538 Effect of the forage-to-concentrate ratio on DMI and ruminal fermentation based on timing of feeding relative to feed restriction. R. I. Albornoz*[1], J. R. Aschenbach[2], D. R. Barreda[3], and G. B. Penner[1], *[1]University of Saskatchewan, Saskatoon, SK, Canada, [2]Free University of Berlin, Berlin, Germany, [3]University of Alberta, Edmonton, AB, Canada.*

The objective of this study was to evaluate the interaction between the forage-to-concentrate ratio (F:C) of diets fed before (baseline) and during short-term feed restriction (FR; collectively denoted as PRE) and those fed post-feed restriction (POST) on DMI and rumen fermentation. Twenty ruminally cannulated heifers (477 ± 38 kg BW) were exposed to 14 d for adaptation followed by 5 experimental periods; 5-d baseline, 5-d FR, and 3 wk of recovery (R1, R2, and R3). Heifers were fed, ad libitum, a high forage diet (HF; F:C = 92:8) or a moderate forage diet (MF; F:C = 60:40) during baseline, and FR was imposed at 25% of ad libitum DMI. During recovery, one half of the HF and MF heifers remained on the same diet, and the other half were exposed to an abrupt switch (e.g., HF/HF, HF/MF, MF/HF, and MF/MF). PRE × period (P = 0.02) and POST × period (P = 0.04) interactions were detected for DMI. Although DMI, within periods, was not different for HF and MF, heifers fed HF PRE increased DMI from R1 to R3. Heifers fed HF POST had higher intake during R1 than heifers fed MF with no differences observed between diets within other periods. A PRE × POST × period interaction was detected for butyrate concentration (P = 0.01). Butyrate was higher for cows fed MF PRE than HF PRE. Butyrate concentration decreased from baseline to FR and returned to baseline values by R3; although the extent of the increase was greater for heifers fed HF PRE than MF PRE. PRE × period (P = 0.02) and POST × period (P < 0.01) interactions were detected for mean pH. For the PRE × period interaction, heifers fed HF had higher pH than those fed MF during baseline, but pH did not differ between diets during FR. Despite this, pH was higher during FR than baseline and decreased for all heifers during R1 with mean pH returning to baseline values by R2 for HF heifers. For the POST × period interaction, mean pH during R1 was lower for MF than HF, but no other differences were detected among treatments. This study indicates that feeding MF before, and HF after FR reduces risk for ruminal acidosis following FR.

Key Words: beef cattle, feed restriction, rumen fermentation

539 Rumen and cecum methane emissions between steers that are either negative or positive for residual gain. H. Freetly*, K. Hales, and J. Wells, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Cattle produce CH_4 in the rumen and the cecum, and it represents a loss of feed energy. A possible cause of variation in feed efficiency may be differences in capacity to produce CH_4. We hypothesized that cattle with a higher residual gain (RG) would have a decreased capacity to produce CH_4. 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 intake was measured using an Insentec RIC Feeding System (Insentec B.V., Marknesse, The Netherlands). The diet consisted of 82.75% rolled corn, 12.75% corn silage, and 4.5% Biegerts supplement (Bradshaw, NE; contains 0.066% monensin, 51% CP). On d 0, 1, 21, 42, 56, 62, and 63 BW was measured, and BW gain was calculated using the regression coefficient. 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 received the diet until they were slaughtered. One positive and negative RG steer were slaughtered at 12, 13, 14, 15, 19, 20, and 21 d after the end of the feeding period. At slaughter, rumen fluid was filtered and placed in a flask in a 39°C waterbath and allowed to settle. Samples were taken from the center layer. Cecum contents were placed directly into an incubation flask. For each sample site, 10 g of sample was anaerobically transferred to incubation bottles (110 mL) that contained 70 mL of buffer (4 replicates/steer). Bottles received 40 mL of hydrogen gas and were incubated in a 39°C shaking waterbath. Gas volume and CH_4 concentrations were determined at 2, 4, 6, and 8 h. Rate of CH_4 production was the average of replicate bottles within steer. Data were analyzed as a 2 × 2 factorial with sample site and RG as fixed effects. Methane production per unit DM ($mmol \cdot g^{-1} \cdot min^{-1}$) was greater in rumen 0.000510 ± 0.000051 than cecum 0.000036 ± 0.000051 samples (P < 0.001). Methane production did not differ between high and low RG (P = 0.98). Partially funded by NIFA Grant 2011-68004-30214 National Program for Genetic Improvement of Feed Efficiency in Beef Cattle. USDA is an equal opportunity provider and employer.

