695 Tumor necrosis factor alpha increases triglyceride content and alters transcript abundance of metabolic genes in the liver of lactating dairy cattle. B. J. Bradford*, L. K. Mamedova, J. E. Minton, J. S. Drouillard, and B. J. Johnson, *Kansas State University*, *Manhattan*.

Recent data have shown that bovine fatty liver is associated with inflammation, but a causative role of inflammatory mediators has not been demonstrated. To determine whether inflammation can induce fatty liver, recombinant bovine tumor necrosis factor alpha (TNF) was administered to late-lactation Holstein cows in a randomized complete block design. Cows (n = 5 per treatment) were blocked by feed intake and milk production and randomly assigned within block to control (saline), TNF at 2 μg/kg per d, or pair-fed control (saline, intake matched) treatments. Treatments were delivered once daily by subcutaneous injection for 7 d. Plasma samples were collected daily for analysis of glucose and non-esterified fatty acids (NEFA) and a liver biopsy was collected on d 7 for triglyceride (TG) and quantitative real-time PCR analyses. Data were analyzed with mixed models using treatment contrasts to assess effects of TNF administration and decreased feed intake. By d 7, feed intake and milk production decreased by 15% and 12%, respectively, for both TNF and pair-fed cows compared to controls. TNF administration significantly increased hepatic TNF mRNA and protein abundance and increased liver TG content by 103% ($P < 0.05$) without affecting plasma NEFA concentration. TNF tended to decrease hepatic carnitine palmitoyltransferase 1 and increase fatty acid translocase (CD36) and 1-acyl-glycerol-3-phosphate acyltransferase transcript abundance (all $P < 0.10$), effects which are consistent with increased NEFA uptake and storage as TG. TNF also decreased transcript abundance for glucose-6-phosphatase ($P = 0.02$) and phosphoenolpyruvate carboxykinase 1 ($P = 0.09$), genes important for gluconeogenesis. Plasma glucose concentration was not affected by treatment. These findings indicate that TNF promotes liver TG accumulation and suggest that inflammatory pathways may also be responsible for decreased glucose production in cows with fatty liver.

Key Words: fatty liver, tumor necrosis factor, inflammation

696 Effects of feeding colostrum on somatotoropic axis, metabolic traits and vital signs of Holstein bull calves. D. Qadimi, A. Zare Shahne, A. Nikkhah, M. Moradi, and R. Masoumi*, *University of Tehran*, *Iran*.

Bovine colostrum contains various essential nutrients, antibodies, hormones, growth factors and antimicrobial peptides (e.g. Lactoferrin, and Lactoperoxidase) that are important for nutrient supply, host defense, growth and for general neonatal adaptation. In this study, effects of colostrum fed for different durations on somatotropic axis, selected metabolic traits, plasma levels of growth hormone and vital sings in the first week of life in calves were examined. Holstein bull calves (n = 18) with mean body weight of 44.6 kg were randomly assigned into three treatment groups and fed colostrum twice daily for 3d (group GrC6) or colostrum only as their first meal (group GrC1) followed by milk replacer up to day 7, or they received only milk replacer but no colostrum (group GrM). Blood samples were taken on days 1,2 and 7 of experiment five minutes before and 0.5, 2, 4 and 7 h after feeding colostrum. Plasma glucose, urea, creatinine and GH were measured. Data were analyzed by Proc GLM of SAS. Postprandial plasma glucose concentration on day 2 increased significantly ($p<0.05$) in groups GrC6 and GrC1 in compare with group GrM and remained elevated up to day 7. Plasma urea concentration on day 1 decreased significantly ($p<0.01$) in groups GrC6 and GrC1 than in group GrM and remained lowered up to day 7. There was not any significant difference in plasma creatinine ($p<0.05$) concentration between treatment groups. Plasma GH concentration was not changed by feeding different levels of colostrum ($p<0.05$) but there was a increasing trend in plasma GH in GrC6. Calves fed colostrums had significantly higher($p<0.01$) rectal temperatures, heart rates and respiratory frequencies than calves provided by milk replacer. The somatotrophic axis is basically functioning in neonatal calves and may be influenced by nutrition. Furthermore, significantly higher circulating glucose and lower Urea levels in calves fed colostum compared with those fed milk replacer, stimulated anabolic processes.

