

Growth and Development

184 Fetal programming of offspring growth due to maternal high protein diet is genotype dependent in mice. M. Langhammer, M. Derno, N. Dietrich, U. Renne, G. Nürnberg, U. Hennig, and C. C. Metzges*, *Research Institute for the Biology of Farm Animals (FBN), Dummerstorf, Germany.*

Poor fetal growth is incompatible with adult health. We have shown in a rat model that maternal dietary high protein (HP) intake throughout pregnancy results in low birth weight and increased body fatness in the offspring. This paper addresses whether effects of a maternal HP diet throughout pregnancy and/or lactation are genotype dependent. Female mice of 3 strains (selected for long distance running, LDR; high body weight, HBW; and unselected control, CON; n=25 each) were fed isoenergetic HP (40% protein) or control (C) diets (20%) from mating to end of lactation (21d). Litters were standardized to 10 pups at birth. Pups were cross-fostered and offspring was tested in 3 combinations of pre- and postnatal dietary exposure: HP-C, C-HP, and C-C (n=10 litters each). In HBW, CON, and LDR maternal growth from mating to term was reduced by 64, 45 and 11% in HP fed dams as compared to C dams (HBW, CON; $P < 0.05$). CON and LDR offspring showed reduced birth weight when their mothers received HP diet throughout pregnancy (CON 1.40 vs. 1.46 g; LDR 1.58 vs. 1.62 g; $P < 0.05$), whereas in HBW no difference between HP and C diet was found (2.17 vs. 2.12 g). Litter size at birth was lower in CON dams fed HP diet (10.96 vs. 12.03 pups in C; $P < 0.05$). Until weaning, losses were highest among C-HP pups (CON 23% and HBW 16% of all litters). In all strains body mass gain per litter between birth and age 21d were lowest in C-HP (CON 43.9; LDR 51.8; HBW 88.1 g), as compared to HP-C (95.1; 71.7; 199.9 g) and C-C (95.7; 78.7; 197.3g) offspring (lactation diets HP vs. C; $P < 0.05$). Lactating dams fed HP diet are less able to support normal growth development in pups until weaning. The LDR strain is less susceptible to early postnatal exposure to maternal HP diet. In the HBW strain fetal growth in offspring of HP dams is maintained presumably due to larger body reserves of their mothers.

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Key Words: Fetal programming, High protein intake, Gestation

185 Development and enteral long-chain n-3 fatty acids differentially alters muscle intracellular pools of free amino acids in the neonate piglet. M. C. Thivierge*¹, K. Bergeron¹, P. Julien², and T. A. Davis³, ¹*Institute of Nutraceuticals and Functional Food (INAF), Université Laval, QC, Canada,* ²*Laval University Medical Ctr. (CHUL), QC, Canada,* ³*USDA/ARS Children's Nutr. Res. Ctr., Baylor College of Medicine, Houston, TX.*

Recent studies suggest that feeding long-chain n-3 fatty acids (LCn-3FA) in the diet may blunt the developmental reduction in insulin sensitivity and anabolism in the neonate piglet. To examine the effect of LCn-3FA on protein anabolism, 2-day-old piglets (n=28) were weaned and assigned to one of two semi-purified milk replacers and raised until 10- or 28-d-old. Milk replacers differed in their fatty acid composition (Control: 0.82% and Enriched: 10.99% LCn-3FA). At either 10 or 28 d of age, phenylalanine kinetics were conducted by simultaneously infusing L-[1-¹³C]phenylalanine (22 $\mu\text{mol/kg}\cdot\text{h}$) along with total parenteral nutrition (7.9 ml/kg $\cdot\text{h}$). After a 4-h infusion period, piglets were killed and longissimus dorsi muscle was sampled. Fractional synthetic rate of muscle proteins (FSR) was not altered by feeding milk replacer enriched in LCn-3FA. However, FSR decreased

between 10 and 28 d of age (from 13 to 8%/d; $P < 0.01$). The age-regulated fall in FSR coincided with reductions in the concentrations of many non-essential amino acids (NEAA) in the cellular milieu (Asp $P = 0.04$; Ala $P = 0.02$; Ser $P < 0.01$; Pro $P = 0.03$). 3-Methyl-histidine, a marker of myofibrillar protein degradation, also decreased ($P < 0.01$) with development. Essential amino acids (EAA) remained mostly unaltered, except Arg ($P < 0.01$) and Phe ($P = 0.03$) concentrations that increased with age. Feeding milk replacer enriched in LCn-3FA reduced the cellular EAA to NEAA ratio ($P = 0.03$). The results suggest that feeding a diet enriched in LCn-3FA blunts the developmental increase in cellular EAA to NEAA ratio but does not block the fall in muscle protein synthesis.

