

Graduate Student Competition—CSAS

265 Diurnal Variation of Blood Metabolites in Response to Time of Feeding and Dietary Forage to Concentrate Ratio in Lactating Dairy Cows.

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The effects of the time of providing fresh total mixed ration and the dietary concentrate level on daily averages and diurnal variation of blood metabolites were examined. Eight lactating Holstein cows (BW = 660 ± 62 kg, 82 ± 22 days in milk; mean ± SD) were used in a 4 × 4 Latin square design with a 2 × 2 factorial arrangement of treatments. Each experimental periods included 2 wk of adaptation followed by 1 wk of sampling. Treatments included two diets (D) and two times of feeding (TF, 9 am and 9 pm). Diets contained either higher concentrate (HC, forage to concentrate ratio (F:C) = 38:62) or lower concentrate (LC, F:C = 49:51). Blood was sampled every 2 h for 24-h periods during each sampling week. Proc MIXED Procedure of SAS with appropriate covariance structure for repeated measures was adopted to assess the fixed effects of D, TF, hour of sampling (H), and their interactions on blood metabolites. Feeding HC vs. LC diet significantly increased blood glucose (P<0.001) and lactate (P<0.05), and decreased β-hydroxybutyrate (BHBA) (P<0.01). Evening feeding tended to increase (P<0.10) daily average of blood lactate compared to morning feeding. Diurnal variations of all blood metabolites were modified (P < 0.01) by time of feeding. Diurnal rhythmicity of blood urea was significantly (P<0.001) entrained by the interaction between diet and TF. Evening fed cows exhibited a prefeeding decline and a postfeeding rise in blood glucose, whereas morning fed cows did not. Primiparous cows showed more variation (P<0.01) in blood NEFA than multiparous cows. Results revealed that TF modified the diurnal variation of blood metabolites and thus may affect peripheral delivery of the nutrients in high-producing lactating cows.

Table 1. Effects of diet (D), time of feeding (TF), and hour of sampling (H) on blood metabolites

	Diet (D)		Time of Feeding (TF)				D	T	H	D*H	T*H	D*H T*H
	HC	LC	Morning	Evening								
Glucose, mg/dL	80.5	76.6	78.5	78.6	***	NS	***	NS	***			
BHBA, mmol/L	470	576	513	533	**	NS	***	NS	***			
NEFA, mEq/L	0.12	0.13	0.13	0.12	NS	NS	NS	†	**			
Urea, mmol/L	4.94	4.75	4.83	4.86	†	NS	***	*	***			
Lactate, mmol/L	0.70	0.65	0.65	0.69	*	†	***	NS	***			

NS= not significant; † P < 0.15; * = P < 0.05; ** = P < 0.01; *** = P < 0.001

Acknowledgements: This study was supported by grants from Dairy Farmers of Canada and Dairy Farmers of Manitoba

Key Words: Time of feeding, Diurnal variation, Blood metabolites

266 Citrulline synthesis limits whole-body arginine synthesis in piglets fed an arginine deficient diet. K. L. Urschel*¹, A. K. Shoveller¹, R. Uwiera², P. B. Pencharz^{1,3}, and R. O. Ball^{1,3}, ¹Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada, ²Health and Laboratory Animal Sciences, University of Alberta, Edmonton, Alberta, Canada, ³Departments of Paediatrics and Nutritional Science, University of Toronto, Toronto, Ontario, Canada.