Key Words: colostrum, metabolism, calves

697 Continuously infused obestatin increased pancreatic β-cell function in response to an intravenous glucose tolerance test. J. R. Roche*[1], A. J. Sheahan[1], L. M. Chagas[1], J. K. Kay[1], and R. C. Boston[2], [1]*DairyNZ*, *Hamilton, NZ*, [2]*University of Pennsylvania*, *Kennett Square*.

At 20 DIM, 51 cows were randomly allocated to one of three treatment groups; a control (CONT) or a group continuously infused with either 0.74 μmol/d of ghrelin (GHRE) or obestatin (OBE) subcutaneously for 8 wk. During wk 5, cows were subjected to an intravenous glucose challenge (300 mg D-glucose/kg BW). Plasma glucose, insulin, NEFA, growth hormone (GH), and ghrelin concentrations were measured prior to glucose infusion and at regular intervals following infusion. Bergman's Minimal Model (MINMOD) and Boston's NEFA model were fitted to each subject's glucose challenge response, and model outputs, area under the curve, peak or nadir concentration, and profile slopes from each hormone/metabolite compared statistically. All treatments exhibited the previously published characteristic post-infusion profiles in plasma glucose, insulin, ghrelin, NEFA, and GH. However, OBE cows produced 50% more ($P< 0.01$) insulin in response to the glucose infusion than either the CONT or GHRE cows (peak insulin at 10 min post-infusion was 22 ± 3.0, 20 ± 1.8, and 35 ± 3.4 μU/mL in CONT, GHRE, and OBE cows, respectively; mean ± SEM). They also had a correspondingly lower nadir plasma NEFA (0.51 ± 0.059, 0.60 ± 0.032, and 0.35 ± 0.033 mmol/L in CONT, GHRE, and OBE cows, respectively), and produced more GH than either GHRE or CONT cows in response to the insulin-mediated decline in blood glucose and NEFA (peak GH 40 to 50 min post-infusion was 7.3 ± 1.10, 10.0 ± 1.53, and 13.2 ± 2.22 ng/mL in CONT, GHRE, and OBE cows, respectively). Model outputs confirm an obestatin effect on insulin and NEFA. The volume of insulin available for glucose disposal (AIRg: a proxy for pancreatic β-cell function) in MINMOD was 45 and 89% greater in OBE cows compared with CONT and GHRE cows, respectively ($P< 0.01$). Boston′s NEFA model highlighted that OBE cows had lower baseline NEFA, and this resulted in a lower nadir NEFA; data imply an effect of obestatin on pancreatic β-cell function, and a corresponding effect on lipid metabolism.

Key Words: glucose tolerance test, ghrelin, obestatin

698 Residual feed intake and heat production of Holstein cows throughout lactation. A. Brosh*[1], A. Asher[1], J. Miron[2], A. Shabtay[1], G. Adin[3], U. Moalem[2], Y. Aharoni[1], and A. Arieli[4], [1]*Agricultural Research Organization*, *Ramat Yishay, Israel*, [2]*Agricultural Research Organiza-*

tion, *Bet-Dagan, Israel*, [3]*Extension Service, Ministry of Agriculture, Bet-Dagan, Israel*, [4]*Hebrew University of Jerusalem, Faculty of Agricultural*, *Rehovot, Israel*.

