cardoso[2], E. Trevisi[1], and J. J. Loor[2], [1]*Università Cattolica del Sacro Cuore, Piacenza, Italy,* [2]*University of Illinois, Urbana-Champaign, Urbana.*

The study was aimed to investigate the mRNA expression linked to systems involved in the metabolic, epithelial integrity, and immune function in ruminal epithelial tissue during the transition period in dairy cattle. Seven multiparous Holstein cows with a ruminal fistula were dried off at −50 d relative to the expected calving and fed a controlled-energy diet (NEL = 1.24 Mcal/kg of DM) until calving, and then a common lactation diet. Ruminal epithelial tissue was biopsied at -14, 10, and 28 d in milk (DIM). Extracted mRNA was used for profiling of 23 genes via quantitative real-time RT-PCR. The expression of genes was normalized using geometric mean of 3 internal control genes (CMTM6, ERC1, and MRPL39). Data were analyzed as a repeated measures study using the MIXED procedure of SAS (SAS Inst. Inc., Cary, NC). The epithelial integrity genes OCLN and TJP1 had a decrease ($P < 0.05$) of expression from -14 to 10 DIM. For genes involved in the immune function, TNF did not change significantly. In contrast, the expression of CD45 decreased ($P < 0.05$) from -14 to 10 DIM and the expression of TL2 and TLR4 decreased ($P < 0.01$) until 28 DIM compared with -14 DIM. The transporters SLC14A1, SLC16A1, and SLC16A3 increased expression during the transition period with highest ($P < 0.05$) values at 28 DIM. The ketogenic gene HMGCS2 had higher ($P < 0.05$) expression at 28 DIM vs. -14 and 14 DIM. Expression of PPARA, PPARD, and PPARG did not change during the transition period; while, the nuclear receptor RXRA decreased ($P < 0.01$)from -14 DIM to 28 DIM. Expression of the insulin receptor (INSR) was lower ($P < 0.05$) at 10 DIM vs. -14 and 28 DIM. Expression of TGFB1, involved in cell growth and proliferation, had the highest ($P < 0.05$)expression at 10 DIM; while, its receptor (TGFBR1) had higher ($P < 0.05$) expression at -14 DIM and subsequently decreased. Results suggest that along with other tissues the ruminal epithelium also experiences changes at the transcriptome level. These are likely important for a successful transition into lactation. The observed changes could be driven by both changes in feed composition and nutrient intake typical of this period, and to the metabolic and hormonal changes that take place in preparation to the time of calving and the onset of lactation.

Key Words: rumen, transition cow, transcriptomics

0502 Energy expenditure is lower in efficient compared with inefficient lactating dairy cattle.

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Measuring the energy expenditure (EE) of an animal, particularly while it is at pasture exhibiting natural behaviours, is of particular importance to improve management, breeding, and feeding practices. Recently, the estimation of EE based on heart rate (HR) has been explored. In cattle, this relationship appears to be more stable than in other nondomestic animals, likely due to the acclimation and low fear response of domestic, particularly dairy, cattle. Sixteen lactating, primiparous Holstein-Friesian cows previously classed as efficient (n = 8) or inefficient (n = 8) based on residual feed intake (RFI) were housed in open circuit respiration chambers for a period of 48 h. Animals were fed lucerne hay cubes ad libitum and recieved 6 kg DM crushed wheat grain (and minerals) at milking (total diet CP 18% and ME 10.5 MJ/kg DM). Real time measurements of methane, CO_2, and O_2 flux were obtained in the chamber and real time HR measurements obtained using a Polar Equine HR monitor fitted to the cows for the duration of the chamber measurement period. Production measures (e.g., intake, milk yield, and milk content), heart rates, and O_2 consumption were not different between the efficiency groups. Oxygen consumption per heart beat (HB), defined as O_2 pulse, was calculated for the first 24 h of the study. The O_2/HB over the entire 24 h there was a significant effect of efficiency group such that efficient cows consumed less (0.01029 g min^{-1} per HB, $P < 0.05$) O_2 per heartbeat than inefficient cows. The finding of a relationship between efficiency and O_2 pulse being present in lactating dairy cattle is novel. Taken together, the lower pulse O_2 in efficient animals without a variance in intake or production indicates that there are fundamental differences in maintenance energy consumption between inefficient and efficient groups. This finding supports the idea that a more efficient animal will deliver less O_2 per HB whilst maintaining a level of health and production similar to that of an inefficient animal.