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Key Words: Muscle amino acid free pools, Fractional synthetic rate, Piglets

186 The adipogenic enzymatic activity of bovine intramuscular, perirenal, and subcutaneous cultured preadipocytes differs, and increases in all depots following exposure to dexamethasone. G. Ortiz-Colón*, A. C. Grant, M. E. Doumit, and D. D. Buskirk, *Michigan State University, East Lansing.*

The objective of this study was to determine if there were differences in adipogenic capacity among bovine preadipocytes derived from intramuscular (IM), subcutaneous (SC), and perirenal (PR) adipose tissue, and to evaluate the effects of dexamethasone (DEX) on the adipogenesis of these preadipocyte populations. Preadipocytes isolated from three steers were grown to confluence in culture and then exposed to 0 (control), 25, or 2500 nM DEX for 48 h. After an additional 10 d in differentiation media, the propensity to differentiate, determined by glycerol-3-phosphate dehydrogenase (GPDH) specific activity and oil red O staining was PR > SC > IM ($P < 0.05$). Compared with control, 2500 nM DEX increased GPDH activity in preadipocytes from all depots ($P < 0.05$). There was no interaction between adipose tissue depot and DEX concentration for GPDH activity ($P = 0.99$). However, the percentage of PR preadipocytes with lipid droplets greater than 10 μm -diameter increased in response to DEX in a dose-dependent manner, but only increased above control in SC preadipocytes exposed to 2500 nM DEX ($P = 0.002$). Furthermore, DEX did not statistically increase the percentage of IM preadipocytes with large ($\geq 10 \mu\text{m}$ -diameter) lipid droplets ($P > 0.27$). These observations reflect an adipose tissue depot by DEX concentration interaction ($P = 0.03$). It appears that for IM preadipocytes, DEX increased the lipogenic activity of the cells more than it increased the number of lipid-filled preadipocytes. Relative differences in adipogenic capacity among preadipocytes isolated from IM, SC, and PR bovine adipose tissue were evident. Dexamethasone enhanced adipogenic enzyme activity in all three depots, but did not enhance morphological differentiation of IM preadipocytes.

Key Words: Bovine, Preadipocyte, Dexamethasone

187 Identification of two cell culture models to study bovine CAT1 activity and expression. S. F. Liao*, C. A. Woods, J. A. Boling, and J. C. Matthews, *University of Kentucky, Lexington.*

Although L-Lysine (Lys) is a dietarily-essential amino acid (AA) for cattle fed a high corn diet, proteins responsible for absorption of Lys by

cattle have not been described. CAT1 is a major intestinal transporter of cationic AA. CAT1 demonstrates a high-affinity (μM) System γ^+ activity that differs from $\text{b}^{0,+}$, $\gamma^+\text{L}$, and $\text{B}^{0,+}$ cationic AA transporter systems due to its independence of Na^+ ($-\text{Na}^+$) and/or insensitivity to neutral AA. This project was conducted to determine if Madin-Darby Bovine Kidney (MDBK) cells and steer hepatocytes express CAT1 activity and/or mRNA. Putative System γ^+ activity was assessed in wells ($n = 8-12$) of 2-d cultured MDBK cells ($250,000/2 \text{ cm}^2$ well) by characterizing the $-\text{Na}^+$ uptake (pmol/mg protein) of Lys ($10 \mu\text{M}$; [H^3]Lys, radiotracer) in the presence and absence of 2 mM L-Arg or L-Leu. System γ^+ Lys uptake accounted ($P < 0.001$) for 50% of total $-\text{Na}^+$ Lys uptake, as did Systems $\text{B}^{0,+}$ and/or $\gamma^+\text{L}$. K_m determination for $-\text{Na}^+$ Lys in the presence of 5 mM L-Leu was $250 \mu\text{M}$, consistent with CAT1 activity. RT-PCR of total RNA extracted from MDBK cells (and bovine kidney, and ileal epithelium), using the full-length pig CAT1 as a template, produced a single cDNA product of about 700 bp. Sequencing of the MDBK and kidney products revealed a 695-bp cDNA that possessed 89, 87, 99% homology with corresponding regions of the pig, human, and predicted bovine CAT1 mRNA, respectively. The expression of System γ^+ activity and CAT1 mRNA next was evaluated in wells (4-6) of 2-d cultured hepatocytes ($200,000/2 \text{ cm}^2$ well) isolated (collagenase perfusion) from the caudal lobe of 30-d old Angus steer livers ($n = 4$), using transport and RT-PCR parameters identical to those used for MDBK cells. Systems γ^+ , $\text{b}^{0,+}$, and $\gamma^+\text{L}$ accounted ($P < 0.034$) for 19, 34, and 47% of $-\text{Na}^+$ Lys uptake, respectively, and RT-PCR yielded a product of about 700 bp. These results demonstrate that MDBK cells and steer hepatocytes express CAT1 activity and mRNA and indicate their usefulness to study bovine CAT1 function and expression.