Serial measurements of cows' individual intake, milk energy, and heat production (HP) using the heart rate Oxygen Pulse method, were obtained from weeks 1 to 11 of lactation (WEL) for 63 Holstein cows, and continue up to WEL 35 for 53 cows. Cows' residual ME feed intake (RFIme, the actual ME intake (MEI) minus the expected MEI, MEIex) were calculated. Similarly cows' residual HP (RHP, the measured HP minus the expected HP, HPex) was calculated. All energy transformation calculations were based on NRC (2001) equations. Dietary NEl concentrations, based on tabular values and not adjusted for level of intake, were 26% higher than the actual dietary NEl based on in vivo measurements of digestibility. Adjusting the tabular dietary NEl concentration for level of intake reduced the magnitude of this overestimation (above the in vivo concentration) by 14.6%, but after this adjustment the calculated dietary NEl concentration was still 8% higher than the NEl concentration based on in vivo digestibility. Milk production in week 1 was 26.8±1 (SE) L/d, 25±0.6 Mcal/d, reached a peak of 55.1±0.9 (L/d), 35.60.5 Mcal/d in WEL 6 and decreased to 36.4±0.8 (L/d), 26.7±0.5 Mcal/d in WEL 35. Cows` BW (kg) and BCS (scale of 1-5) in the first WEL were respectively 658 and 2.98, decreased to the lowest values of 612 and 2.64 in WEL 6 and increased up to 625 and 2.71 in WEL 35. The average MEI (Mcal/d; based on in vivo digestibility) were 41±1 in WEL 1, reached a peak of 64±1 in WEL 11, and decreased to 56±6 in WEL 35. The in vivo values of NEl and ME were used to calculate RFIme and RHP (Mcal/day) for all individual cows. Unexpectedly, a trend of changes was calculated in the RFIme and in the RHP of the weeks' average (N=35), a quadratic regression of RFIme = -0.0061WEL^2^ +0.3272 WEL-1.5155, R^2^= 0.312, (P<0.001) and of RHP = -0.0109WEL^2^+0.3849WEL-5.3623, R^2^=0.285, P<0.001. RHP was positively correlated to the cows` HP (R^2^=0.67, P<0.001). It can be concluded that the tested cows were less efficient than expected according to NRC (2001), and that coefficients of transforming MEI to energy in milk may not be constant during lactation.

Key Words: cow, lactation, efficiency

699 IGF-1 concentrations following sustained release growth hormone treatment in ewes. T. A. Wilmoth*, J. M. Koch, C. O. Lemley, and M. E. Wilson, *West Virginia University*, *Morgantown*.

Low birth weight lambs have higher mortality rates in the first few days following birth than normal birth weight lambs. Treatment of ewes with growth hormone (GH) around the time of conception increases birth weight of lambs, therefore increasing their chance of survival. Treatment of ewes with GH at the time of conception does not cause a difference in the number of cells in the trophectoderm or inner cell mass of the embryo compared to embryos from control ewes. However, treatment of ewes with GH caused an increase in placental efficiency compared to control ewes, which may indicate prolonged alterations in uterine environment. Growth hormone causes an increase in insulin like growth factor-1 (IGF-1), which increases cell growth and somatostatin production, but causes a decrease in growth hormone releasing hormone and GH. Concentrations of IGF-1 in the serum are correlated to the concentration of GH at peak amplitude. The objective of this experiment was to determine the effective duration of sustained release GH using IGF-1 as a proxy for GH. Ewes were synchronized with 2 prostaglandin injections 8 days apart and penned with a fertile ram. At the time of the second injection, rbST (Posilac) was administered and a blood sample collected (week 0). Jugular blood samples were collected weekly and plasma was used for determining IGF-1. For weeks 1, 2, 3 and 4, treated ewes had an increased IGF-1 concentration compared to control ewes (3, 5, 4 and 2.5-fold, respectively). By week 8, control and treated ewes had similar concentrations of IGF-1. Periconceptional treatment with sustained release GH causes IGF-1 to remain elevated for the first half of gestation, potentially altering the uterine environment during a crucial developmental period. The timing of the elevation in IGF-1 following periconceptional GH treatment leads us to suggest that its effect on birth weight is mediated by a change in placental function as IGF-1 concentrations are similar in control and treated ewes during the second half of gestation in which the fetus will undergo the most growth.

Key Words: growth hormone, IGF-1, fetal programming

700 Transcriptional adaptations in mesenteric and subcutaneous adipose tissue from non-lactating cows in response to plane of dietary energy. M. Mukesh, J. K. Drackley, P. Ji*, M. Bionaz, S. L. Rodriguez-Zas, R. E. Everts, H. A. Lewin, and J. J. Loor, *University of Illinois*, *Urbana*.