Arginine in sows' milk is low and intake in suckling piglets could limit growth. Piglets can synthesize arginine from proline, but there is an upper limit to this synthesis and piglets fed a deficient arginine diet have diminished whole-body arginine status. The objective of this experiment was to elucidate where the limitation in this metabolic pathway occurs by supplementing an arginine deficient diet (basal) with equimolar (9.18 mmol kg⁻¹ d⁻¹) quantities of either pro-

line (+PRO), ornithine (+ORN), citrulline (+CIT) or arginine (+ARG). Male piglets (n=25, ~1.7 kg) were fitted with gastric catheters (IG) for diet and isotope infusion, jugular vein catheters (IV) for isotope infusion, and femoral vein catheters for blood sampling (d 0). Piglets were given a complete diet until d 3 and then received one of the 5 test diets for the remainder of the trial. Beginning on d 5, piglets received 3 primed, constant infusions on separate days: [guanido-¹⁴C]arginine given IG and IV to calculate arginine flux, and [U-¹⁴C]proline given IG to calculate proline conversion to arginine. Compared to piglets fed the basal, +PRO and +ORN diets, piglets fed the +CIT and +ARG diets had lower plasma ammonia (P<0.05) and urea (P<0.05) concentrations, higher plasma arginine concentrations (P<0.0001), and higher IV and IG arginine fluxes (P<0.05). These results demonstrate that citrulline, but neither ornithine nor proline, is an effective precursor for arginine synthesis in week-old piglets. The conversion of proline to arginine, as a % of arginine flux, was greatest in piglets fed the +PRO diet (44.5%), followed by the basal (25.8%), +ORN (22.5%), +ARG (6.2%) and +CIT (5.7%) diets (SEM = 3.1%; P<0.0001). This shows that citrulline addition to an arginine deficient diet spared the use of proline in arginine synthesis. Citrulline synthesis appears to be the limiting factor for arginine synthesis in piglets. Strategies aimed at improving arginine status in young piglets should focus on increasing citrulline concentrations.

Acknowledgements: This study was funded by NSERC.

Key Words: Piglet nutrition, Arginine biosynthesis, Amino acid metabolism

267 Early weaning up-regulates the capacity of the small intestinal

sucrase-isomaltase and maltase-glucoamylase hydrolysis of maltose in the neonatal pig. D. Lackeyram*¹, D. Pham¹, Q. Liu², Y. Mine¹, M. Bakovic¹, B. L. Nichols³, and M. Z. Fan¹, ¹University of Guelph, Guelph, Ontario, Canada, ²Agri-Food Canada, Guelph, Ontario, Canada, ³Baylor College of Medicine, Houston, Tx.

Sucrase-isomaltase (SI) and maltase-glucoamylase (MGA) are small intestinal brush border membrane enzyme complexes responsible for the hydrolysis of maltose. SI is capable of hydrolysing both sucrose and maltose where MGA serves as the final pathway of starch digestion to glucose in the neonate. This study investigated combined changes in the capacity of intestinal MGA and SI in the hydrolysis of maltose as affected by early weaning (EW) stress. Eight Yorkshire piglets, with an average BW of 3 kg at the age of 10 d, were weaned from sows and fed a corn and soybean meal-based diet for 12 d in comparison with 8 suckling (SU) piglets. The entire small intestine was collected and divided into 4 regions: duodenum, proximal jejunum, distal jejunum, and terminal ileum. Homogenized intestinal tissue from each of the regions was used to conduct kinetic experiments of combined MGA and SI activity with six concentrations of purified maltose (0-75 mM) at 37°C and pH 6.0. Weaning increased (P<0.05) the combined maximal specific enzyme activities (V_{max}: EW, 29.42±0.60 vs. SU, 24.69±0.39, nmol/mg protein.min, n=48) by 19% and the combined enzyme affinities (K_m: EW, 4.16±0.37 vs. SU, 5.86±0.68, mM, n=48) by 29% primarily in the jejunum. Weaning also increased (P<0.05) the digestive capacity of the combined enzyme action (EW, 169.29±3.49 vs. SU, 135.54±3.16, mol/kg BW.d, n=16) by 25%. Thus, early weaning up-regulates the capacity of the intestinal SI and MGA to hydrolyse maltose by increasing the combined enzyme activities and their affinities as an adaptation to weaning on vegetal diets.