Key Words: cattle, methane

540 Evaluation of a complete-feed (RAMP) receiving diet. C. J. Schneider*[1], B. L. Nuttelman[1], W. A. Griffin[1], D. B. Burken[1], R. A. Stock[2], T. J. Klopfenstein[1], and G. E. Erickson[1], *[1]University of Nebraska-Lincoln, Lincoln, [2]Cargill Inc., Blair, NE.*

Two receiving trials were conducted in 2010 and 2011 to evaluate effects of feeding RAMP on cattle performance during the receiving period. Crossbred steers (yr 1: n = 642; BW = 264 ± 12.3 kg, yr 2: n = 758; BW = 257 ± 15.3 kg) were received over 2 consecutive d in 2010 and 2 d, one wk apart in 2011. Steers were blocked by arrival date and location within the feedlot yielding 2 blocks in yr 1 and 3 blocks in yr 2. Cattle were randomly allocated based on processing order to 34 pens in yr 1 and 44 pens in yr 2, within block, resulting in 15 to 20 cattle per pen. Treatments included a control receiving diet (CON;35% alfalfa hay, 30% sweet bran, 30% dry rolled corn, and 5% supplement, DM basis; 16.7% CP, 36.7% NDF) and RAMP (21.9% CP, 41.9% NDF), a complete feed (formulated and provided by Cargill Inc., Blair, NE) that contained a high level of sweet bran with a minimal amount of forage. All diets contained 27.6 mg/kg monensin and 26.5 mg/kg thiamine. Cattle were offered ad libitum access to treatment diets for 30 or 31 d in yr 1 and 21, 24, or 28 d in yr 2. Following the feeding period, cattle were limit-fed a common diet (47.5% sweet bran, 23.75% grass hay, 23.75 alfalfa hay, and 5% supplement, DM basis) for 5 d before to collecting final BW to minimize variation in gut fill. Final BW were averages of 2-d weights. There was a year × treatment interaction for ADG (P = 0.05) and DMI (P < 0.01). RAMP increased ADG (P < 0.01) compared with CON in yr 1 (1.63 and 1.47 kg, respectively), but in yr 2 ADG was not different (P = 0.93) at 1.59 kg for CON and 1.60 kg for RAMP. In yr 1 DMI were not different (P = 0.11) with 7.11 and 7.34 kg/d for CON and RAMP, respectively. However, in yr 2, DMI was different (P < 0.01) with 6.37 and 5.82 kg/d for CON and RAMP, respectively. Across both yr, RAMP increased (P < 0.01) G:F compared with CON (0.250 and 0.230, respectively). Incidence of BRD was not different (P = 0.27) for CON and RAMP across both years. Feeding RAMP improved G:F compared with feeding a traditional receiving diet.