The transcriptional machinery of cow adipose tissue depots and the role of dietary energy on gene networks remain poorly characterized. Effects of moderate excess (M) or low dietary energy (L) on mesenteric (MES) and subcutaneous (SubQ) adipose tissue transcript profiles were assessed in 10 non-pregnant dry cows. Cows were assigned to either an M (NE_L = 1.61 Mcal/kg) or L (NE_L = 1.37 Mcal/kg) diet for 8 wk. The M diet contained 74.5% (DM basis) forage without straw, while the L diet contained 84.6% forage including 41.9% wheat straw and met cow NE_L requirements at ad libitum DMI. At slaughter, SubQ and MES were sampled and used for microarray analysis using a 13,000 annotated bovine oligonucleotide microarray. Cows fed M had greater MES weight. Statistical analysis (FDR $\leq$ 0.2; unadjusted $P < 0.007$) revealed 427 and 312 differentially expressed genes (DEG) due to tissue site and diet. Pathway analysis showed that the most-enriched functions among DEG between tissues were cellular growth (greater in MES), synthesis and accumulation of lipid (greater in MES), and transcription regulation (e.g. NFκB binding site activation, greater in MES). Network analysis among DEG higher in MES suggested a central role of CCAAT/enhancer binding protein beta (CEBPB). Among DEG due to energy intake were several involved in cell viability (greater in L), development of leukocytes (greater in M), cytostasis of connective tissue (greater in M), and activation and binding of cells (both immune and non-immune; greater in M). Pathways of synthesis and sensitivity to growth factors (FGF, HGF) as well as sphingolipid synthesis had more DEG with M than L. Most DEG due to energy intake level were involved in response to stimulus (e.g., immune response; greater in M) and components of protein complex (e.g., translation; greater in L). Glucocorticoid receptor (GRLF1) and E2F transcription factor 7 (E2F7) were the transcription factors most affected by dietary energy. Results provide evidence of adipose site-specific and energy-responsive transcriptomic signatures.

Key Words: genomics, overnutrition, lipogenesis

701 Effect of plane of nutrition and feed deprivation on insulin responses in dairy cattle during late gestation. K. M. Schoenberg*, R. M. Ehrhardt, and T. R. Overton, *Cornell University*, *Ithaca, NY*.

Nonlactating Holstein cows (n=12) in late pregnancy were used to determine effects of plane of nutrition followed by feed deprivation on

responses to insulin. Beginning 48±4.5 d prior to calving, cows were fed either a high (H) or low (L) diet to meet 139 and 84% of calculated energy requirements, respectively. Cows were subjected to an intravenous glucose tolerance test (GTTa; 0.25 g dextrose/kg BW) on d 14 of treatment and a hyperinsulinemic-euglycemic clamp (HECa; 1μg/kg of BW/h) on d 15. Following a 24 h fast, cows were subjected to GTTb on d 17 and HECb on d 18. During the feeding period, NEFA were higher for cows fed L vs. H (73.1, 163.6 μEq/L; P<0.001). For all cows, glucose was lower after 48 vs. 24 h of fasting (54.6, 67.6 mg/dL; P<0.001) but NEFA were higher (792.6, 219.3 μEq/L; P<0.02). Glucose area under the curve (AUC) across both GTT were higher for cows fed L than cows fed H (5437, 4532 mg/dL x 180 min; P <0.04) and was higher during GTTb (6778, 3192; P<0.001) than GTTa, suggesting slower clearance of glucose during negative energy balance either pre- or post-fast. This corresponded with a higher dextrose infusion rate during HECa than HECb (203.3, 90.1 ml/hr; P = 0.001). Plasma NEFA decreased at a faster rate during GTTb than GTTa (-22.5, -4.8 μEq/L*min; P<0.001). NEFA suppression was highest for cows on the L diet during GTTb, and lowest for cows fed H during GTTa (68.6, 50.3 μEq/L; P = 0.07). Cows fed L had greater NEFA AUC than those fed H (-48726, -26068 μEq/L x 180 min; P< 0.02), as did cows during GTTb vs. GTTa (-64016, 10778 μEq/L x 180 min; P<0.001). During HECa, NEFA were 21% below basal for cows fed the H diet, 69% below basal for cows fed the L diet and NEFA were 88 and 66% below basal respectively during HECb (treatment x HEC; P<0.001). These results suggest that cows fed below energy requirements or feed-deprived have slower clearance of glucose and larger NEFA responses to glucose challenge; overall, effects of feed deprivation were larger than plane of nutrition.