Key Words: energy expenditure, efficiency, residual feed intake

0503 Supplementation of OmniGen-AF during the receiving period modulates the metabolic response to a lipopolysaccharide challenge in feedlot steers.

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The use of probiotic feed supplements to enhance animal health and growth are of great interest to the beef industry. Studies have demonstrated that some probiotic supplements may affect metabolism, and therefore influence an animal's response to an immune challenge. This study was designed to determine the effect of supplementing feedlot steers with OmniGen-AF (Prince Agri Products Inc., Quincy, IL) during the receiving period on the metabolic response to a lipopolysaccharide (LPS) challenge. Steers (n = 18; 270 ± 5 kg BW) were obtained and transported to the University of Nebraska Agricultural Research and Development Center feedlot. Upon arrival steers were processed and separated into 2 treatment groups (n = 9/treatment): 1 group was fed a standard receiving diet (Control, Cont) and the other group was fed the same receiving diet supplemented with OmniGen-AF at 4 g/45.4 kg BW/d for 29 d (OmniGen-AF). On d 27, steers were fitted with indwelling jugular cannulas and placed in individual stalls. On d 28, steers were challenged i.v. with LPS (0.5 µg/kg BW at 0 h), and blood samples were collected at 30-min intervals from -2 to 8 h and at 24 h postchallenge. Serum was isolated and stored at −80°C until analyzed for glucose, NEFA, and blood urea nitrogen (BUN) concentrations. Data were analyzed using the Mixed procedure of SAS (SAS Inst. Inc., Cary, NC) specific for repeated measures. Glucose concentrations were affected by treatment (P = 0.009) and time ($P < 0.001$). Glucose was greater in OmniGen-AF steers compared with Cont steers (76.4 ± 1.1 mg/dL vs. 72.4 ± 1.0 mg/dL). For NEFA concentrations, there was a treatment ($P < 0.001$) and time ($P < 0.001$) effect. Specifically, Cont (0.210 ± 0.007 mmol/L) steers had greater NEFA concentrations than OmniGen-AF steers (0.101 ± 0.010 mmol/L). There was a tendency (P = 0.07) for a treatment × time interaction such that NEFA concentrations were greater ($P \leq 0.03$) in Cont steers than OmniGen-AF steers from 3 to 8 h after LPS challenge. For BUN, there was a treatment ($P < 0.001$) effect such that concentrations were greater in Cont steers (12.4 ± 0.1 mg/dL) than OmniGen-AF supplemented steers (11.5 ± 0.1 mg/dL) throughout the study, and were not affected by time (P = 0.28). These data suggest that OmniGen-AF supplementation modulates the metabolic response to a LPS challenge and provides an indication that supplementation of feedlot steers with OmniGen-AF may prevent the breakdown of other substrates (e.g., protein and fat) for energy during an immune challenge.

Key Words: cattle, metabolism, OmniGen-AF

0504 Supplementation of *Saccharomyces cerevisiae* modulates the metabolic response to a lipopolysaccharide challenge in feedlot steers.

