

Ruminant Nutrition: Beef: Efficiency of Production

430 Effects of cow size on dry matter and residual feed intake of lactating beef cows. R. S. Walker^{*1}, R. M. Martin², L. Gentry³, G. Gentry², and G. Scaglia⁴, ¹LSU AgCenter Hill Farm Research Station, Homer, LA, ²LSU AgCenter School of Animal Sciences, Baton Rouge, LA, ³Louisiana Tech University, Ruston, ⁴LSU Iberia Research Station, Jeanerette, LA.

Thirty-eight Angus cross lactating beef cows (BW = 582 ± 51.3 kg, BCS = 5.0 ± 0.5) were used to determine if differences in DMI and residual feed intake (RFI) exist based on cow size. Cows were housed in individual pens (2.2 × 9.1 m) equipped with 2.2 m of bunk space and fed a diet formulated to meet or exceed maintenance requirements consisting of 30% dry bermudagrass hay and 70% ryegrass baleage (DM = 49.3%, CP = 13.2%, NDF = 54.9%, TDN = 63%) for a 14 d adaptation and 70 d feeding period. Individual daily feed intakes, BW, BCS, and hip height were recorded and cow was the experimental unit. Feed intakes were used to calculate RFI for each cow as the difference between actual and expected feed intake. Blood samples were obtained on d 0 and 70 and analyzed for glucose, insulin, and leptin. Cows were assigned to a light (L; 558 ± 23.6 kg) or heavy (H; 626 ± 38.6 kg) weight group based on d 0 BW adjusted to a 5 BCS for differences in DMI and RFI. Based on RFI, cows were classified as positive (POS; 1.65) or negative (NEG; -1.48) for first analysis and low (LOW; -2.28), medium (MED; -0.04), or high (HI; 2.35) for second analysis of d 0 BW, glucose, insulin, and leptin. Cows in the L group had a lower ($P < 0.01$) daily DMI (15.6 ± 1.2 kg) compared with cows in the H group (16.7 ± 1.1 kg); however, mean RFI was not different. Day 0 BW was similar for cows classified as POS (586 ± 50.4 kg) compared with NEG (580 ± 53.5 kg) RFI. Glucose and insulin levels were similar for both POS and NEG RFI groups; however, leptin levels tended to be higher ($P < 0.10$) on d 0 and 70 for cows classified as NEG (0.84 ng/mL) compared with POS (0.58 ng/mL) RFI. Day 0 BW was similar for cows classified as either HI (582 ± 51.7 kg), MED (593 ± 54 kg), or LOW (570 ± 50 kg) RFI. Glucose and leptin levels were similar among HI, MED, and LOW RFI groups; however, insulin levels were higher ($P < 0.01$) on d 0 for HI and LOW RFI groups compared with MED and tended ($P < 0.10$) to be higher on d 70 for HI compared with MED and LOW RFI groups. While differences in DMI were associated with cow size, mature BW is not a good predictor of feed efficiency in beef cows using RFI.

Key Words: cattle, residual feed intake, dry matter intake

431 Effects of feeding a natural biopolymer (chitosan) on methane emissions and performance in beef cattle. D. D. Henry^{*1}, M. J. Ruiz-Moreno¹, F. M. Ciriaco¹, M. Kohmann², V. R. G. Mercadante¹, G. C. Lamb¹, and N. DiLorenzo¹, ¹North Florida Research and Education Center, University of Florida, Marianna, ²Department of Agricultural and Biological Engineering, University of Florida, Gainesville.

Recent in vitro experiments indicate that the natural biopolymer chitosan could modify ruminal fermentation and decrease methane production. Our objective was to evaluate the natural biopolymer chitosan as a feed additive to mitigate in vivo methane emissions and increase performance in beef cattle. Twenty-four crossbred heifers (BW = 252 ± 24 kg) were used in a randomized block design replicated in 2 periods. Heifers were randomly assigned to 12 pens (2 heifers/pen) and pens were randomly assigned to 1 of 6 treatments in a 2 × 3 factorial arrangement. Factors included diet [high concentrate (HC) or low concentrate (LC)] and either 0.0, 0.5 or 1.0% of chitosan dietary inclusion on a DM basis.