Key Words: insulin clamp, glucose tolerance test

702 The acute phase response: Differentiating corticotrophin-releasing hormone (CRH)- versus lipopolysaccharide (LPS)-induced proinflammatory cytokine and acute phase protein profiles in beef calves. J. A. Carroll*[1], L. E. Hulbert[1], N. C. Burdick[1,2], L. C. Caldwell[2,3], M. A. Ballou[4], J. D. Arthington[5], R. C. Vann[6], A. N. Loyd[2,3], T. H. Welsh, Jr.[2], and R. D. Randel[3], [1]*Livestock Issues Research Unit, USDA-ARS, Lubbock, TX*, [2]*Texas AgriLife Research, Texas A&M System, College Station*, [3]*Texas AgriLife Research Center, Texas A&M System, Overton*, [4]*Department of Animal and Food Sciences, Texas Tech University, Lubbock*, [5]*University of Florida - IFAS, Range Cattle Research and Education Center, Ona*, [6]*MAFES, Mississippi State University, Raymond*.

Development of methods to effectively attenuate potentially detrimental effects of various stressors encountered by livestock depends on understanding unique stressor-specific responses. The objective of this study was to profile indicators of the acute phase immune response to compare and contrast potential differences between CRH- and LPS-induced stress responses. Purebred Brahman bull calves (n = 11; 226.9±12.6 kg) were transported 770 km from Overton, TX to Lubbock, TX and fitted with indwelling jugular catheters after 24 h of rest. Twenty-four h afterwards, blood samples were collected at 30-min intervals from -2 to 8 h, and again at 12 and 24 h, relative to an i.v. infusion of either LPS (0.25 μg/kg BW) or CRH (0.5 μg/kg BW) at 0 h. Serum was stored at -80°C until analyzed for tumor necrosis factor-alpha (TNF-α), interleukin 6 (IL-6), interferon gamma (IFN-γ) and haptogolobin (Hp). Compared to pre-challenge concentrations, CRH induced a single peak in serum TNF-α starting at 2.5 h (P≤0.01) and lasting until 4 h (P≤0.07) whereas LPS induced a biphasic response beginning at .5 h (P≤0.04) with peaks at 1.5 and 3.5 h, and lasting until 7.5 h (P≤0.01). For IL-6, CRH induced a single peak beginning at 3 h (P≤0.01) and only lasting for .5 h. In contrast, LPS induced a biphasic IL-6 response beginning at 1.5 h (P≤0.01), peaking at 2.5 h and 6 h, and lasting until 12 h (P≤0.03). For IFN-γ, CRH induced a single peak at 3 h (P≤0.01), beginning at 2.5 h (P≤0.07) and lasting until 3.5 h (P≤0.01). LPS induced a multiphasic IFN-γ response beginning at .5 h (P≤0.01) and lasting until 24 h (P≤0.01) with peaks at 2.5, 3.5 and 6 h. For Hp, CRH-induced a single spike at 4 h (P≤0.02) that had ended by 6 h (P≥0.14) whereas LPS induced Hp concentrations continued to escalate even at the 24 h time period (P≤0.01). These data demonstrate that the stress response in beef calves either simulated by CRH or induced by endotoxin is comprised of specific immunological profiles that may be as unique as the stressor itself.

Key Words: cattle, immunity, stress

703 Fibroblast growth factor 21 (FGF21) expression is increased in hepatic tissue of feed-restricted cows and during the transition from pregnancy to lactation. K. J. Harvatine*[1] and Y. R. Boisclair[2], [1]*Penn State University, University Park*, [2]*Cornell University, Ithaca, NY*.

Fibroblast growth factor 21 (FGF21) is a recently discovered hormone that is induced in liver during fasting. FGF21 promotes adaptations to the fasted state, including coordination of hepatic oxidation of free fatty acids with their mobilization from adipose tissue. Interestingly, exogenous administration of FGF21 reduced hepatic triglyceride concentration and improved insulin sensitivity in obese mice. Our objective was to determine if FGF21 is regulated similarly in the cow. To investigate the role of FGF21 in regulation of energy homeostatis in the dairy cow we measured hepatic FGF21 expression in liver during positive and negative energy balance. First, liver biopsies were collected from five non-pregnant late-lactation cows when fed 120% of energy requirement or restricted to 30% of maintenance requirement. Statistical analysis included the random effect of cow and the fixed effect of treatment. Feed restriction resulted in a 37 fold increase in hepatic FGF21 expression compared to control (P<0.001). Secondly, liver biopsies were collected from ten cows during the transition from pregnancy to lactation. Statistical analysis included the random effect of cow and the fixed effect of stage of lactation. Hepatic FGF21 expression was increased over 10 fold 8 d after parturition compare to 28 d prior to calving (P = 0.001). Feed restriction and the transition to lactation resulted in a large negative energy balance, increased adipose tissue mobilization, and increased plasma NEFA concentration. Hepatic FGF21 synthesis may play a determinant role in regulating the rate of utilization of lipid reserves in energy-deficient dairy cows.