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Live yeast has the potential to serve as an alternative to the use of low-dose supplementation of antibiotics in cattle due to the ability to alter ruminant metabolism; which in turn may influence the immune response. Therefore, the objective of this study was to determine the metabolic response to a lipopolysaccharide (LPS) challenge in feedlot steers supplemented with *Saccharomyces cerevisiae CNCM I-1079* (SC). Steers (n = 18; 266 ± 4 kg BW) were processed and separated into 3 treatment groups (n = 6/treatment): (1) steers were fed a standard receiving diet and served as the control (Cont); (2) steers were fed the receiving diet supplemented with SC (Lallemand, Inc.) at 0.5 g·animal^{-1}·d^{-1} (SC-0.5); and (3) steers were fed the control diet supplemented with SC at 5.0 g·animal^{-1}·d^{-1} (SC-5.0) for 29 d. On d 27, steers were fitted with indwelling jugular cannulas and rectal temperature (RT) probes, and were placed in individual stalls. On d 28, steers were challenged i.v. with LPS (0.5 µg/kg BW at 0 h), and blood samples were collected at 30-min intervals from -2 to 8 h and at 24 h postchallenge. Serum was isolated and stored at −80°C until analyzed for glucose, NEFA, and blood urea nitrogen (BUN) concentrations. There was a treatment (P = 0.02) and time effect (P < 0.001) for glucose; SC-0.5 steers had greater glucose concentrations (77.8 ± 1.6 mg/dL) than Cont (71.5 ± 1.3 mg/dL) and SC-5.0 steers (71.6 ± 1.4 mg/dL). Glucose concentrations also increased (P < 0.001) over time in response to LPS challenge. Concentrations of NEFA were also affected by time (P < 0.001) but were not affected by treatment (P = 0.42). For all treatments, NEFA concentrations increased in response to LPS challenge. There was a treatment (P < 0.001) and a time (P < 0.001) effect for BUN concentrations; BUN concentrations were greater (P < 0.001) in SC-0.5 steers (14.5 ± 0.2 mg/dL) than Cont (12.8 ± 0.2 mg/dL) and SC-5.0 (12.8 ± 0.2 mg/dL) steers. For all 3 groups, BUN concentrations increased (P < 0.001) in response to LPS challenge. These data demonstrate that *S. cerevisiae* supplementation may alter the metabolic response to LPS challenge. Repartitioning of nutrients may help explain the variations in the acute phase response observed in cattle supplemented with *S. cerevisiae*. Data from this study suggest that *S. cerevisiae* products may be useful as alternatives to antibiotic use in feed to enhance cattle health.

Key Words: cattle, live yeast, metabolism

0505 Circulating amino acids and biomarkers of metabolism and inflammation during the peripartal period in cows with different liver functionality index.

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Objectives were to profile AA and biomarkers of inflammation during the peripartal period. Eighteen multiparous cows were used from -21 through 56 d around parturition. Cows were monitored for health status, milk yield, and DM intake. Body weight and BCS were measured every week. Blood samples were obtained twice weekly or daily from -10 to 10 d. Cows were ranked retrospectively in tertiles according to the liver functionality index (LFI), which includes 3 liver biomarkers of hepatic function: albumin, cholesterol, and total bilirubin. The LFI measures the relevant changes in concentrations between 3 and 28 d, standardized with the optimal pattern of change for the 3 parameters obtained from healthy cows at the same stage of lactation. A high LFI (better liver function) is characterized by lower bilirubin and higher cholesterol and albumin, and the opposite is true for low LFI. Although DMI (16.8 kg/d) and BCS (2.45) did not differ (P > 0.05) due to LFI or the interaction, cows in the high (39.2 kg/d) and medium (34.8 kg/d) vs. low (30.8 kg/d) LFI had greater (P < 0.05) milk production. As expected, there was a significant interaction (P < 0.05) for the concentration of albumin, cholesterol, and bilirubin such that cows in low vs. high LFI had lower cholesterol and albumin but greater bilirubin namely after calving. There was no interaction or LFI effect (P > 0.05) for NEFA, hydroxybutyrate, and haptoglobin but concentrations increased (P < 0.05) after calving. The interaction (P = 0.06) effect observed for concentration of essential AA was due in part to greater values in high and medium LFI cows namely during d 7 through 14. A similar type of response resulted in a trend (P = 0.10) for an interaction in the concentration of branched-chain AA (BCAA). There was no LFI or interaction effect (P > 0.05) for concentration of Lys, which decreased (P < 0.05) markedly from -21 d to calving followed by a gradual increase to prepartal values by d 14. In contrast, concentration of Met decreased markedly between -21 d and calving but did not reach prepartal values until d 42. Results suggest some alterations in postpartal EAA and BCAA concentration such that cows with high vs. low LFI produce more milk and maintain greater concentrations of these AA.

