

Ruminant Nutrition: Beef: Feed Additives

W250 Live yeast and adaptation protocols on finishing feedlot Nellore cattle fed high concentrate diets. P. L. Alvarez,* S. L. Silva, L. S. Martello, M. R. Mazon, L. S. Oliveira, P. H. Cancian, A. C. Ianni, L. Z. Zandoni, R. F. Carvalho, A. P. S. Silva, and P. R. Leme, *Universidade de São Paulo, Faculdade de Zootecnia e Engenharia de Alimentos, Pirassununga, SP, Brazil.*

Adaptation period on feedlots is a critical step for rumen stability. Inclusion of live yeast on high concentrate diets has been reported to be an alternative to reduce nutritional disorders such as acidosis and ruminitis on beef cattle. The aim of this work was to evaluate the performance and carcass traits of finishing feedlot Nellore (*Bos indicus*) cattle fed high concentrate diets with (LY) or without (CON) live yeast under 2 different adaptation protocols. Forty-8 Nellore bulls (24 intact and 24 castrated) (372 ± 22.5 kg BW; 20-mo) were distributed in individual pens in a randomized block (initial BW) and fed LY or CON diets. Diets were composed by 85% of concentrate (corn grain, corn gluten, soybean meal, mineral salt and monensin) and 15% of sugarcane bagasse as roughage source. Animals were adapted to final diets using step-up (ST) or feed intake restriction (FR) methods. The ST group started with 30% of concentrate increasing 15% each 2 d until it reached 85% while the FR group started with 4.5 kg of final diet increasing one kg each 2 d. Both groups achieved the final diets after 10 d. After that, animals were fed for 56 d with LY or CON diets. Feed and orts were registered daily for DMI and F:G determinations. Animals were weighed at the beginning and at the end of adaptation period and then every 28 d. Ultrasound measurements of LM area (LMA) and backfat thickness (BFT) between 12th/13th ribs were collected every 28 d intervals. Fixed effects of initial BW (block), adaptation protocol, treatment and adaptation protocol x treatment interaction were evaluated using GLM procedure of SAS system. No interactions were observed for any trait. There was no effect of treatment on ADG and DMI on adaptation period. Animals fed FR protocol had higher ADG (1.121 vs 0.580 kg/day; $P = 0.0417$) and F:G (0.158 vs 0.085 kg ADG / kg DMI; $P = 0.0599$) than those fed ST but they did not differ for BW (379 kg) and DMI (6.6 kg). After adaptation period final BW (497 kg), ADG (1.72 kg), DMI (12.2 kg), F:G (0.143 kg ADG/kg DMI) LMA (76.1 cm²) and BFT (4.1 mm) were not affected by treatments or adaptation protocols. Use of FR protocol improves performance on adaptation period but has no effect on post-adaptation period. LY does not affect feedlot performance.

Key Words: beef cattle, performance, probiotics

W251 Effect of slow release urea supplementation during the dry season on Nellore cattle performance in Brazil. D. P. Pantoni*¹, D. S. Graça¹, M. H. Ramos², and P. C. Molina¹, ¹Federal University of Minas Gerais, Belo Horizonte, Minas Gerais, Brazil, ²Research Institute Flávio Guarani - Rehagro, Belo Horizonte, Minas Gerais, Brazil.

This study was developed to synchronize the release of nitrogen from supplement with carbohydrate from pasture. Forty Nellore bulls (average weight 446 kg \pm 24.6) were allowed to graze pastures of *Brachiaria brizantha* 'Marandu' during the dry season (June to September of 2010). Pastures were divided into 3 paddocks of 10 ha each with water and mineral ad libitum and managed in a rotation system. Dry matter availability averaged 5,200 kg of DM/hectare. Forage quality average 6% for CP, 69% for NDF and 51% for IVDMD. Treatments were: only mineral (T1), supplement containing 6% Urea (T2), supplement containing 3% Urea and 3% of slow release Urea (T3), supplement containing

6% of slow release Urea (T4). All supplements contained 15% soybean meal, 67% ground corn and 12% mineral with 200 mg of monensin. Pasture intake was measured using lignin as an internal marker. Cattle was brought together every day, divided by their treatments into pens, and allowed to eat the supplement (average of 1 kg/animal). Statistical analysis was performed using PROC MIXED of SAS (SAS Institute, Cary, NC) with treatment as the experimental unit for performance and animal as the experimental unit for nitrogen variables. There was no difference ($P > 0.05$) in forage consumption expressed as a percentage of BW (2.3, 2.1, 2.2, and 2.1; respectively for T1, T2, T3, and T4). There was no difference ($P > 0.05$) in ADG (316, 327, and 286 kg/d for T2, T3, and T4, respectively) and total gain (22, 23, and 20 kg, for T2, T3, and T4 respectively) between the urea treatments. Blood urea nitrogen (mg/dL) was not different ($P > 0.05$) between T2, T3, and T4. Allantoin (microbial marker) was not different ($P > 0.05$) between treatments (250, 327, 349, and 351 mg/dL, respectively for T1, T2, T3, and T4). Internal rate of return was greater for T2 followed by T3, T4, and finally T1 (19, 17, 10, and -2%, respectively). We concluded that slow release urea did not provide any benefit over conventional urea when Nellore bulls were offered low quality pastures.

