
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-eight Nellore bulls (24 intact and 24 castrated) (372 ± 22.5 kg BW; 20-20 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


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 588 kg ± 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 IVDM. 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 interaction (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, braquiiaria, cattle

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 ± 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 IVDM. 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 interaction (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, braquiiaria, cattle

Ruminant Nutrition: Beef: Feed Additives
either concentrate level or SRU level \((P > 0.05)\). The average \(K_4\) 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 lindomycin 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. Hubbert 2, M. L. Galyean 3, 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 lindomycin 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 \((P < 0.05)\) with dietary LP level. Daily 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 BW, 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 \((P < 0.05)\) 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, lindomycin 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. Graungard*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 \((P < 0.05; \text{fold-change} \geq 1.1; 124 \text{upregulated, 146 downregulated})\) and at d160, 399 genes were affected \((176 \text{upregulated, 223 downregulated})\) 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 \((P = 0.04)\). The average \(K_d\) for peroxisome proliferator-activated receptor gamma coactivator 1 alpha 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:** alpha-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 \((5 \times 10^9 \text{cfu/kg feed})\). 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 Roughtage 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 \((2.05 \pm 0.09 \text{kg/d vs} 1.80 \pm 0.28 \text{kg/d}; P < 0.05)\). Moreover, the homogeneity of growth was increased in the SC group. Consumption of feed was higher in the SC group \((8.01 \pm 0.73 \text{kg DM/head per day vs} 7.48 \pm 0.49 \text{kg DM/head per day}; P < 0.05)\). The feed conversion ratio was enhanced by the SC in the diet \((3.92 \pm 0.35 \text{kg DM/kg live weight for SC vs} 4.22 \pm 0.43 \text{kg DM/kg live weight for C}; P < 0.1)\). The SC supplemented animals also showed a different feeding behavior \((\text{higher number of visits to the RIC, shorter feeding time per visit and lower quantity ingested per visit}; P < 0.05)\). 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. Branne1*, 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 x 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 absorb data were collected. MFA x WDGS interactions were not observed for any growth, health, or carcass parameter. Growth rate between MFA programs did not differ (P ≥ 0.05); however, DM intake tended to be greater (P ≤ 0.10) for LP/CTC and feed efficiency improved (P ≤ 0.05) by M/T. Carcass measurements and liver abscess incidence were not affected (P ≥ 0.05) by MFA program. Linear (P ≤ 0.01) and cubic effects (P ≤ 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 ≤ 0.05) with higher WDGS levels. Overall morbidity at the 30 and 45% WDGS levels was increased (P ≤ 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: forage; concentrate, NPN, ruminant


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-hydroxy-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 x 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 Mintrex 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 MFP 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

W257  Basal diet affects ruminal in situ degradation rate of urea and Optigen II in steers. V. B. Holder1*, 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 forage:concentrate, NPN, ruminant diet containing varying levels of WDGS. 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

W259  The effect of combination of metal amino acid chelates, Se yeast, mannooligosaccharides, and dietary antioxidants on the health and growth performance of high-risk calves. T. J. Wistuba1*, 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

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 Nellore 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: feedlot diet, pH, ruminal ammonia

W261 Ruminal 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*2, 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, 2Altech 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 SRU 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: beef cattle, chitosan, metabolism

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* core group of methanogens and differences in ruminal methane emissions. 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 adapters 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

---

**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, 1Animal and Bioscience Department, Animal and Grassland Research and Innovation Centre, Teagasc, Grange, Co. Meath, Ireland, 2School of Agriculture, Food Science and Veterinary Medicine, University College Dublin, Belfield, Dublin 4, Ireland.

Methane (CH\(_4\)), a potent greenhouse 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 adapters 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