Key Words: transition period, inflammation, immunometabolism

0506 Peripheral leukocytic responses to ultraviolet radiation in prepubertal rabbits fed a turmeric-supplemented diet. V. A. Togun*, *Ladoke Akintola University of Technology, Ogbomoso, Nigeria*.

This study investigated the antioxidant/antiinflammatory effect of turmeric (*Curcuma longa*) to enhance developmental resilience in stress induced, UV irradiated (*R*) rabbits indexed by peripheral leukocytic responses. This study was conducted for a total of 85 d in 3 phased periods: 40 d preirradiation, 5 d irradiation, and 40 d postirradiation in 72 acclimatized prepubertal, unsexed rabbits of average body weight range of 600 g, randomly assigned to 6 groups of 12 rabbits each and treated as follows: Group 1 served as control; they were fed unsupplemented diet and forage (*Tridax procumbens*) basal diet (BD) for the entire study periods without any treatment. Group 2 animals were fed BD supplemented with 2% crude pulverized turmeric (T) during Periods 1, 2, and 3, but were not irradiated. Group 3 animals were fed unsupplemented BD at Periods 1, 2, and 3 and irradiated. Group 4 rabbits were fed supplemented BD during Periods 1 and 2 only, and irradiated. Group 5 animals were fed supplemented BD at Periods 1, 2, and 3 and irradiated. Group 6 animals were fed BD in Periods 1 and 2, and irradiated at Period 2, following which supplemented BD was served in Period 3. Blood was collected on d 86 from 00.09 h. Feed and water were available ad libitum. The experimental design was completely randomized block design. Data were analysed by ANOVA with graphic post-hoc test of significance. Evident from Table 0506 with data for all the periods, UV irradiation significantly ($P < 0.05$) suppressed WBC and absolute lymphocytic count. Turmeric supplementation significantly ameliorated these UV effects ($P < 0.05$).

Key Words: turmeric, leukocytic-response, ultraviolet radiation, rabbits

Table 0506. Table of results[1]

S/N	GROUP *n*	WBC (10^3)	LYM, %	ABS
1	CONTROL	6.00 + 1.01†	69.12 + 6.0	3954 + 722.65
2	T + T + T	5.88 + 0.80^{ns}	77.72 + 4.60*,**	4651 + 830.72*,**
3	– + R +–	4.53 + 1.18*	71.93 + 3.34^{ns}	3183 + 662.50*
4	T + TR +–	6.85 + 1.09**,^{ns}	68.87 + 6.27^{ns}	4526 + 667.66*
5	T + TR + T	9.98 + 1.74*,**	69.64 + 5.32^{ns}	5524 + 1269.08*,**
6	– + R + T	5.78 + 0.91**,^{ns}	70.64 + 5.96^{ns}	4080 + 750.69^{ns}

n, number of animals = 12; †mean + SEM; T, turmeric; R, UV irradiation; LYM, lymphocyte; ABS, absolute lymphocyte count, WBC, white blood cell count.

$P < 0.05$ vs. control.

**$P < 0.05$ vs. UV irradiation; not significant (ns) vs. control.

0507 Regulation of adipogenesis and key adipogenic gene expression by retinoic acid in 3T3–L1 preadipocytes. S. Ji*[1], M. Du[2], and R. A. Hill[1], *[1]University of Idaho, Moscow, [2]Washington State University, Pullman.*