Key Words: urea, braquiaria, cattle

W252 Intake, digestibility and digestion kinetics of beef steers supplemented with slow-release urea in diets with two concentrate levels. P. D. B. Benedeti, P. V. R. Paulino,* T. S. Martins, E. F. Lisboa, L. H. P. Silva, C. R. V. Teixeira, L. C. Alves, M. S. Duarte, R. Mezzomo, J. C. M. Lima, J. P. I. S. Monnerat, M. I. Marcondes, and S. C. Valadares Filho, *Universidade Federal de Viçosa, Viçosa, MG, Brazil.*

This study evaluated the effects of replacing soybean meal (SBM) by slow-release urea (SRU) in beef cattle diets containing 2 concentrate levels on intake, partial and total digestibility and digestion kinetics in finishing beef steers. Eight crossbred steers were used (average BW of 418 kg) fitted with ruminal and abomasal cannulas. Total fecal collections were performed to determine digestibility and rumen evacuation was used to determine passage and digestion rates. The animals were distributed in 2 groups of 4 steers, when each group received one of the 2 levels of concentrate (40 or 80% of the total DM). The experiment was designed as a Latin square in 2 x 4 factorial scheme, with 2 concentrate levels in the diet, and within each square, 4 levels of SBM protein replacement by SRU: 0, 33, 66 and 100%. The interaction of concentrate level x SRU levels was not significant ($P > 0.05$) for any variable measured. Dry matter (DM) intake, as well as organic matter (OM) intake and crude protein (CP) intake decreased linearly ($P < 0.05$) as SBM was replaced by SRU. For each percentage unit of SRU added to the diet there was a reduction of 5.80, 5.17 and 0.58 g in DMI, OMI and CPI, respectively. The intake of non-fiber carbohydrates (NFC) was higher ($P < 0.05$) in the diet containing 80% concentrate when compared with the 40% concentrate diet, whereas neutral detergent fiber (NDF) intake was greater ($P < 0.05$) on the low concentrate diet when compared with the high concentrate diet. Ruminal digestibility coefficient of OM tended to be greater ($P < 0.074$) for the 40% concentrate diet, whereas all other ruminal, intestinal and total digestibility parameters evaluated were not statistically different ($P > 0.05$) among treatments. DM and OM passage rates (K_p) were greater ($P < 0.05$) on the 80% concentrate diet than on the 40% concentrate diet. Replacing SBM by SRU up to 100% on the diet did not lead to any modification ($P > 0.05$) on DM, OM, CP and NDF passage rate. Digestion rates (K_d) were also not affected by

either concentrate level or SRU level ($P > 0.05$). The average K_d for DM, OM, CP and NDF were 3.82, 4.21, 1.13, and 2.20%/h, respectively.

Key Words: soybean meal, nonprotein nitrogen, feedlot

W253 Dose response effects of laidlomycin propionate plus chlortetracycline or monensin plus tylosin on growth performance, carcass merit and health of growing-finishing beef steers. M. E. Branine^{*1}, M. E. Hubbert², M. L. Galyean³, and B. D. Hunsaker⁴, ¹Pfizer Animal Health, Canon City, CO, ²New Mexico State University, Clayton, ³Texas Tech University, Lubbock, ⁴Summit Research LLC, Wellington, CO.