Key Words: beef cattle, feedlot, receiving

541 Effects of RAMP on feed intake and ruminal pH during adaptation to finishing diets. C. J. Schneider*[1], A. L. Shreck[1], R. A. Stock[2], T. J. Klopfenstein[1], and Galen Erickson[1], *[1]University of Nebraska-Lincoln, Lincoln, [2]Cargill Inc., Blair, NE.*

A metabolism trial was conducted using 6 ruminally fistulated steer calves (BW = 255 ± 30 kg) to evaluate using RAMP, a complete feed provided by Cargill containing Sweet Bran and minimal forage, to adapt cattle to finishing diets. Steers were gradually adapted to finishing diets using 4 adaption diets followed by 7 d feeding a common finishing diet for a total of 5 periods consisting of 7 d each. Treatments were imposed during grain adaption using 2 programs. One treatment used RAMP by decreasing RAMP (100 to 0%) while increasing inclusion of the finishing diet (0 to 100%). For this treatment RAMP was mixed with the finishing ration and fed as a single diet. The control adaptation treatment (CON) contained (DM basis) 25% sweet bran, 5% supplement, with alfalfa hay inclusion decreasing from 45 to 7.5% while increasing a 60:40 blend of high-moisture corn and dry-rolled corn from 25 to 62.5%. All diets contained 27.6 mg/kg monensin and 26.5 mg/kg thiamine. Steers were offered ad libitum access to feed and water and fed once daily at 0800 h. Ruminal pH was recorded every min continuously for all 5 periods using wireless pH probes. Adapting cattle with RAMP increased DMI ($P < 0.01$) by 45% relative to CON in period 1 and by 25% in period 3 ($P = 0.04$). Intakes were not different during periods 2 and 4 ($P = 0.14$ and $P = 0.12$, respectively). RAMP adaptation tended to increase DMI ($P = 0.09$) compared with CON when cattle were fed the common finishing diet (6.05 and 7.35 kg for CON and RAMP, respectively). Maximum pH tended ($P = 0.07$) to be higher for CON compared with RAMP in period 2, but maximum pH was not different ($P > 0.28$) between treatments for other periods. Average ruminal pH, minimum pH, time below pH 5.6 and area below 5.6 were not affected ($P > 0.23$) by adaption method in any period. Adapting cattle with RAMP had no effect ($P > 0.11$) on magnitude of pH change or ruminal pH variance in any period. Adapting cattle to high-grain finishing diets using RAMP increased DMI but did not affect ruminal pH.

Key Words: beef cattle, grain adaptation, metabolism

542 Effect of maturity on the yield and in situ digestibility of whole-crop cereals. C. L. Rosser*[1], A. Beattie[1], H. C. Block[2], J. J. McKinnon[1], H. A. Lardner[1,3], and G. B. Penner[1], *[1]University of Saskatchewan, Saskatoon, SK, Canada, [2]Agriculture and Agri-Food Canada, Brandon, MB, Canada, [3]Western Beef Development Centre, Humbolt, SK, Canada.*

The objective of this study was to determine the optimal maturity at harvest for common whole-crop cereals used in swathgrazing systems in western Canada. Four replicate plots of barley (*Hordeum vulgare* L. 'CDC Cowboy'), millet (*Panicum milliaceum* 'Red Proso'), oat (*Avena* spp. 'CDC Weaver'), and wheat (*Triticum aestivum* L. '07FOR21') were grown. Subsections in each replicate were randomly assigned to 1 of 4 harvest maturities (cut at a 5-cm stubble height); head elongation, late milk to early dough, hard dough, and fully mature. At each stage of maturity, the wet and DM yields and chemical composition (DM, OM, NDF, crude fat, and NFC) were determined. Whole-crop samples were ground to pass through a 2-mm screen, weighed into nylon bags, and exposed to rumen incubation for 0, 2, 4, 8, 16, 24, 48 and 72 h. Rates of degradation were determined using a first-order kinetic model. Data were analyzed with stage of maturity as a fixed effect and plot as a random effect. For all crops evaluated, DM yield increased ($P < 0.001$) with advancing maturity. The concentration of CP, and NDF decreased ($P \leq 0.012$) while the concentrations of OM and NFC increased ($P < 0.001$) with advancing maturity for all crops investigated. Despite the large increase for DM yield, the yield of CP was not affected by advancing maturity for all crops except that it increased for wheat ($P < 0.001$), whereas, the yields of OM, NDF, NFC, and crude fat increased ($P < 0.023$) for all crop types. The DM degradation rate (%/h) was not affected by maturity, but the rate for NDF degradation decreased for millet and oat as plants matured ($P \leq 0.031$). However, the stage of maturity did not affect NDF degradation rate for barley or wheat. The yield of effectively degradable DM for barley ($P = 0.196$) was not affected by maturity, but increased for millet ($P = 0.016$), oat ($P = 0.004$), and wheat ($P < 0.001$) with advancing maturity. These findings suggest that harvesting whole-crop annual cereals at a mature stage may maximize the yield of effectively degradable DM.