Adipogenesis plays an important role in metabolic homeostasis and nutrient pathways, and is crucial for regulating body fat reserves and body weight of mammals. The transcriptional control of adipogenesis requires a sequential series of gene expression events and activation of a number of key signaling pathways. Retinoic acid is considered as a potent inhibitor of adipogenesis for decades, and understanding the mechanism of retinoic acid regulation of adipogenesis is useful for helping to control body fat and to manipulate meat quality in the beef industry. To investigate the function of retinoic acid in regulation of adipogenesis, adipocyte differentiation and key adipogenic gene expression were studied in 3T3-L1 preadipocytes. Lipid accumulation was measured by Oil Red O staining, and expression of key adipogenic genes was quantified using quantitative real-time PCR. Adipogenic responses to different concentrations of retinoic acid were determined on d 2, 4, 6, 8, and 10 after stimulation of adipogenesis with the traditional hormonal cocktail (dexamethasone, isobutyl-1-methylxanthine and insulin) in the absence or presence of retinoic acid. In response to high concentrations (10^{-6}, 10^{-7} M) of retinoic acid, lipid accumulation and the expression of PPARγ, C/EBPα, FABP4, and SCD-1 were inhibited through d 8, but on d 10, lipid accumulation and the expression levels of these genes rebounded to levels comparable with the control. Interestingly, the greatest effects of retinoic acid treatments were on expression of FABP4. However, expression of SREBP-1c was not affected. The lowest retinoic acid concentration (10^{-10}M) did not affect adipocyte differentiation or expression of adipogenic genes. These results indicate that retinoic acid inhibited adipogenesis via suppressing adipogenic specific genes, especially FABP4. Our data indicate that a deeper understanding of the roles of retinoic acid in regulating adipogenesis will be informed by further study of adipogenic specific gene promoter activity.

Key Words: adipogenesis, transcription factors, retinoic acid

0508 Cholesterol metabolism, transport, and hepatic regulation during negative energy balance in early and mid-lactation in dairy cows.

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The negative energy balance (NEB) in early lactation has considerable effects on the cholesterol metabolism of dairy cows. The objective of this study was to investigate the response of plasma and milk lipids, enzyme activities, and hepatic mRNA expression of transcripts encoding for factors involved in cholesterol metabolism to a NEB in early and mid-lactation. Fifty multiparous Holstein dairy cows (25 control [C], 25 feed-restricted [R]) were studied from wk 1 postpartum (pp) until wk 17 pp, with an almost 50% feed-restriction from wk 14 to 17 pp. Blood samples, liver biopsies, and milk samples were taken in wk 1, 14, and 17 pp. Blood and milk lipid concentrations [triglycerides (TG), cholesterol, lipoproteins] and enzyme activities [phospholipid transfer protein (PLTP), lecithin-cholesterol acyltransferase (LCAT)] related to cholesterol homeostasis were analyzed. Hepatic gene expression of 3-hydroxy-3-methylglutaryl-coenzyme A (HMGC) synthase 1 (HMGCS1) and HMGC reductase (HMGCR), sterol regulatory element-binding factor (SREBF)-2, microsomal triglyceride transfer protein (MTTP), ATP-binding cassette transporter (ABC) A1, and ABCG1 were measured. While values were lower for cows in wk 1 pp, plasma concentrations of TG, cholesterol, VLDL-cholesterol (VLDL-C) and LDL-C increased in R cows from wk 14 to 17 pp compared with C cows. Whereas in wk 1 pp, PLTP activity was increased and LCAT activity was lower, activities of PLTP and LCAT did not differ between wk 14 and 17 pp in C and R cows. Cholesterol concentration in milk did not change from wk 14 to 17 pp, whereas cholesterol mass in milk was decreased in wk 17 pp for R cows and tended to be lower in R cows compared with C cows. On the contrary, cholesterol concentration and mass in milk were higher in wk 1 pp. SREBF-2, HMGCS1, HMGCR, MTTP, ABCA1, and-G1 showed no changes during the experiment. In contrast, during the NEB at the onset of lactation the expression of HMGCS1, HMGCR, SREBF-2, and ABCA1 were increased. In conclusion, increased plasma concentrations of TG, cholesterol, VLDL-C, and LDL-C during the feed restriction period suggest that in later stages of lactation the liver is able to enhance the export of generated TG as VLDL. The diminished milk cholesterol mass might represent a measure to save cholesterol for the constitution of VLDL.

Key Words: cholesterol metabolism, lipoprotein, dairy cow