Key Words: Intestinal sucrase-isomaltase, Maltase-glucoamylase, Weaned piglets

268 Ultrasonic evaluation of intramuscular fat content in yearling beef bulls. R. Bergen*, S. Miller, I. Mandell, and C. Campbell, *University of Guelph, Guelph, Ontario, Canada.*

Two commercially available software programs were used by trained and experienced ultrasound technicians to predict 12/13th rib intramuscular fat percentage in 88 crossbred yearling (435 ± 37 d, 633 ± 78 kg, 5.3 ± 2.1 mm rib fat depth) bulls prior to slaughter. Marbling score and chemical intramuscular fat percentage (2.66 ± 1.08 %) were evaluated post-slaughter. A base model including year indicated that neither ultrasound ($R^2 = 0.59$ vs. 0.46, residual standard deviation = 0.70 vs. 80%, respectively) nor marbling score ($R^2 = 0.45$, $rsd = 0.81$ %) was particularly effective at predicting chemical intramuscular fat content. Combining intramuscular fat estimates produced by both ultrasound programs in the same model did not improve prediction of chemical intramuscular fat percentage ($R^2 = 0.60$, $rsd = 0.69$ %). Including ultrasound fat depth, breed composition, hip height, and squared terms of ultrasound intramuscular fat percentage in the model improved ultrasound-based predictions of intramuscular fat percentage ($R^2 = 0.64$ vs. 0.55, $rsd = 0.67$ vs. 0.75 %). Scan age, live weight, and other linear body size measurements did not contribute to the prediction models. Further research is needed to assess whether multiple trait evaluations incorporating additional indicator traits may benefit genetic improvement programs for carcass quality.

Acknowledgements: Agriculture and Agri-food Canada's Agriculture Adaptation Council Beef Improvement Ontario Canadian Foundation for Innovation Ontario Cattlemen's Association Ontario Innovation Trust Ontario Ministry of Agriculture and Food

Key Words: Carcass, Marbling, Genetic

269 Evaluation of the NRC (1996) model for predicting feed requirements for beef cows in western Canada. J. L. Bourne*, J. J. McKinnon¹, H. C. Block¹, and H. A. Lardner², ¹University of Saskatchewan, Saskatoon, SK, Canada, ²Western Beef Development Centre, Humboldt, SK, Canada.

A trial was conducted to evaluate the 1996 NRC beef model's ability to predict DMI and ADG of pregnant cows under western Canadian conditions. Over 2 consecutive years, 90 Angus (587 ± 147 kg) cows assigned to 15 pens (N=6) were fed typical winter diets *ad libitum*, formulated to stage of pregnancy. Data collection included pen DMI and ADG (corrected for pregnancy), calving date, calf weight, body condition scores and ultrasound fat measurements, weekly feed samples and daily ambient temperature. Pen DMI and ADG in each trimester was predicted using the 1996 NRC beef model. The results indicate that in the 2nd and 3rd trimester of both years the model over predicted ($P < 0.05$) DMI required to support observed ADG, and under predicted ($P < 0.05$) ADG based on observed DMI. *Ad libitum* intake was over predicted ($P < 0.05$) in all cases except for the 2nd trimester of year 2, where predicted *ad libitum* intake was not different ($P > 0.05$) from observed intake. A second evaluation was carried out assuming thermal neutral (TN) conditions. In this case, it was found that during the 2nd trimester of year 1 predicted DMI and predicted ADG were not different ($P > 0.05$) from observed DMI and ADG, however in year 2 predicted DMI was less ($P < 0.05$) than observed DMI, and predicted ADG was greater ($P < 0.05$) than observed ADG. In the 3rd trimester of both years the DMI under TN conditions was under predicted ($P < 0.05$), and the ADG was over predicted ($P < 0.05$) indicating some negative effect of environment. Assuming TN conditions resulted in DMI and ADG predictions being closer to actual performance. These results suggest current energy equations for modeling environmental stress over predict maintenance requirements for wintering beef cows in western Canada.