Key Words: harvest maturity, in situ, swathgrazing

543 Rumen bacterial population responses to inclusion of wet distillers grains plus solubles in finishing diets of feedlot cattle. G. M. Shipp*[1], W. E. Pinchak[2], D. W. Pitta[3], B. Milligan[4], S. L. Ivey[4], and J. C. MacDonald[1], *[1]Texas AgriLife Research, Amarillo, [2]Texas AgriLife Research, Vernon, [3]Department of Clinical Studies, School of Veterinary Medicine, University of Pennsylvania, Kennett Square, [4]New Mexico State University, Las Cruces.*

A 6 × 6 Latin square with repeated measures design with dry rolled (DRC), steam flaked corn (SFC), and SFC with levels of wet distillers' grains plus solubles (WDGS) at 15%, 30%, 45% and 60%. Rumen samples collected at 0 and 4 h post feeding on d 21 of each period were strained into fluid and solid fractions (FRAC) and archived. Genomic DNA was extracted for amplification of V4 region of 16S rDNA gene and sequenced utilizing a Roche 454 FLX platform. Phylogenetic distribution of taxa, multivariate non-metric multidimensional scaling (NMDS) to compare community populations and Proc MIXED models were used to determine the influence of diet, time, FRAC and their interactions on rumen bacterial communities. Total sequences (1,747,630) were assigned to taxa. Different rumen bacterial communities developed in response to diet ($P < 0.05$) and FRAC within diet ($P < 0.01$) but not time ($P > 0.05$) and were readily differentiated utilizing NMDS at respective taxa level. The phyla *Firmicutes* dominated solid FRAC (up to 85%) while *Firmicutes* and *Proteobacteria* co-dominated (up to 95%) fluid FRAC. In contrast, *Bacteriodetes* constituted < 5% of all communities. Quantitative differences ($P < 0.05$) in *Firmicutes*, *Proteobacteria*, *Cyanobacteria*, and *Tenericutes* existed among diets. The family *Lachnospiracea* dominated the solid FRAC and decreased with WDGS inclusion. In contrast, *Rumincocacceae*, increased with all levels of WDGS. *Veillonellaceae*, exhibited a quadratic ($P < 0.05$) response by decreasing above 30% WSDGS. Genera *Eubacterium*, *Schwartzia*, and *Acidaminococcus* were dominant at ≥30% WDGS compared with DRC, SFC and 15% WDGS diets. *Paralactobacillus*, *Slackia*, and *Desulfovermiculus* were unique to WDGS diets and associate to specific functions. In summary, decreased animal performance observed with increasing WDGS inclusion in SFC diets supports our tenant that the rumen microbiome plays a key role in production efficiency of feedlot cattle.