Doses of laidlomycin propionate plus chlortetracycline (LP/CTC) or monensin plus tylosin (M/T) were evaluated in an experiment with growing-finishing steers. No ionophore, low, moderate, and high levels of LP (50, 100 and 150 mg/animal per day) and M (150, 300 and 450 mg/animal per day), respectively were compared. Chlortetracycline (350 mg/animal per day) or T (90 mg/animal per day) were fed in combination with LP or M, respectively. Four-hundred 20 steers (average initial wt. 357 kg) were randomized by initial BW to 6 blocks (7 pens/block). Steers were on feed for 153 d (3 heavy weight blocks) or 175 d (3 lightweight blocks) at a commercial feedlot facility before slaughter. Ionophores, CTC, and T were added to a non-medicated basal diet using a micro-ingredient allocation machine. Linear (L) and quadratic (Q) effects of ionophore dose were evaluated for growth performance and carcass measurements. Carcass-adjusted final BW, ADG, and hot carcass weights indicated a Q increase ($P \leq 0.05$) with dietary LP level. Dry matter intake and carcass-adjusted DM feed:gain ratio were not affected by LP dose. Neither L nor Q responses were observed for M level on DMI, carcass-adjusted BW, growth performance, or DM feed:gain ratio. Hot carcass weight was not affected by M level. Increasing M level increased number of Prime/Choice carcasses (L and Q); increased marbling score (L and Q); twelfth rib fat thickness (Q); and calculated yield grade (Q). Incidence and severity of liver abscesses were not affected by ionophore type or level. Morbidity and mortality rates from respiratory disease were minimal across treatments. Across dose levels, mean ionophore effects indicated LP increased ($P \leq 0.05$) carcass-adjusted final BW, ADG, DMI and hot carcass weight compared with M, with no difference between ionophores for carcass-adjusted DM feed:gain ratio. Growth performance responses of feedlot cattle may be modified by medicated feed additive program and dietary level of ionophore.

Key Words: ionophore level, laidlomycin propionate, monensin

W254 Adipose gene expression patterns in finishing steers fed steam-flaked corn diets supplemented with dietary *Aspergillus oryzae* extract containing α -amylase activity. D. E. Graunard^{*1}, K. M. Brennan¹, J. S. Jennings¹, and J. J. Wagner², ¹Alltech Center for Animal Nutrigenomics and Applied Animal Nutrition, Nicholasville, KY, ²Southeast Colorado Research Center, Colorado State University, Lamar.

We evaluated the effect of dietary *Aspergillus oryzae* extract on lipogenic gene expression in finishing beef cattle. Cross-bred yearling steers were randomly assigned to 2 groups (n = 135/treatment). From receiving until d21, starter and step-up diets were fed to acclimate steers to steam-flaked corn. Steers were then fed a finishing diet ad libitum until harvest that met or exceeded NRC requirements: basal diet with or without 5 g/hd/d *A. oryzae* extract (Amaize, Alltech Inc.) containing α -amylase (AMZ). On d70 and at harvest (d160), adipose tissue was sampled from one steer per pen (n = 15/treatment). Gene expression was profiled using

the Affymetrix Bovine Genome Array. Of the 24,000 probe sets on the array, ~60% were expressed in subcutaneous adipose tissue. At d70, 270 genes were affected ($P \leq 0.05$, fold-change ≥ 1.1 ; 124 upregulated, 146 downregulated) and at d160, 399 genes were affected (176 upregulated, 223 downregulated) by AMZ. At both times the main functions affected were lipid metabolism, cellular development and cell-to-cell signaling/interaction. Gene classification based on gene ontology (GO) using the PANTHER database revealed the most affected GO term was metabolic processes (d70, 90 affected genes; d160, 149 affected genes). Analysis of individually affected genes showed a 1.42-fold ($P = 0.04$) increase in AMZ steers at d70 of peroxisome proliferator-activated receptor gamma coactivator 1 α mRNA, a key gene in fat and energy metabolism. Results suggest AMZ added to a steam-flaked corn finishing diet affects expression of genes involved in metabolism, growth and cellular development in steer adipose tissue. These results offer genomic support to previous findings that AMZ supplementation results in improved performance and carcass characteristics in finishing steers.

Key Words: amylase, beef, gene expression

W255 Effect of *Saccharomyces cerevisiae* CNCM I-1077 supplementation on zootechnical performances and feeding behavior of dairy bull calves during growing period. C. Loncke¹, L. Van Nespen¹, C. Launay¹, E. Sulmont¹, L. Dussert^{*2}, and V. Demey², ¹INZO, Chierry, France, ²Lallemand SAS, Blagnac, France.