Heifers were housed in the University of Florida-Feed Efficiency Facility in Marianna, FL. Diets were offered ad libitum and intake was recorded by a GrowSafe system (GrowSafe Systems, Airdrie, Alberta, Canada). After at least a 14-d adaptation period, methane emissions were measured using the SF₆ tracer technique for 5 consecutive d in each sampling period. Performance data were collected for the heifers. Data were analyzed using the MIXED procedure of SAS (SAS Institute, Cary, NC). No effects ($P > 0.10$) of chitosan or chitosan × diet interaction were found for DMI or methane emissions. A diet effect ($P < 0.01$) was found for methane emissions expressed as g/d, as g/kg of BW^{0.75}, and as g/kg of DMI. Heifers consuming a LC diet produced 130 g of CH₄/d vs. 45 g of CH₄/d in the HC diet. When adjusted for intake, heifers produced 18.2 and 7.1 g of CH₄/kg of DMI in LC and HC, respectively. The addition of up to 1% of chitosan did not affect ($P > 0.10$) methane emissions or growth performance in heifers consuming either diet. Heifers consuming a LC diet had decreased ($P < 0.01$) ADG and G:F and produced 2.9 times more methane per day than those fed a HC diet. However, when expressed as methane produced per kg of DM consumed, heifers consuming a LC diet produced 2.6 times more methane than those consuming a HC diet.

Key Words: beef, methane, chitosan

432 Ruminal methanogens in steers that are negative or positive for residual gain. H. Freetly^{*}, J. Wells, M. Kim, K. Hales, and A. Lindholm-Perry, USDA, ARS, US Meat Animal Research Center, Clay Center, NE.

Cattle produce CH₄ in the rumen and it represents a loss of feed energy. A possible cause of variation in feed efficiency may be differences in capacity to produce CH₄. We hypothesized that cattle with a higher residual gain (RG) would have a lower abundance of methanogens in the rumen. Individual DMI and BW gain were determined on crossbred steers (n = 132, initial age = 348 ± 1 d and BW 444 ± 4 kg) for 56 d. Steers were offered feed ad libitum and individual intake was measured. The diet consisted of 82.75% rolled corn, 12.75% corn silage, and 4.5% supplement (0.066% monensin and 51% CP). Residual gain was calculated from the regression of BW on DMI; $f(x) = (0.1262 \pm 0.0128)x + (25.7 \pm 9.9)$, $R^2 = 0.43$. The 7 animals with the most extreme positive and negative RG that were within 32% of the STD of the mean DMI (772 ± 90 kg) were sampled. Steers were slaughtered and mixed rumen fluid was strained through cheesecloth and frozen. DNA was isolated from rumen content, and bacterial DNA was quantified using PCR with unique amplicons and is expressed as the log of the DNA concentration. Total archaea bacteria standardized to total bacterial DNA (16S) did not differ between High and Low RG ($P = 0.96$). High and Low RG steers did not differ for *Methanobrevibacter ruminantium* + *Mbb. cuticularis* ($P = 0.56$), *Methanosarcina barkeri* ($P = 0.58$), or *Methanobacterium ruminantium* ($P = 0.54$) after standardizing for total archaea bacteria. The concentration of *Mbb. smithii* + *wolinii* + *thaueri* + *gottschalkii* + *woesii* tended to be greater in the High RG steers ($P = 0.06$). While species composition may shift between cattle with different RG, total methanogens did not differ suggesting that differences in feed efficiency may not be a function of rumen microbial capacity to produce methane. Partially funded by National Institute of Food and Agriculture Grant 2011-68004-30214 National Program for Genetic Improvement of Feed Efficiency in Beef Cattle.

Key Words: cattle, methane, methanogen

433 Assessing body fat chemical composition in F1 Nellore × Angus bulls and steers through the use of biometric measures. M. A. Fonseca^{*1,2}, L. O. Tedeschi¹, S. C. Valadares Filho², N. F. De Paula³, H. J. Fernandes⁴, and L. D. Silva², ¹Texas A&M University, Department of Animal Science, College Station, ²Federal University of Vicosa, Department of Animal Science, Vicosa, Minas Gerais, Brazil, ³Federal University of Mato Grosso, Department of Animal Science, Cuiaba, Mato Grosso, Brazil, ⁴Mato Grosso do Sul State University, Department of Animal Science, Aquidauana, Mato Grosso do Sul, Brazil.