Key Words: CAT1, SLC7A1, MDBK, Hepatocytes

188 Leptin increases IGF-I-induced expression of SOCS3 mRNA in prepubertal heifer mammary parenchyma. B. E. Etchebarne^{*1}, L. F. P. Silva², J. S. Liesman³, and M. J. VandeHaar³, ¹Stanford University, Palo Alto, CA, ²University of Sao Paulo, Pirassununga, SP, Brazil, ³Michigan State University, East Lansing.

High-energy diets promoting body growth rates $>1 \text{ kg/d}$ impair mammary development in prepubertal dairy heifers. Biological mechanisms to explain this result are not well understood, but the hormones insulin-like growth factor-I (IGF-I) and leptin likely play a role. Adipocytes produce the protein leptin, and leptin concentrations increase with increased fat deposition in the body and mammary gland. IGF-I stimulates and leptin inhibits proliferation of mammary epithelial cells in vitro and in vivo in cattle. We hypothesize that leptin inhibits the mammogenic action of IGF-I, and diets that promote rapid prepubertal body growth inhibit mammary development if fat deposition is increased. Our objectives were to elucidate the effects of IGF-I and leptin infusion on cell cycling in mammary epithelial cells, by identifying key genes controlling the interaction of these two hormones in bovine parenchyma. Selected genes were measured using quantitative real-time-PCR to analyze mammary tissue collected from six prepubertal Holstein heifers after 7 d of intramammary hormone infusions of IGF-I, leptin, IGF-I plus leptin, or saline control. Addition of leptin to IGF-I treated quarters increased suppressor of cytokine signaling (SOCS)-3 mRNA 2.3-fold relative to IGF-I-infused quarters. Assuming protein changes follow mRNA expression, increased SOCS3, which signals within the JAK/STAT cell proliferation pathway, could possibly explain the inhibition of IGF-I-induced mammary epithelial cell proliferation. We propose that a SOCS-mediated feedback mechanism exists in which SOCS3 decreases MEC sensitivity

to the IGF-I mitogenic effect, reduces the progression of cells into the S-phase of the cell cycle, and thereby prevents IGF-I-stimulated mammary epithelial cell proliferation during periods of high energy feeding or increased adiposity in the ruminant.

Key Words: IGF-I, Leptin, Mammary

189 Cellular and biochemical features of skeletal muscle and subcutaneous adipose tissue in pigs differing in IGF-II genotype. D. Gardan^{*1}, I. Louveau¹, K. Van den Maagdenberg², N. Buys³, S. De Smet², and F. Gondret¹, ¹INRA/Agrocampus Rennes, Systèmes d'Élevage, Nutrition Animale et Humaine, Saint Gilles, France, ²Laboratory for Animal Nutrition and Animal Product Quality, Department of Animal Production, Ghent University, Melle, Belgium, ³Division of Gene Technology, Department of Biosystems, K.U. Leuven, Heverlee, Belgium.

In pigs, a mutation in the regulatory sequence of the paternally imprinted IGF-II gene (Q allele) is associated with increased muscle mass and decreased backfat thickness. This study aimed to determine the impact of this mutation on some cellular and biochemical features of skeletal muscle and adipose tissue. Muscle (trapezius) and subcutaneous adipose tissue (SCAT) were collected in pigs (average weight at slaughter 106 kg) differing in IGF-II genotype (Qpat, $n = 6$; qpat, $n = 7$). Tissue lipid content, cell size and activities of lipogenic enzymes were determined using standard assays. Real-time PCR was performed to examine mRNA expressions of IGF-II gene and of genes involved in lipogenesis or lipolysis. Levels of IGF-II mRNA were higher in muscle from Qpat than qpat pigs ($P < 0.05$), but did not differ ($P > 0.1$) between the two groups in SCAT. Muscle lipid content and intramuscular adipocyte size were not influenced by IGF-II genotype. In contrast, lipid content was lower ($P < 0.05$) in SCAT from Qpat than qpat pigs. In this tissue, adipocytes were smaller ($P < 0.05$) while their number tended to be higher ($P = 0.06$) in Qpat than in qpat pigs. Expressions and/or activities of malic enzyme, fatty acid synthase and hormone-sensitive lipase were not influenced by IGF-II genotype in the examined tissues. Our results suggest that IGF-II mutation may favor adipocyte proliferation in SCAT at the expense of differentiation process.