The aim of this study was to evaluate the effectiveness of supplementation with *Saccharomyces cerevisiae* CNCM I-1077 (SC) in the diet of the growing period of dairy bull calves. Sixteen Montbéliarde calves aged 6 mo and weighing on average 251 ± 22 kg at the beginning of the adaptation period were used. The trial was preceded by 28 d of adaptation during which the animals all received the same ration composed of corn silage and 2.5 to 3 kg of concentrate. During the trial's experimental phase, the animals were fed either with control diet (C), or an experimental diet supplemented with SC (5×10^9 cfu/kg feed). Both groups received corn silage as forage. Animals were fed according to the following program: 1 kg concentrate /100 kg BW and 1 kg DM forage /100 kg BW. The animals were placed in a Roughage Intake Control system (RIC) (8 animals per box, 4 animals per trough), which allowed to record individual feed intake as well as feeding behavior. The experimental period lasted for 56 d. The animals were weighed every 28 d and individual consumption was recorded. The results show that the supplementation with live yeast SC positively influenced the animals ADG compared with C (2.05 ± 0.09 kg/d vs 1.80 ± 0.28 kg/d; $P \leq 0.05$). Moreover, the homogeneity of growth was increased in the SC group. Consumption of feed was higher in the SC group (8.01 ± 0.73 kg DM/head per day vs 7.48 ± 0.49 kg DM/head per day; $P \leq 0.1$). The feed conversion ratio was enhanced by the SC in the diet (3.92 ± 0.35 kg DM/kg live weight for SC vs 4.22 ± 0.43 kg DM/kg live weight for C; $P \leq 0.1$). The SC supplemented animals also showed a different feeding behavior (higher number of visits to the RIC, shorter feeding time per visit and lower quantity ingested per visit; $P \leq 0.05$). This trial shows that the incorporation of live yeast SC stimulates the consumption of dairy bull calves, involving thus a higher weight gain of these animals. The inclusion of SC also reduces the heterogeneity of growth of young bulls during the early stage of fattening.

Key Words: fattening beef, *Saccharomyces cerevisiae* CNCM I-1077

W256 Effects of medicinal feed additive (MFA) program fed with varying levels of wet distillers grains (WDGS) on growth performance, carcass characteristics and health of growing / finishing beef steers. M. E. Branine^{*1}, M. E. Hubbert², and B. D. Hunsaker³, ¹Pfizer Animal Health, Canon City, CO, ²New Mexico State University, Clayton, ³Summit Research LLC, Wellington, CO.

Dose level effects of wet corn distillers grains (WDGS) and medicinal feed additive (MFA) program were evaluated. Three hundred twenty yearling steers (average initial weight 320 kg) were randomized in a 2 × 4 factorial arrangement (4 blocks / treatment) with main effects of MFA program consisting of laidlomycin propionate (LP; 11.1 g/DM ton) plus chlortetracycline (350 mg/animal per day; CTC) or monensin (M; 28 g/ton DM) plus tylosin (T; 90 mg/animal per day) and 0, 15, 30 and 45% dietary (DM basis) inclusion level of WDGS. A single source of WDGS was used throughout the study with cattle fed once daily. Cattle were on feed for a total of 179 d before being shipped to a commercial plant for slaughter where carcass and liver abscess data were collected. MFA × WDGS interactions were not observed for any growth, health, or carcass parameter. Growth rate between MFA programs did not differ ($P \geq 0.05$); however, DM intake tended to be greater ($P \leq 0.10$) for LP/CTC and feed efficiency improved ($P \leq 0.05$) by M/T. Carcass measurements and liver abscess incidence were not affected ($P \geq 0.05$) by MFA program. Linear ($P \leq 0.01$) and cubic effects ($P \leq 0.06$) of dietary WDGS were present for bodyweight, growth rate and carcass weight with 15% WDGS having greater response than the 0% diet and 30 and 45% WDGS. Feed efficiency and DM intake were not affected by WDGS level. Marbling score was linearly decreased with increased WDGS level. Overall health was not affected by MFA program; however, apparent morbidity from respiratory disease, while low, was increased ($P \leq 0.05$) with higher WDGS levels. Overall morbidity at the 30 and 45% WDGS levels was increased ($P \leq 0.01$) compared with 0 and 15% inclusion levels, with no differences among WDGS levels for mortality. Alternative MFA programs may have application in feedlot diets containing varying levels of WDGS

Key Words: Ionophore, laidlomycin propionate, wet distillers grains

W257 Basal diet affects ruminal in situ degradation rate of urea and Optigen II in steers. V. B. Holder^{*1}, J. S. Jennings², and J. M. Tricarico³, ¹University of Kentucky, Lexington, ²Alltech, Brookings, SD, ³Innovation Center for U.S. Dairy, Rosemont, IL.

The objective of this study was to determine whether basal diet would have an effect on the ruminal degradation of urea and a slow release urea product (Optigen II). The basal diets were 30% vs. 100% forage. The 30% forage diet was offered at 2.4% of BW and was based on fescue hay, cracked corn, cottonseed hulls, soybean meal and urea. The 100% forage diet was offered ad libitum and consisted of fescue hay plus a vitamin and mineral supplement. Intake of the 100% forage diet was approximately 2.2% of BW. Steers were fed once daily at 7am. Four Angus steers (BW = 311 kg) were used in a crossover design with 3 weeks of adaptation to diets before each in situ experiment. Experiments were conducted independently for urea and Optigen II respectively. Triplicate 10-g samples of Optigen II and urea in 5 × 10 cm polyester bags were sequentially inserted into the rumen before simultaneous removal to achieve various incubation times. Incubation times were 0, 5, 10, 15, 20, 30, 40, 50 and 60 min for urea and 0, 1, 2, 6, 10 and 24 h for Optigen II. In situ residues were processed by flash freezing in liquid N then subsequently dissolving residues in a known amount of 1 M HCl. Resulting solutions were incubated at 100°C for 25 min to ensure total dissolution of urea. The determination of urea concentration of the solutions allowed direct quantification of urea disappearance from