Key Words: cattle, microbial ecology, rumen microbiology

544 Effect of sugarcane fiber digestibility and mode of conservation on intake and rumen pH of growing Nellore steers. D. O. Souza, B. S. Mesquita, J. Diniz-Magalhães, F. D. Rodriguez, B. S. Marques, and L. F. P. Silva,* *Universidade de São Paulo, Pirassununga, SP, Brazil.*

Sugarcane attains maturity and is available for daily harvest during the dry season; however, ensiling is an effective option for reducing labor costs. The objective of this study was to evaluate the effects of sugarcane

stalk fiber digestibility (NDFD), and of mode of conservation on intake and rumen pH. Eight ruminally cannulated Nellore steers (275 ± 20 kg BW) were used in a replicated 4 × 4 Latin square design. Two sugarcane genotypes with differing NDFD were used: IAC2480 with higher NDFD (15% 30-h NDF digestibility), and IAC2094 with lower NDFD (6.5% 30h-NDF digestibility). Treatment diets contained 40% sugarcane, of total DM, as sole roughage source given as freshly chopped, or as silage, to evaluate the possible interaction between NDFD and mode of conservation on DM intake. Diets were formulated to provide daily gain of 1.2 kg/d. Animals were housed individually in a tie-stall with free access to water and fed ad libitum with 10% orts. Periods lasted for 14d, being 10d for adaptation, and 4d for sample collection. DM intake was determined on d 10, 11 and 12, and rumen pH on d 14 at 6 time points: 0, 1, 3, 6, 9 and 12h after the morning feeding. Main effects of sugarcane genotypes (CANE), of mode of conservation (CONS), and their interaction were tested by ANOVA. Feeding sugarcane with higher NDFD increased DM intake (5.7 vs. 5.1 ± 0.5 kg/d, $P < 0.01$), however the interaction CANE x CONS was significant ($P = 0.04$). The effect of greater NDFD on DM intake was only significant when feeding sugarcane as silage ($P < 0.01$), having no effect on DM intake when sugarcane was offered and freshly cut ($P = 0.53$). The mode of conservation did not affect DM intake ($P > 0.05$). Regarding rumen pH, there was no effect of CANE, nor there was a CANE × CONS interaction ($P > 0.30$). Feeding sugarcane as silage, as opposed to freshly cut, increased mean rumen pH (6.69 vs. 6.37 ± 0.08, $P < 0.01$). There was a clear reduction of pH during the day ($P < 0.01$), but there was no effect of TIME x CONS on rumen pH ($P = 0.23$). We conclude that sugarcane silage with higher NDFD increased DM intake, and feeding silage as opposed to freshly cut increased rumen pH.

Key Words: cattle, NDF digestibility, sugarcane silage

545 Impact of diet on the abundance and diversity of fecal *Escherichia coli* shed from cattle in overwintering environments. K. Christiuk,* D. O. Krause, K. Ominski, T. De Kievit, and E. Khafipour, *University of Manitoba, Winnipeg, Manitoba, Canada.*

The objective of this study was to determine the effect of diet and overwintering strategy on *E. coli* populations in beef cattle during 2, 21-d periods. Sixty beef cows were assigned to 3, replicated feeding strategies, each with 10 cows. Four groups of cows were fed using a bale-grazing strategy while the other 4 groups of cows were fed in dry lot pens. During period 1, 2 pens in the bale graze system received grass hay supplemented with DDGS (dried distiller's grains with solubles; 2.5 kg/cow every third day) while the remaining 4 pens received grass hay only. During period 2, the DDGS supplemented cows remained on the same diet while the other 4 pens received 1 kg/cow/day of barley. Three cows in each pen were randomly selected and individual fecal samples were collected and cultured on selective media (Eosin Methylene Blue Agar). Colonies of *E. coli* were counted and 3 isolates were selected for DNA extraction. Isolates were subjected to PCR in search of 18 selected genes encoding for a range of virulence factors, including adhesins, aggregation factors, toxins, pathogenicity islands, autotransporters, and capsule synthesis. There were no significant differences in *E. coli* numbers between the treatments ($\alpha = 0.05$; P-value = 0.06) but the highest number of *E. coli* were isolated from bale grazed cows receiving barley (6.71 log cfu/g) and the lowest number were from bale grazed DDGS cows (5.78 log cfu/g). Comparison of the virulence genes present in the *E. coli* isolates resulted in a significant difference in *cnf* (cytotoxic necrotizing factor; induces prominent stress fiber formation and increase adherence to epithelia) between treatments ($\alpha = 0.05$; P-value < 0.001). Contrast analysis of the virulence data by diet resulted in significant differences in the presence of *aidA* (adhesion involved in diffuse adherence), *fliC* (flagellan structural gene), and *cnf*. The data suggests that diet may affect the abundance of *E. coli* shed in the feces and increase the presence of *E. coli* harbouring particular virulence genes that mediates adhesion of the bacterium to the epithelial surfaces.