Acknowledgements: Saskatchewan Agriculture Development Fund

Key Words: NRC evaluation, Feed requirements, Wintering beef cow

270 Postnatal changes of pancreatic and hepatic fractional protein synthesis rates in piglets measured by an intraperitoneal flooding dose of L-[ring-2H5]phenylalanine. X. Yang*, L. Liu¹, G. Werchola¹, Y. Mine¹, Q. Liu², and M. Fan¹, ¹University of Guelph, Guelph, ON, Canada, ²Agriculture and Agri-Food Canada, Guelph, ON, Canada.

This study examined the hypothesis that postnatal changes of pancreatic and hepatic fractional protein synthesis rates (FSR) were associated with plasma cortisol and insulin levels in piglets. Thirty six littermate purebred Yorkshire gilts were divided into suckling groups at ages of d 1, 4, 6, 12, 20, and one week post-weaning group at d 28, respectively, and injected intraperitoneally a flooding dose of L-[ring-2H5]phenylalanine (Phe) in saline. Plasma, pancreatic and hepatic samples were collected for the determination of cortisol and insulin concentrations by radioimmunoassay and the tracer Phe enrichments with gas chromatography-mass spectrometry. Postnatal changes of plasma hormone levels were observed ($P < 0.05$) for cortisol (quadratic effects) and insulin (quadratic and cubic effects). The average tracer Phe enrichments in the plasma, pancreatic, and hepatic free pools were 27.4, 28.9 and 32.8 molar%, respectively. There was a quartic pattern ($P < 0.05$) of pancreatic and hepatic FSR changes during the postnatal development. Only the postnatal changes of pancreatic FSR were positively ($P < 0.05$) correlated with plasma insulin levels. In conclusion, there are postnatal changes in the pancreatic and hepatic FSR. Insulin and cortisol effects on pancreatic and hepatic FSR may be tissue and age specific.

Key Words: pancreatic and hepatic fractional protein synthesis rates, cortisol and insulin, piglets

271 Changes in the plasma citrulline concentration are a predictor of alterations in gut mucosal morphology and functions in the piglet. D. Lackeyram*, D. G. Burrin², Y. Mine¹, and M. Z. Fan¹, ¹University of Guelph, Guelph, ON, Canada, ²Baylor College of Medicine, Houston, TX.

This study determined quantitative relationships between the plasma urea and amino acid (AA) concentrations and the gut mucosal morphological changes and body weight gains in early weaning (EW) and suckling piglets. The study was conducted for 12 d with 24 Yorkshire piglets of an average initial body weight of 3.4 kg at d 10 of age. The weaned pigs were fed a corn and soybean meal-based diet. There was no sex effects ($P > 0.05$) on any of the endpoint measurements. The EW pig had 32% ($P < 0.05$) of the whole body growth rate of the suckling pigs. The EW pig experienced an elevated whole body AA catabolism ($P < 0.05$) as indicated by significant increases in plasma urea concentration. Weaning decreased ($P < 0.05$) the total counts of mucin-filled goblet cells along the crypt-villus axis. Weaning also caused gut mucosal villus atrophy and crypt hyperplasia ($P < 0.05$) in comparison with suckling piglets. There were linear relationships ($P < 0.05$) between the plasma urea concentration and average daily gain and gut mucosal morphological measurements, supporting the concept that gut mucosal crypt cells are metabolically of a catabolic phenotype, whereas the villus cells are predominantly of an anabolic phenotype. There were also linear relationships ($P < 0.05$) between plasma concentrations of urea and several AA including carnitine, citrulline, glutamate, glutamine, phenylalanine, and taurine. Similarly, there were linear relationships ($P < 0.05$) between the gut mucosal morphological measurements and several AA, with citrulline showing the best correlation. In conclusion, gut mucosal crypt hyperplasia is partially responsible for the weaning-associated elevation in whole body AA catabolism and growth repression. Change in the plasma citrulline concentration is a reliable plasma marker for predicting alterations of gut mucosal morphology and functions in piglets.