This study was conducted to assess the body fat chemical composition through the use of biometric (BM) and postmortem (PM) measurements taken in 40 F₁ Nellore × Angus bulls (B) and steers (S) under feedlot conditions. The animals had 12.5 ± 0.51 mo of age, and shrunk BW (SBW) of 233.03 ± 23.47 and 238 ± 24.58 kg for B and S, respectively. Animals were fed 60% corn silage and 40% concentrate. Eight animals were slaughtered at the beginning (4 B, 4 S), and the remaining animals were randomly assigned into a factorial 2 (gender) × 3 (slaughter weights) arrangement of treatments for the entire trial. The subsequent slaughters were performed when the group of animals reached an average BW of 380 (6 B, 5 S), 440 (6 B, 5 S), and 500 kg (5 B, 5 S). The day before the slaughter, the following BM were taken: hook bone width (HBW), pin bone width (PBW), abdomen width (AW), body length (BL), rump height (RH), height at withers (HW), pelvic girdle length (PGL), rib depth (RD), girth circumference (GC), rump depth (RuD), and thorax width (TW). The PM collected were empty BW (EBW) subcutaneous fat (SF), internal fat (InF), intermuscular fat (ImF), carcass and empty body physical fat, fat thickness at the 12th rib (FT), and 9 – 11th rib section fat (HHF). Additionally, the amount of carcass (CF_{ch}) and empty body (EBF_{ch}) chemical fat contents were estimated by ether extraction of the carcass and empty body constituents. The equations were developed using a stepwise procedure to select the variables with the best goodness-of-fit and the least root mean square error (RMSE). There was an effect of gender ($P < 0.05$) and the equations were developed separately: $EBF_{ch}(kg) = -8.7312 + 1.5672 \times CF_{ch} + 0.5599 \times RuD$ ($r^2 = 0.995$ and $RMSE = 2.73$) and $CF_{ch}(kg) = -123.8316 + 3.7369 \times AW$ ($r^2 = 0.901$ and $RMSE = 6.92$) for S, and $EBF_{ch}(kg) = 34.7554 + 0.3735 \times SBW - 2.4676 \times PGL$ ($r^2 = 0.952$ and $RMSE = 6.70$) and $CF_{ch}(kg) = 44.4023 - 0.3932 \times EBW - 2.5457 \times PGL$ ($r^2 = 0.959$ and $RMSE = 6.21$) for B. The observed BM that most affected the CF_{ch} and EBF_{ch} in this database were RuD and AW for S, and PGL for B, respectively.

Key Words: carcass fat estimation, empty body fat estimation, modeling

434 High energy diet enhances stearoyl-CoA desaturase (SCD) expression in Hanwoo skeletal muscle. K. Y. Chung*, S. H. Lee, S. S. Chang, Y. M. Cho, E. M. Lee, and H. S. Kang, Hanwoo Experiment Station, NIAS, RDA, Pyeongchang, Korea.

High energy diet has been used for enhancing intramuscular adipose tissue in high quality beef cattle. The aim of this experiment was to determine the effect of high energy diet on the level of SCD gene expressions and genotypes. We hypothesized that SCD expression is increased in beef cattle muscle tissue when fed a high energy diet and that this is related to SCD genotypes (CC, CT, TT). A 2 × 3 factorial arrangement (High, Control, vs. CC, CT, TT) in a completely random design was used to feed 24 Hanwoo steers. Two steers were fed in same pen and 12 pens were used for treatment. Blood was drawn from each steers on every first week from 11 to 28 mo. Longissimus dorsi (LD) muscle was collected within 10 min of harvest for analysis of mRNA SCD abundance. Overall ADG were not different between high energy diet and control diet ($P > 0.05$). However, 22 and 27th mo ADG were

increased ($P < 0.05$) by high energy diet compare with control diet. Overall serum NEFA concentrations were not affected by high energy diet ($P > 0.05$), but 22nd and 26th mo NEFA concentrations were increased ($P < 0.05$) by high energy diet. Marbling score and yield grade were not affected by high energy diet ($P > 0.05$). There was a negative correlation ($R^2 = 0.7868$) between concentrations of stearic and palmitoleic acid. Palmitoleic acid was lowest in control-fed CT group and highest in control-fed TT group. Real-time quantitative PCR revealed that the mRNA content of SCD in muscle from high energy diet cattle increased ($P < 0.05$) as compared with the control group. These data indicated that high energy diet increased relative mRNA level of SCD, and these effects may be mediated monounsaturated fatty acid composition in Hanwoo LD muscle.

Key Words: genotype, Hanwoo, SCD

435 Metabolic imprinting effect during early growth on extra cellular matrix construction in Wagyu (Japanese Black steers). A. Nomura^{*1}, R. Fujimura¹, A. Saito⁴, S. Khounsakunalath¹, K. Saito², K. Sakuma², T. Abe², H. Hasebe², S. Kaneda², T. Etoh¹, Y. Shiotsuka¹, S. Maak³, E. Albrecht³, H. Takahashi¹, T. Gotoh¹, ¹Kuju Agricultural Research Center, Kyushu University, Taketa, Oita, Japan, ²National Livestock Breeding Center, Nishigo, Fukushima, Japan, ³Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany, ⁴Zenrakuren, Tokyo, Japan.