both sources. Urea disappearance reached a maximum (100%) by 10 min of incubation. Urea disappearance was higher on the 100% forage diet than the 30% forage diet at 5 min (95.3 vs. 77.5%, $P < 0.05$). Urea disappearance from Optigen II was higher on the 100% forage diet than the 30% forage diet for all time points from 2 h onwards ($P = 0.0005$) and the difference was maximum at 24 h (78 vs. 87%, $P < 0.05$). These data demonstrate that diet does affect the degradation characteristics of protected urea. Forage:concentrate affects ruminal pH, passage, viscosity, and lipase and urease activities all of which may contribute to the observed differences.

Key Words: forage:concentrate, NPN, ruminant

W258 Effect of feeding chelated forms of Zn, Cu, and Mn in combination with methionine on growth and reproductive development of heifers. R. Harvey^{*1}, Y. Wang², G. I. Zanton², T. J. Wistuba², and M. S. Kerley¹, ¹University of Missouri, Columbia, ²Novus International Inc., St. Charles, MO.

Heifer production across most of the US is based upon forage-dominant diets. Methionine is typically the first-limiting amino acid in a forage-based diet. Forages can also vary widely in mineral composition, often being deficient relative to the animal's micromineral requirement. Therefore, the objective of this study was to determine the effect of 2-hydroxyl-4-methyl-thio butanoic acid (HMTBA; MFP) and/or organic trace mineral in the form of Zn, Cu, and Mn (HMTBA; Mintrex), Novus International) supplied to a forage-fed diet on growth and reproductive characteristics of developing heifers. The experiment was carried out in a 2 × 2 factorial design plus negative control. The treatments consist of Negative Control (NEG)- heifers were fed diet without additional Zn, Cu, Mn and MFP supplement; ITM- heifers were fed inorganic Zn, Cu, and Mn (30, 10, 20 mg/kg respectively); ITM + MFP- Supplemental MFP at 15 g/d with inorganic Zn, Cu, and Mn (30, 10, 20 mg/kg respectively); CTM- No MFP- Supplemental Mintrex to supply Zn, Cu, and Mn (30, 10, 20 mg/kg respectively); CTM + MFP- Supplemental Mintrex at levels delivered in Mintrex treatment, MFP was given at 15 g/d. Sixty purchased, weaned and prepubertal heifers were used in this experiment (252.3 ± 23.3 kg). Data were analyzed as a completely randomized design with repeated measurements using MIXED procedure of SAS. There was no significant treatment effect on DMI, ADG, and RTS ($P > 0.05$). Heifers fed MFP had a tendency for higher gain efficiency ($P = 0.10$), compared with no MFPTM heifers. A trend for a mineral by MFP interaction was observed ($P = 0.06$) in serum antibody titer after 4 weeks of vaccination. The combination of CTM and MFP had the greatest serum antibody titers ($P < 0.05$), and CTM, and ITM+MFP treatments had the least. Therefore, supplementation of HMTBA and chelated minerals was effective at improving efficiency and health responsiveness of developing heifers.

Key Words: heifer development, methionine, microminerals

W259 The effect of combination of metal amino acid chelates, Se yeast, mannaoligosaccharides, and dietary antioxidants on the health and growth performance of high-risk calves. T. J. Wistuba^{*1}, G. I. Zanton¹, D. Nuzback¹, M. Andersen¹, and E. Larsen², ¹Novus International Inc., St. Charles, MO, ²Larsen Nutritional Solutions, Fowler, CO.

Calves that are new to the feedyard are often exposed to numerous stressors (weaning, transportation, commingling, dietary restriction, etc.) that cause oxidative stress and compromise health and performance. Cu, Mn and Zn play a role in superoxide dismutase activity and Se in