Key Words: Citrulline, Gut mucosal morphology, Piglets

272 Effect of pelleted barley on performance and carcass quality of feedlot steers. L. M. Williams^{*1}, J. J. McKinnon¹, V. R. Racz¹, D. A. Christensen¹, and K. Ataku², ¹University of Saskatchewan, Saskatoon, SK, Canada, ²Rakuno Gakuen University, Ebetsu, Hokkaido, Japan.

Development of export markets for cereal grains necessitates shipping grain in processed forms; however, excessive processing can lead to problems such as acidosis. A trial was conducted to evaluate the performance of beef steers fed diets containing ground, pelleted barley as the concentrate. Weaned steers (N=350; 285±22kg) were assigned to one of 12 pens and fed either pelleted or rolled barley as the concentrate. During backgrounding, cattle were fed 42% concentrate (DM), consisting of 85% pelleted or rolled barley and 15% canola meal. During finishing the concentrate was fed at 86% of the diet (DM) and consisted of 94% pelleted or rolled barley and 6% canola meal. Steers were weighed every 4 weeks during growing and every 2 weeks during finishing. Ultrasound backfat (USBF) and *longissimus dorsi* (LD) area were measured

monthly. Animals were slaughtered at 12mm of USBF or 625 kg. Carcass data included weight, LD area, grade fat, marbling score, and liver abscess score. Rib fat, lean and bone %, LD and fat color, and marbling fat content were determined on 8-bone rib samples from 40 randomly selected steers. Steers fed pelleted barley had lower ($P<0.05$) ADG during finishing (1.80 vs. 2.00 kg/d) and for the total trial (1.60 vs. 1.70 kg/d), as well as more ($P<0.05$) days on feed (196 vs. 186). DMI was lower ($P<0.05$) for cattle fed pelleted barley throughout the trial. Feed efficiency (kg feed/kg gain) was superior ($P<0.05$) for the group fed pelleted barley during finishing (6.03 vs. 6.21) and the total trial (6.27 vs. 6.64). Both diets produced similar carcasses, but inter-muscular fat % was higher ($P<0.05$) for the rolled barley group (60.0 vs. 57.4%), as was ($P<0.05$) grade fat (11.2 vs. 10.7 mm). Results from this study indicate that pelleted barley can be used effectively in growing and finishing diets, however further research is required to discover why intake of pelleted barley is reduced.

Key Words: Pelleted barley, Carcass quality, Finishing steers

Growth and Development: Postnatal Development as a Harbinger of Future Performance

273 Hormone and growth factor regulation of tissue remodeling in the mammary gland. D. Flint^{*1}, G. Allan¹, J. Beattie¹, M. Travers¹, M. Barber¹, A. Kolb¹, C. Whitelaw², M. Boutinaud³, N. Binart⁴, and P. Kelly⁴, ¹Hannah Research Institute, Ayr, UK, ²Roslin Institute, Midlothian, Edinburgh, UK, ³INRA Unite Mixte de Recherches Sur la Production du Lait, Saint Gilles, France, ⁴Inserm Unit 584, Hormone Targets, Faculty of Medicine Rene Descartes, Paris.