Key Words: *Escherichia coli*, dried distillers grains with solubles, virulence genes

546 Comparison of different supplemental cobalt forms on fiber digestion and cobalamin levels. W. L. Kelly*[1], C. K. Larson[2], M. K. Petersen[1], and R. C. Waterman[1], *[1]USDA-ARS, Fort Keogh Livestock and Range Research Laboratory, Miles City, MT, [2]Zinpro Corporation, Eden Prairie, MN.*

Cobalt (Co) is essential for rumen microbial metabolism to synthesize methane, acetate and methionine. It also serves as a structural component of vitamin B_{12}, which functions as a coenzyme in energy metabolism. A study was conducted to determine if Co form (cobalt carbonate vs. cobalt glucoheptonate) supplemented above NRC requirements would improve fermentability of a low quality forage diet and change serum cobalamin concentrations. Twenty ruminally-cannulated cows (577 ± 13 kg) were individually fed in a completely randomized experimental design. Cows were fed a grass hay diet (7.9% CP, 56% TDN, 63% NDF, 87% DM) at 2.25% of BW for a 62 d study, which consisted of 3 periods: acclimation (AC), treatment (TR), and residual (RE). Cows were stratified by age (5 ± 0.37 yr) and lactational history, and assigned to receive 12.5 mg supplemental Co in 1 of 2 forms: (1) 27.2 mg of cobalt carbonate (CC, n =11 cows) or (2) 50 mg of cobalt glucoheptonate (CGH, n = 9 cows). Supplementation was administered daily via a gelatin capsule placed directly into the rumen 2 h after daily feeding. During the last 96 h of each period, forage fermentability was measured using an in situ nylon bag technique. Serum samples were collected 4 and 6 h following feeding, 24 h before the end of each period. Measurements taken in the AC period were used as covariates for analysis in the TR and RE periods. A treatment × period interaction ($P = 0.03$) was exhibited for in situ OM fermentability at 96 h; (TR period, 68.44 and 70.83 ± 0.81%, and RE period, 67.61 and 66.82 ± 0.75%, for CC and CGH; respectively). Once inclusion of Co in the CGH group was removed, fermentability was reduced by 4.01% compared with 0.82% in the CC cows. The NDF disappearance (OM basis) was lower for the TR period compared to the RE period at 48 h ($P < 0.001$; 62.95 and 65.18 ± 0.39%; respectively). However, by 96 h the NDF disappearance was higher for TR period than the RE period ($P = 0.02$; 70.44 and 68.89 ± 0.44%; respectively). No differences were detected for cobalamin serum levels or rate of fiber fermentation. The outcomes of this research signify that while there are no residual effects of Co supplementation on fermentation, there is an indication that Co glucoheptonate supplementation does enhance the overall extent of fermentation. The extent of fiber disappearance is also improved with Co supplementation regardless of form.