glutathione peroxidase activity. Dietary antioxidants have been shown to improve overall anti-oxidant status, and mannanoligosaccharides improve the body's natural defense mechanisms. Therefore, the objective of this study was to evaluate the effects of feeding the combination of trace minerals chelated to glycine (MAAC-Zn, -Cu and -Mn), Se yeast (Zorien) dietary antioxidant (Agrado Plus), and mannanoligosaccharide (Zorien MOS) on growth performance, feed efficiency, and health in receiving calves. The study utilized 955 calves (742 steers and 213 bulls) that were obtained from 2 order buyers through sale barns in SE OK and SE TX with an average initial body wt of 233.6 ± 0.4 kg. The dietary supplements (Control or Treatment) were formulated to contain the same amount of supplemental Zn (320 mg), Cu (120 mg), Mn (200 mg), and Se (0.6 mg) from either organic or inorganic sources. In addition, calves consuming the Treatment supplement were fed 2 g/hd/d Agrado Plus and 20 g/hd/day Zorien MOS. After initial processing, calves were blocked by truckload (1–12), origin (TX vs OK), sex (bull vs steer), and individual body wt (light to heavy). No differences ($P > 0.14$) in body wt, gain, intake, or feed conversion were detected during the 42 d receiving period between Control and Treatment supplement calves. Calves were highly stressed as evidenced by the high morbidity (68% treated at least once). No differences ($P > 0.27$) between treatments were detected for morbidity, days between re-pulls, medicine cost, realizers, or total out. However, approximately 50% less ($P = 0.05$) calves died when fed the Treatment (1.04%) compared with the Control (2.09%). Therefore, the combination of organic trace minerals, dietary antioxidants and mannanoligosaccharides was an effective way to reduce death loss in highly stressed receiving cattle.

Key Words: health, oxidative balance, receiving calves

W260 Effect of addition of increasing doses of chitosan in diets of Nelore cattle on the intake and digestibility total nutrients. R. V. Barletta,* A. P. C. Araújo, R. Gardinal, R. D. Mingoti, B. C. Venturelli, J. E. Freitas Jr., T. H. A. Vendramine, J. R. Gandra, M. C. B. Santos, B. C. Benevento, V. G. C. Lacuna, and F. P. Rennó, *1University of Sao Paulo, Sao Paulo, Brazil.*

The objective of this study was to evaluate the inclusion of different doses of chitosan in the diet of beef cattle on intake and total apparent digestibility of nutrients. Eight Nelore steers (540 ± 28.5 BW/kg of SD) cannulated in the rumen were used and divided into 2×4 balanced Latin squares with an experimental period of 21 d, being 14 d for adaptation and 7 d of sample collection. The daily doses of chitosan (0, 50, 100 and 150 mg/kg BW) were inserted directly through the rumen cannula, twice daily. Daily intake was measured individually so to be kept a percentage of orts between 5 and 10% of the total supplied in the previous day. The total apparent digestibility of nutrients, was determined by the concentration of indigestible acid detergent fiber (iADF). There was quadratic effect ($P < 0.05$) to the NDF intake with the inclusion of chitosan in the diets (2.99; 3.06; 3.09 and 2.91 to the doses CH0, CH50, CH100 and CH150 respectively). The inclusion of chitosan in the diets caused linear increase ($P < 0.05$) to the NDF digestibility (56.62, 60.19, 60.69 and 60.59% for the doses CH0, CH50, CH100 and CH150 respectively). There was increase ($P < 0.05$) to the crude protein digestibility with the inclusion of the chitosan in the diets (63.12, 64.92, 66.49 and 67.51 CH0, CH50, CH100 and CH150 respectively). The total carbohydrate digestibility was positively influenced by dose of the chitosan, probably by effects of the NDF digestibility. The inclusion of the chitosan increased ($P < 0.05$) the total nutrients digestibility, resulting in linear increase (68.07, 70.97, 71.59 and 72.10 to the doses CH0, CH50, CH100 and CH150 respectively). At the significance level of 5% in the analysis by SAS PROC MIXED the inclusion of chitosan

in the diet did not affect dry matter intake and obtained positive effects on total apparent digestibility of nutrients.

Key Words: beef cattle, chitosan, metabolism

W261 Ruminant parameters, microbial protein production, protein efficiency and nitrogen balance on beef steers supplemented with slow-release urea in diets with two concentrate levels. P. D. B. Benedeti¹, P. V. R. Paulino*¹, T. S. Martins¹, E. F. Lisboa¹, L. H. P. Silva¹, C. R. V. Teixeira¹, L. C. Alves¹, M. S. Duarte¹, R. Mezzomo¹, J. C. M. Lima¹, J. P. I. S. Monnerat¹, M. I. Marcondes¹, S. C. Valadares Filho¹, and M. Manella², *¹Universidade Federal de Viçosa, Viçosa, MG, Brazil, ²Alltech do Brasil, Curitiba, PR, Brazil.*