Key Words: Adipocytes, IGF-II, Lipid metabolism

190 Evaluation of a mathematical model to estimate total feed required for pen-fed Santa Gertrudis steers and heifers based on performance and diet composition. B. Bourg^{*1}, L. O. Tedeschi¹, G. E. Carstens¹, E. Brown¹, and D. G. Fox², ¹Texas A & M University, College Station, ²Cornell University, Ithaca, NY.

The Cornell Value Discovery System (CVDS) was developed to predict growth and body composition based on animal, diet, and environment information. This model has been adapted to facilitate individual management of pen-fed cattle, and to harvest animals at the most profitable USDA quality and yield grade endpoints. The CVDS is also used to allocate feed to individual cattle fed in pens. The objective of this study was to evaluate the model's effectiveness in predicting total DM required (DMR) for Santa Gertrudis steers and heifers ($n = 457$) fed in five separate pens at the King Ranch feedyard. Pens 1 and 4 contained heifers only, pens 3 and 5 contained steers only, and pen 2 contained a mix of both heifers and steers. The cattle were fed three step-up rations and one finishing ration, that ranged from 2.3 to 2.82 Mcal ME/kg. Dietary ME was calculated using actual feed analysis in the Cornell Net Carbohydrate and Protein System (CNCPS) model.

Animal performance and carcass traits (HCW, backfat, ribeye area, and marbling scores) were used to compute the BW at 28% empty body fat (EBF) for each animal. The CVDS model with the adjustment of ME efficiency for composition of gain was used to predict individual DMR and to estimate total DMR of the pen. The 90% confidence interval of predicted EBF at the harvest BW was similar between steers and heifers and ranged from 25-36% EBF. The mean bias, calculated as the difference between DMR and feed fed divided by feed fed and weighed by animals per pen, was 4.64% and 1.46% for heifers and steers respectively, with an overall value of 2.43% ($P = 0.16$). A sensitivity analysis of the dietary ME (± 5 and $\pm 10\%$) indicated the accuracy decreased when dietary ME used was lower or higher than the CNCPS predicted value. Our findings suggest the CVDS accurately predicted feed requirements for Santa Gertrudis steers and heifers.

Key Words: Finishing cattle, Feed intake, Modeling

191 Using ultrasound to determine body composition of breeding heifers. M. J. Baker^{*1}, L. O. Tedeschi², D. G. Fox¹, W. R. Henning³, and D. J. Ketchen¹, ¹Cornell University, Ithaca, NY, ²Texas A&M University, College Station, ³Pennsylvania State University, College Park.

Carcass traits and ultrasound have been used to predict empty body fat (EBF) of steers and yearling bulls, which is used to predict their energy and DM requirements for growth. This study was conducted to develop equations to predict EBF from ultrasound measurements in

breeding heifers for use in predicting their individual DM requirements when fed in group pens. One hundred eighteen spring-born purebred and crossbred beef heifers (BW=271 kg) were sorted into 3 marketing groups on projected days to USDA low Choice Quality grade and fed a common high energy diet in twelve slatted floor pens (10 hd/pen) until estimated to average the target quality grade. The heifers were evaluated for body composition with ultrasound at approximately one year of age. Ultrasound measurements included backfat (uBF), rump fat (uRmpFt), ribeye area (uREA) and intramuscular fat (IMF); hot carcass weight (HCW) was predicted with an equation (pHCW). Carcass data collected included HCW, backfat over the 12th-13th rib (BF), marbling score (MRB), and ribeye area (REA). The 9-11th rib section was removed and dissected into soft tissue and bone. Chemical fat determined by ether extract was used to compute carcass fat (CF) and EBF. Regression analysis showed that carcass measurements explained 62% of the variation (RMSE = 1.42) in EBF ($23.6 + 3.16*BF + 0.0138*HCW + 0.778*MRB - 0.0894*REA$). Adding body density (final SBW divided by volume predicted from girth circumference, width, and length) accounted for 70% of the variation in EBF. The equation developed with ultrasound measurements on the live heifers ($EBF = 14.7 + 8.73*uRmpFt + 11.4*uBF - 0.0669*uREA + 0.452*IMF + 0.0148*pHCW - 6.267*uRmpFt*uBF$), explained 61% of the variation (RMSE = 1.5). The measured EBF was 31.3% and the predicted EBF was 31.6% and 31.5% using the carcass and ultrasound equations, respectively. Ultrasound can be used as effectively as direct measure of carcass traits in predicting EBF in breeding heifers.