Key Words: FGF21, transition cow

704 Expression of thyroid hormone responsive spot 14 and a homologous protein (MIG12) are dynamically regulated in adipose tissue of dairy cows during modification of energy balance. K. J. Harvatine*[1], Y. R. Boisclair[2], and D. E. Bauman[2], [1]*Penn State University, University Park*, [2]*Cornell University, Ithaca, NY*.

Thyroid hormone responsive spot 14 (S14) and MID1 interacting protein 1 (MIG12) share sequence homology and may encode proteins with redundant function, although a specific biochemical function of their gene products is not clear. Regulation of S14 is well described in other species where it is predominantly expressed in lipogenic tissue and dynamically altered by transcriptional regulation under dietary conditions affecting energy balance. Expression and regulation of MIG12 has not been well described. Our objective was to characterize

the metabolic responsiveness of S14 and MIG12 in the bovine using real-time RT-PCR. Our initial study compared the expression of S14 and MIG12 in a panel of 9 tissues collected from lactating dairy cows. S14 was predominantly expressed in adipose tissue and moderately expressed in liver, mammary tissue, and skeletal muscle. MIG12 was predominantly expressed in skeletal muscle and moderately expressed in adipose tissue and liver. Next, we investigated the regulation of S14 and MIG12 in the adipose tissue of dairy cows experiencing periods of positive and negative energy balance. Firstly, adipose tissue biopsies were collected from five non-pregnant late-lactation cows when fed 120% of energy requirement or restricted to 30% of maintenance requirement. Feed restriction resulted in over a 90% and 78% decrease in the expression of S14 and MIG12, respectively ($P = 0.02$ and $P < 0.01$). Secondly, adipose tissue biopsies were collected from ten cows during the transition from pregnancy to lactation. Expression of both S14 and MIG12 was decreased over 95% by 8 d postpartum as compared to 28 d prepartum (both $P < 0.001$). Overall, results indicate both S14 and MIG12 are responsive to energy status and that the induction of a negative energy balance, whether by feed restriction or the transition from pregnancy to lactation, results in a down regulation in the expression of S14 and MIG12 in adipose tissue.

Key Words: S14, MIG12, ;ipogenesis

705 TNFα and factors related to insulin signaling in adipose tissue of dry- and early lactating dairy cows. H. Sadri[1,2], A. van Dorland[1], G. R. Ghorbani[2], H. R. Rahmani[2], and R. M. Bruckmaier*[1], [1]*University of Bern, Vetsuisse Faculty, Veterinary Physiology*, *Bern, Switzerland*, [2]*Isfahan University of Technology, Department of Animal Science*, *Isfahan, Iran*.

This study was conducted to clarify the mechanisms of insulin resistance in adipose tissue during late gestation and early lactation in dairy cows. The mRNA expression of TNFα, insulin receptor (INSR), insulin receptor substrates (IRS1 and IRS2), regulatory (p85) and catalytic subunit of PI-3 kinase (p110), insulin independent (GLUT1) and responsive (GLUT4) glucose transporters in adipose tissue was measured by real-time RT-PCR, and their relationship with plasma NEFA concentrations was evaluated. Biopsies from subcutaneous fat were taken at the tail head from 30 dairy cows in wk 8 antepartum (a.p.), on d 1 postpartum (p.p) and in wk 5 p.p.. Blood samples were collected every two weeks. The mRNA abundance of TNFα was higher ($P < 0.05$) during p.p. compared to that in a.p. The mRNA encoding for GLUT1 and GLUT4 on d 1 p.p. was lower ($P < 0.05$) compared to the other time-points. There was a trend ($P = 0.09$) for increased mRNA abundance of INSR in p.p. relative to a.p., and decreased mRNA abundance of IRS1 on d 1 compared to wk 5 p.p. The mRNA encoding for IRS2, p85 did not change over time. A tendency ($P<0.15$) was observed for a negative correlation between plasma NEFA concentration and GLUT4 mRNA abundance in wk 8 a.p., and on d 1 p.p. There was a trend ($r = 0.30$, $P = 0.11$) for a positive correlation between TNFα mRNA abundance and plasma NEFA concentration in wk 5 p.p.. Results show a local role for adipocyte-derived TNFα, and suggest its contribution in adaptation of adipose tissue towards catabolism. Down regulation of GLUT4 expression may be involved in insulin resistance shortly after calving, and may be mediated in part by TNFα and elevated NEFA concentration. The slight decrease in mRNA abundance of IRS1 on d 1 compared to wk 5 p.p. may show an involvement of IRS1 in insulin resistance at the onset of lactation. Changes in gene expression of INSR, IRS2 and p85 show no involvement in promoting insulin resistance in adipose tissue of dairy cows.