This study evaluated the effects of replacing soybean meal (SBM) by slow-release urea (SRU) in beef cattle diets containing 2 concentrate levels, on ruminal parameters, microbial protein production, protein efficiency and nitrogen balance in finishing beef steers. Eight cross-bred steers (average BW of 418 kg) fitted with ruminal and abomasal cannulas were used. The animals were distributed into 2 groups of 4 steers each, and each group received one of the 2 levels of concentrate (40 or 80% of the total dry matter). The experiment was designed as a double Latin square in a 2×4 factorial scheme, with 2 concentrate levels in the diet, and within each square, 4 levels of replacement of soybean meal protein by slow-release urea: 0, 33, 66 and 100%. The diets with different levels of concentrate were applied independently in each Latin square and were fed once daily. Ruminal fluid samples were taken every 2 h after feeding throughout a 24 h period to determine pH and ammonia concentration. A cubic effect ($P < 0.05$) of SBM replacement by SRU on ruminal ammonia (N-NH₃) concentration in relation to the hours of collection was detected. A quadratic effect of replacing SBM by SRU was observed ($P < 0.05$) on pH and on the excretion of urea N in urine, expressed both as g/day or mg/kg of BW. The animals had higher ($P < 0.05$) total N excretion in urine, in g/day, as the slow-release urea levels were increased in the diet, but no significant effects were observed ($P > 0.05$) for total N in urine in mg/kg BW (average of 148.56 mg/kg BW) and for the concentration of urea N in the serum (average value of 11.53 mg/dL). Nitrogen intake, N excreted in feces, nitrogen balance and efficiency of nitrogen use decreased linearly ($P < 0.05$) as the levels of SRU increased in the diet, whereas the amount of nitrogen compounds excreted in urine increased linearly ($P < 0.05$) as SRU replaced SBM in the diet. The production of microbial nitrogen and microbial efficiency were not significantly affected by the experimental treatments ($P > 0.05$) obtaining average values of 173.75 g/day and 128.36 g/kg TDN ingested, respectively. Replacing SBM by SRU decreases nitrogen efficiency utilization in beef steers.

Key Words: feedlot diet, pH, ruminal ammonia

W262 Impact of an all-natural liquid fermentation prototype on performance of feedlot cattle. M. Scott*¹, J. Miles², H. Vermaak³, and S. Schalk³, *¹Diamond V, Cedar Rapids, IA, ²University of Pretoria, Pretoria, Gauteng, South Africa, ³Essential Nutrient Systems, Pretoria, Gauteng, South Africa.*

As feed costs continue to rise, new technologies that will improve feed efficiency in a safe and consistent manner will become more critical for beef cattle production. With this in mind, a randomized complete block design study utilizing 144 bonsmara-type steers (233 ± 0.8 kg BW) was conducted to examine the effect of a liquid *Lactobacillus* fermentation prototype (LFP; Diamond V, Cedar Rapids, IA) on performance of feedlot cattle. The 134 d study was conducted on a commercial beef

research facility in South Africa. Upon arrival, cattle received a feedlot ID tag, were vaccinated and treated for parasites, and were allocated to a free-range pasture for 8 d. On d 9, cattle received a trial ID tag and growth implant, and were re-vaccinated, castrated, and dehorned. Steers were then blocked by arrival body weight and randomly assigned to one of 3 treatments with 8 pens per treatment and 6 steers per pen. Dietary treatments included a control diet that contained 0, 5, or 10 g LFP per head daily. Treatments were provided in the starter (d 9 to 29) and grower diets (d 30 to 43), and in the finishing diet that contained 49% hominy chop, 23% maize, 20% maize plant, 3% soya oil cake, and 5% supplement (DM basis). Data were analyzed using Proc Mixed procedures of SAS with pen as the experimental unit. Data were considered significant at $P < 0.05$ and tendency at $0.05 < P < 0.10$. No differences were detected ($P > 0.10$) among treatments for BW, ADG, or DMI. From d 107 to 134, steers supplemented with 5 g LFP had numerically higher ADG ($P = 0.11$; 1.57 vs. 1.39 kg/d) and improved F:G ($P = 0.16$; 6.54 vs. 7.03) compared with 0 g LFP. Overall (d 9 to 134), F:G was improved ($P = 0.03$) for 5 g LFP supplemented steers compared with those receiving 0 or 10 g LFP (4.70 vs. 4.82, 4.86). Results from this study suggest that LFP does improve feed efficiency of beef cattle fed a typical South African feedlot diet and that the effect was dose dependent.