Key Words: Beef heifers, Ultrasound, Body composition

Lactation Biology

192 Effects of CLA on bioenergetic and milk production parameters in grazing dairy cows offered ad libitum or restricted pasture. J. K. Kay^{*1,2}, T. R. Mackle¹, D. E. Bauman³, N. A. Thomson¹, and L. H. Baumgard², ¹Dexel, Hamilton, New Zealand, ²University of Arizona, Tucson, ³Cornell University, Ithaca, NY.

Conjugated linoleic acid (CLA) reduces milk fat synthesis in grazing and TMR-fed dairy cows and often improves calculated net-energy balance (EBAL). Study objectives were to determine if CLA-induced milk fat depression could be utilized during times of nutrient limitations (i.e. droughts) to improve bioenergetic and milk production parameters. Twelve multiparous mid-lactation rumen-fistulated Holstein cows were offered ad libitum (AL) or restricted (R) pasture allowances and abomasally infused twice daily with 0 (0) or 50 (50) g/d CLA (containing a variety of CLA isomers) in a crossover design. Treatment periods lasted 10 d and were separated by a 10 d washout period. Milk and plasma samples were averaged from d 9 and 10, and EBAL was calculated from d 6-10 of the infusion period. Pasture restriction reduced the yield of milk ($P<0.01$; 15.7, 15.4, 11.5, 11.9 kg/d for AL0, AL50, R0 and R50, respectively) and milk components. CLA reduced ($P<0.01$) milk fat yield by 45 and 46% in AL and R, respectively. There was no CLA effect on milk yield nor milk lactose content or yield, however milk protein content increased ($P<0.05$) in both AL and R, resulting in an increased ($P<0.05$) protein yield of 6 and 9% in AL and R, respectively. The CLA-induced changes to milk fat and protein increased ($P<0.01$) the protein:fat ratio by ~2-fold in both AL and R. Milk fat trans-10, cis-12 CLA content increased following CLA infusion ($P<0.01$; 0.10, 0.64, 0.09, 0.74 % for AL0, AL50, R0, R50, respectively). Calculated net-EBAL improved following CLA infusion (-1.8 vs. 11.2 and 1.6 vs. 13.8 MJ/cow/d for AL and R, respectively;

$P<0.05$), however CLA did not alter plasma bioenergetic markers (including insulin, NEFA, BHBA, urea, glucose and AST). Data indicate that during short periods of nutrient restriction, CLA may provide an alternative management tool to improve the milk protein:fat ratio and calculated EBAL, however further studies are required to determine if CLA is effective at improving bioenergetic parameters during long term feed shortages.

Key Words: CLA, Milk fat, Pasture

193 Variation in milk yield response to once-daily milking in Friesian-Jersey crossbred cattle. S. Davis^{*}, L. McNaughton, G. Bracefield, K. Sanders, and R. Spelman, *Livestock Improvement Corporation, Hamilton, New Zealand.*

Once-daily milking (OAD) of cows in New Zealand is an increasingly popular management option. The major constraint to adoption of OAD is the production loss which is variable between individual cows and differs significantly between Friesian and Jersey breeds. The objective of this study was to identify animals consistently showing a minimal loss in production during 7-day periods on OAD in mid and late lactation and to examine the relationship between losses in short (7d) and long-term (70d) OAD challenges. The first study used 306 crossbred cattle (from 6 sires) all in their 2nd lactation and grazing rye-grass/white clover pasture. Mean twice-daily yields in mid-and late-lactation were 16.1 and 10.3 l/d respectively. Mean OAD yield loss after 7d on OAD was 3.6 ± 1.5 (SD) (22.4%) and 1.3 ± 1.0 (SD) (12.7%) l/d. at the same stages. Yield loss ranged from 0 to 8.1 l/d at mid and 0-4.3l/d in late-lactation. 20 animals showed a yield loss of