The extracellular matrix (ECM) physically supports tissue structures by forming junctions with surrounding macromolecules. In muscle, the ECM supports the contraction of myofibers and is an important factor affecting the tenderness of meat. A previous study reported that supplementation with ground maize increased the quantity of heat-soluble collagen and improved meat tenderness in beef produced from grazing Holstein bulls. This suggests that early nutrition may change the quantity of heat-soluble collagen in beef. This phenomenon is referred to as “metabolic imprinting or metabolic programming” based on medical research regarding “the developmental origins of health and disease (DOHaD).” We examined how metabolic imprinting during early nutrition affects the expression of genes related to the ECM in muscles of Japanese Black cattle fattened on grass. Twenty-three steers were divided into 2 feeding groups. One group was intensively nursed with milk replacer (maximum 1800 g/d) and was fed concentrate and roughage after weaning (HE: n = 12). The other group was normally nursed with milk replacer (maximum 600 g/d) and was fed roughage alone after weaning (R: n = 11). The longissimus thoracis muscle (LT) was sampled by needle biopsy at 3 and 10 mo and DNA microarray analysis was performed. Expression levels of some of the genes related to the ECM were significantly different between the HE and R groups. In this study, we focused on 2 genes: (1) fibronectin, which connects cells to other macromolecules of the ECM, and (2) type IV collagen, which surrounds cells as a component of the endomysium and is a heat-soluble collagen. Gene expression for fibronectin was greater in the HE than in the R animals at both 3 and 10 mo. Conversely, gene expression of type IV collagen was greater in the R than in the HE animals at 3 mo, but this result was reversed at 10 mo. In conclusion, our data suggest that early nutrition may affect the formation of the ECM in the muscle of Japanese Black cattle.

Key Words: cattle, ECM, metabolic imprinting

436 Metabolic imprinting effect in beef production: Influence of nutrition manipulation during an early growth stage on adipogenesis in the longissimus muscle in Wagyu (Japanese Black). R.

Fujimura¹, K. Etoh¹, S. Khounsaknalath¹, K. Saito², K. Sakuma², K. Kaneda², T. Abe², T. Etoh¹, Y. Shiotsuka¹, H. Hasebe², H. Hasebe², S. Maak³, A. Elke³, H. Takahashi¹, T. Gotoh^{*1}, ¹*Kuju Agricultural Research Center, Kyushu University, Taketa, Oita, Japan*, ²*National Livestock Breeding Center, Nishigo, Fukushima, Japan*, ³*Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany*, ⁴*Zenrakuren, Tokyo, Japan*.

Japanese Black cattle (Wagyu) are known to accumulate high levels of intramuscular fat. This experiment was conducted to clarify how early nutrition affected adipogenesis in Japanese Black steers fattened on roughage as metabolic imprinting effect. Japanese Black steers were randomly allocated into 2 groups. The high-energy group (Imp: n = 12) received intensified nursing until 3 mo of age and was then fed a high-concentrate diet from 4 to 10 mo of age. The roughage group (Cont: n = 11) received normal nursing until 3 mo of age and was then fed only roughage from 4 to 10 mo of age. From 10 mo of age, both groups were fed only roughage until slaughter at 31 mo of age. Muscle samples were biopsied from the longissimus muscle (LM) at 3, 10,

14, 20 and 30 mo of age. Three genes relating to glucose metabolism, PPAR γ 2, SCD, C/EBP α , Leptin, and FASN were investigated in each LM sample by qPCR analysis. The expression of PPAR γ 2 was significantly higher in group Imp than in group Cont at 3 and 10 mo of age ($P < 0.05$) and conversely significantly lower at 20, and 30 months of age ($P < 0.05$). The expression of C/EBP α was lower in group Imp than in group Cont at 30 mo of age ($P < 0.1$). The expression of SCD was significantly higher in group Imp than in group Cont at 10 mo of age ($P < 0.05$) and conversely significantly lower at 20 and 30 mo of age ($P < 0.05$). The expression of FASN was significantly higher in group Imp than in group Cont at 10 mo of age ($P < 0.01$) and conversely lower at 20 ($P < 0.1$) and 30 mo of age ($P < 0.05$). The expression of Leptin was significantly higher in group Imp than in group Cont at 14 mo of age ($P < 0.05$). These results indicate that the high energy treatment during the early growth phase would influence or disturb adipogenesis timing in grass-fattening of Japanese Black steers.

Key Words: cattle, metabolic imprinting, adipogenesis