Key Words: beef cattle, cobalt, vitamin B12

547 Comparison of animal and dietary effects on ruminal methanogens and their association with protozoa in beef cattle. M. Zhou*[1], M. Hünerberg[1], K. A. Beauchemin[2], T. A. McAllister[2], E. K. Okine[1], and L. L. Guan[1], *[1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada, [2]Agriculture and Agri-Food Canada Lethbridge Research Centre, Lethbridge, Alberta, Canada.*

This study investigated the effects of animal (host) and diet on the variation in ruminal methanogenic communities of 4 beef heifers

sequentially adapted to corn- (CDDGS), wheat-based (WDDGS) dried distillers grain with solubles (DDGS), and WDDGS plus pure corn oil. The methanogenic diversity was examined using PCR-denaturing gradient gel electrophoresis (PCR-DGGE) and methanogen abundance was measured quantitative real-time PCR (qRT-PCR). The methanogen DGGE profiles were analyzed using BioNumerics software and Global R statistics. Methanogen abundance was compared host-wise and diet-wise using Analysis of Variation (ANOVA) and the correlation between methanogens and protozoa was analyzed using PROC CORR within SAS. Observed DGGE patterns of methanogens were similar among the 4 diets but distinctive within each individual animal (Global R = 0.87, $P < 0.01$). Methanogenic phylotypes displayed unique responses to the different sources of DDGS, and the ecological shifts were host-specific. Populations of methanogens and protozoa varied among animals and diets, while densities of *Methanobrevibacter* sp. AbM4 and *Methanosphaera stadtmanae* only differed among animals. The diversity and abundance of methanogenic community adapted to different diets uniquely within individuals. In addition, *Mbb.* sp. AbM4 and total number of protozoa ($P < 0.01$) were positively correlated within animal. In conclusion, the response of ruminal methanogenic community to different diets was host dependent, suggesting that the host biology should not be ignored if dietary strategies are used to manipulate ruminal methanogens.

Key Words: diet effect, host effect, methanogenic ecology

548 Withdrawn by author

549 Assessing how RFI classification in the growing phase predicts RFI classification in the finishing phase. D. Johns,* G. Vander Voort, C. Campbell, M. Quinton, and I. Mandell, *Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada.*

Residual feed intake (RFI) is being used to replace feed efficiency due to its accuracy in determining production efficiency. The objective of this study was to examine whether assessment of production efficiency via RFI in the growing phase (GP) accurately predicts production efficiency in the finishing phase (FP). RFI was calculated at the end of an 84 d GP for 204 crossbred steers. Steers were then allocated to one of 5 finishing management regimens (based on an 87% concentrate diet) designed to produce a wide range in growth performance (average daily gain (ADG), feed:gain (F:G), RFI) and carcass traits. Management regimens included a nonimplanted control (CON), Synovex implant (SYN), Revalor implant (REV), REV plus the β agonist (βA), Optaflexx (OPT), and REV plus the βA, Zilmax (ZIL). The allocation evenly distributed Low (RFI^-) and High (RFI^+) cattle from the GP across all finishing management regimens. Post-slaughter, RFI was calculated for the FP and the overall trial to examine how GP RFI classification predicted performance in the FP. FP ADG ranged from 1.60 (CON) to 2.23 (REV/ZIL) kg/d; F:G ranged from 7.17 (CON) to 5.61 (REV/ZIL). Over the entire trial ADG ranged from 1.72 (CON) to 1.94 (REV/ZIL) kg/d; F:G ranged from 6.37 (CON) to 5.68 (REV/ZIL). RFI ranged from −0.61 to 1.60 in the GP, −2.20 to 2.49 in the FP and −3.15 to 3.61 for the trial overall. The lowest overall and FP RFI was found in ZIL (−0.14 and −0.25 respectively), indicating the most efficient conversion of feed to gain. Overall RFI was improved in all management regimens using REV, with increased efficiency vs. GP RFI. There was limited improvement in efficiency for CON and SYN cattle between GP and FP RFI. For 14.4% of steers, RFI ranking changed from RFI^+ rank in the GP to RFI^- in the FP, becoming more efficient; 19.4% of steers became less efficient while 66.3% kept the same RFI ranking. RFI classification in the GP did not accurately predict RFI classification in the FP for all cattle. More work is needed to examine when RFI should be determined for predicting finishing performance.

Key Words: beef cattle, RFI, growth performance