Key Words: TNF, adipose tissue, cow

706 Differential effects of propionate on mRNA abundance of adiponectin receptors and G protein-coupled receptor GPR41 in bovine subcutaneous and perirenal adipose tissue explants *in vitro*. A. Hosseini*, H. Sauerwein, and M. Mielenz, *University of Bonn*, *Bonn, Germany*.

Ruminants entirely depend on the ruminal production of short-chain fatty acids (SCFA) as the main energy source. The SCFA propionate (C3) is an important stimulus to insulin secretion in ruminants. Insulin (100 nM) increases leptin mRNA in bovine adipose tissue (AT) explants (1). C3 activates members of the family of fatty acid binding receptors, e.g. GPR41, which in turn stimulates leptin mRNA in mice (2). In goats, we have previously demonstrated that C3 differentially increases the mRNA abundance of putative GPR41 in subcutaneous (SC) and perirenal (PR) AT *in vivo*. The adiponectin system improves insulin sensitivity in monogastrics but less is known about the situation in ruminants. Therefore, we established an AT explant model for both SC and PR for characterizing the response of the adiponectin receptors (AdipoR1 and AdipoR2) mRNA to C3 *in vitro*. SC and PR AT were obtained from 7 slaughtered Holstein Friesian cows. The tissue was incubated 4 h in basal medium (DMEM/Ham's F-12 with L-Glutamine) or in medium supplemented with either 100 nM insulin or with 0.5, 1, 2, or 3 mM C3. The mRNA of AdipoR1, AdipoR2 and GPR41 was quantified by real-time-PCR. The data were analyzed using the Paired-samples t-test ($P\leq0.05$; trend: $P\leq0.11$). C3 significantly, or as a trend, increased the mRNA expression of AdipoR1 and AdipoR2 dose dependent only in SC AT explants. No influence of C3 on the mRNA of GPR41 was observed. Insulin did not influence the mRNA expression of AdipoR1 and AdipoR2, but a trend was observed for GPR41 in SC AT. Our results indicate that short-term C3 treatment *in vitro* affects AdipoR1 and AdipoR2 mRNA only in SC AT which might increase glucose uptake and lipid metabolism or accumulation under increased energy load. Likewise *in vivo* studies, an influence of C3 treatment on GPR41 mRNA in SC AT might not be ruled out. (1) Houseknecht et al. 2000. J Endocrinol 164. 51 (2) Xiong et al. 2004. Proc Natl Acad Sci U S A. 101. 1045

Key Words: adipose tissue explants, adiponectin receptors, GPR41

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707 Effect of grain type and processing method on rumen fermentation and milk rumenic acid production. R. Mohammed*[1], J. J. Kennelly[1], J. K. G. Kramer[2], K. A. Beauchemin[3], C. S. Stanton[4], and J. J. Murphy[4], [1]*University of Alberta*, *Edmonton, AB, Canada*, [2]*Agriculture and Agri-Food Canada*, *Guelph, ON, Canada*, [3]*Agriculture and Agri-Food Canada*, *Lethbridge, AB, Canada*, [4]*Teagasc*, *Moorepark, Co. Cork, Ireland*.

Eight Holstein cows in mid-lactation were assigned to 4 diets - rolled barley, ground barley, rolled corn and ground corn containing similar starch contents in two 4 × 4 Latin squares with 21-day periods to investigate the effect of grain type and processing method on milk rumenic acid (RA) production. Diets were supplemented with sunflower seed and had forage:concentrate ratios of 42:58. Rumen and milk samples were collected in the third week of each period. Data were analysed by the