Key Words: beef cattle, feedlot, *Lactobacillus* fermentation prototype

W263 Effect of β -carotene supplementation on fatty acid profile and expression of genes involved in vitamin A metabolism in beef cattle. K. N. Condron,* J. N. Waddell, M. C. Claeys, R. P. Lemenager, and J. P. Schoonmaker, *Purdue University, West Lafayette, IN.*

Thirty Angus-cross calves allotted to 5 treatments were used to examine the effects of dietary β -carotene (β C) or vitamin A (VA) on fatty acid profile and expression of genes involved in VA and lipid metabolism. Treatments consisted of retinyl palmitate (RP) supplemented at the NRC vitamin A requirement (2200 IU/kg), synthetic β C supplemented at 1 \times , 5 \times , and 10 \times the NRC VA requirement, and natural β C (50/50 mix of all-trans and 9-cis- β C) supplemented at 5 \times the NRC VA requirement. Longissimus muscle (LM), liver, and small intestinal (SI) tissues were collected immediately after slaughter, snap frozen in liquid nitrogen, and stored at -80°C for subsequent analysis of fatty acid profile and mRNA expression by quantitative PCR. β -Carotene monooxygenase 1 (β CMO1) and β -carotene oxygenase 2 (β CO2), the enzymes responsible for symmetrical and asymmetrical cleavage of β C, respectively, were both expressed in the SI. Liver and LM tissues did not express β CMO1, but did express β CO2. Natural β C tended ($P < 0.10$) to increase expression of β CMO1 in the SI relative to 5 \times synthetic β C. Expression of β CO2 was not different among treatments ($P > 0.54$) in the liver, but in LM β CO2 expression was increased ($P < 0.01$) in 1 \times β C compared with VA, tended to decrease ($P < 0.10$) in 5 \times β C vs natural β C, and decreased linearly ($P < 0.02$) as synthetic β C concentration increased. Expression of alcohol dehydrogenase (ADH1), an enzyme that converts retinol to retinaldehyde, tended ($P < 0.06$) to decrease in the SI as synthetic β C supplementation increased, but did not differ in the liver ($P > 0.36$). The polyunsaturated fatty acid (PUFA) to saturated fatty acid (SFA) ratio

increased linearly ($P < 0.05$) as dietary synthetic β C increased because of a linear decrease in SFA concentration ($P < 0.08$), including C16:0, as well as a tendency ($P < 0.10$) for a linear increase in PUFA concentration, including C18:2, as synthetic β C supplementation increased. β C fed at 1 \times the NRC requirement decreased ($P < 0.04$) the concentration of CLA relative to VA supplemented at the NRC requirement. In conclusion, β C supplementation seems to inhibit expression of enzymes involved in metabolism of β C and VA, potentially allowing these metabolites to accumulate in muscle, thus altering fatty acid profile and fat deposition.

Key Words: beef cattle, β -carotene, gene expression

W407 Analysis of rumen methanogen diversity in cattle divergent for residual feed intake using next generation sequencing technology. C. A. Carberry*^{1,2}, D. A. Kenny¹, C. J. Creevey¹, and S. M. Waters¹, ¹*Animal and Bioscience Department, Animal and Grassland Research and Innovation Centre, Teagasc, Grange, Co. Meath, Ireland,* ²*School of Agriculture, Food Science and Veterinary Medicine, University College Dublin, Belfield, Dublin 4, Ireland.*

Methane (CH_4), a potent green house gas, is an undesirable end product of fermentation activity of ruminal methanogens. Production of CH_4 in the rumen represents a significant source of energy loss in cattle, accounting for up to 15% of dietary gross energy intake. Improved residual feed intake (RFI), a measure of energetic efficiency, has been associated with reduced ruminal CH_4 emissions in cattle. However there is little published information on whether the ruminal methanogenic population varies between animals of different RFI phenotype and in particular across different dietary regimen. The aim of this study was to analyze the rumen methanogen community in cattle divergent for RFI using 454 pyrosequencing. Yearling Limousin sired heifers ($n = 86$) were ranked on the basis of phenotypic RFI over an 80 d period while consuming a 30:70 maize silage to concentrate diet. The 7 highest (HRFI; inefficient) and 7 lowest (LRFI; efficient) ranking animals were selected for use in this study. Both groups had similar mean bodyweight and ADG but HRFI had, on average, 20% higher DMI. Following ranking on RFI all animals were offered (i) a low energy, high forage grass silage diet, followed by (ii) a high energy, low forage, concentrate based diet. Both diets were offered ad libitum for a 6-wk period. Ruminal fluid was sampled at the end of both periods using a specialized trans-esophageal sampling device. Total microbial DNA was isolated from the rumen fluid and amplified using fusion primers, which included sequencing adaptors and a unique 8-base barcode designed to amplify ca. 550-bp region of the 16S rRNA gene. Across RFI phenotype and diet *Methanobrevibacter* spp. were found to dominate, with *Methanobrevibacter smithii* the most abundant species within this genus. Rare phylotypes contributing <5% of sequences were also detected, and were influenced by both host feed efficiency and diet. Thus the rumen microbiome appears to harbour a core group of methanogens and differences in ruminal methane emissions between efficient and inefficient cattle may be due to variation in the relative abundance of specific rare microbial phylotypes.

Key Words: bovine rumen methanogens, pyrosequencing, residual feed intake