Insulin-like growth factor binding protein-5 (IGFBP-5) production increases dramatically during forced involution of the mammary gland in rats, mice and pigs. Growth hormone (GH) increases production of the survival factor IGF-I, whilst prolactin enhances the effects of GH by inhibiting IGFBP-5 synthesis which would otherwise prevent the actions of IGFs. A causal relationship between IGFBP-5 and cell death was demonstrated in transgenic mice expressing IGFBP-5 specifically in the mammary gland. DNA content in the mammary glands of transgenic mice was decreased as early as day 10 of pregnancy and remained so during the first 10 days of lactation. The concentration of caspase-3 was increased in transgenic animals whereas the concentrations of two pro-survival molecules Bcl-2 and Bcl-xL were decreased. Furthermore, IGF receptor- and Akt-phosphorylation were both inhibited. We also demonstrated that the effects of IGFBP-5 could be mediated in part by IGF-independent effects involving the plasminogen system, and matrix metallo-proteinases (MMPs). Treatment with prolactin was able to inhibit early involutory processes in normal mice but was unable to prevent this in mice over-expressing IGFBP-5, although it was able to inhibit expression of MMPs. Thus IGFBP-5 simultaneously inhibits IGF action and activates the plasminogen system, thereby coordinating cell death and tissue remodelling processes. The ability to separate these properties, using mutant IGFBPs, is currently under investigation. We have also developed a mouse model of diet-induced obesity which shows numerous abnormalities relating to mammary gland function. Animals ate approximately 40% more calories, gained weight at three times the rate of controls and exhibited reduced conception rates, increased peripartum pup mortality and impaired lactogenesis. Despite access to high energy diets, the obese animals mobilised even more adipose tissue during lactation than their lean counterparts. Obese animals also exhibited marked abnormalities in ductal branching morphogenesis and alveolar development of the mammary gland, which may partially explain the delay in differentiation evident during lactogenesis.

Key Words: IGF, Proteases, Obesity

274 Effects of modified calf growth on mammary development, endocrine physiology, and performance. M. Vestergaard^{*1}, S. Purup¹, M. S. Weber Nielsen², Y. R. Boisclair³, and K. Sejrsen¹, ¹Danish Institute of Agricultural Sciences, Tjele, Denmark, ²Michigan State University, East Lansing, ³Cornell University, Ithaca, NY.

The purpose of rearing heifers comprises a utilization of the genetic potential of the animal to achieve the most favorable body and mammary gland development by optimizing feeding and rearing conditions. Our research has led to the concept of a 'critical period' before puberty, where reproductive and thus mammary development can be negatively affected by high levels of nutrition. Since then focus has been devoted to exploring the possibilities of promoting a high rate of gain without negatively affecting mammary gland growth and milk yield potential. In vivo studies on the effects of nutrition, somatotropin axis activity, and steroid hormone activity or pubertal stage on mammary development have shown that classical endocrine factors, such as somatotropin and estrogen, are involved in the regulation of normal growth and development, but their role in mediating the effects on mammary development is less clear. Most evidence suggests that the key regulation takes place locally in the mammary gland. Investigations on local regulation of mammary development have included functional receptor studies in specific tissues and in vitro cell culture experiments using tissue and serum from in vivo experiments. The results indicate that locally produced IGFs and IGF-binding proteins play a role, but many other factors, such as TGF β and leptin, likely also contribute. The importance of other body tissues and the interaction between the mammary gland and other tissues as well as the cross-talk within the mammary gland are less well-studied. However, both the endocrine actions of various growth factors, such as the IGFs, which target most tissues, and the tissue-specific expression and production of important paracrine and endocrine factors have to be considered to further elucidate the complex regulation of mammary gland and body development. We expect that future research will have to focus more on the interactions and synergism among different types of tissues during calf development.

Key Words: Cattle, Mammary, Endocrinology

275 Tissue proteolytic enzymes: Modifiers of muscle and adipose tissue. G. Hausman^{*}, USDA ARS, Athens, GA.

A fundamental aspect of tissue remodeling is the breakdown and degradation of connective tissue and extracellular matrix (ECM) proteins. Degradation or proteolysis of ECM proteins is implicated in cell attachment, cell migration, ECM invasion, angiogenesis and release and processing of membrane bound cytokines and growth factors. Extracellular proteolysis involves several families of proteolytic enzymes, including the plasminogen activator (PA) - plasmin system, the adamalysins (ADAMs) family and the matrixin matrix metalloproteinases