GROWTH & DEVELOPMENT

0370 Whole or ground oats in calf starters: Effects on rumen fermentation and rumen development.
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A series of 3 trials were conducted to determine effects of whole or ground oats in starter grain on rumen fermentation and development of preweaned calves. Male Holstein calves (43.1 ± 2.3 kg BW at birth; n = 8, 9, and 7 for trials 1, 2, and 3 respectively) were housed in individual pens in a heated facility; bedding was covered with landscape fabric to avoid any consumption of bedding. In trials 1 and 2 only, calves were fitted with a rumen cannula by wk 2 of life. Water was offered free choice, and milk replacer was fed to 12% of birth BW. In all trials, a fixed amount of starter (containing 25% oats either ground and in the pellet or whole; 18.7% CP, 12.7% NDF) was offered daily based on average intakes of calves on similar milk replacer diets; orts were fed through the cannula in Trials 1 and 2. Calves were randomly assigned to all pelleted starter (Ground, n = 11) or pellets plus whole oats (Whole, n = 13). Rumen contents (Trials 1 and 2) were sampled weekly at −8, −4, 0, 2, 4, 8, and 12 h after grain feeding for pH and VFA determination. Calves were euthanized 3 wk (Trial 1) or 4 wk (Trials 2 and 3) after grain was offered; organs were harvested, emptied, rinsed, and weighed to gauge digestive organ development. Experimental design was complete randomized block. Starter intake was not different between treatments by design (P > 0.05); weekly intakes were 481 ± 24, 1575 ± 30, 3176 ± 48, 4656 ± 143 g for wk 1 to 4 of grain feeding. Weekly measurements of rumen digesta pH and molar proportion of individual VFA did not change with diet. Molar proportion of butyrate and pH linearly decreased with age, while acetate proportion increased. Reticulorumen weight (569 ground vs. 503 whole ± 24 g) and papillae length (0.75 ground vs. 0.68 whole ± 0.03 mm) tended to be greater for ground (P < 0.1) while abomasum weight (240 ground vs. 274 whole ± 9 g) was greater for whole (P < 0.05). Liver and omasum weights were not different. Under the conditions of this study, physical form of oats in starter grain did not affect rumen fermentation parameters; greater rumen weight and papillae length in Ground may be a result of greater nutrient availability of ground oats.

Key Words: rumen-development, oats

0371 Rumen epithelial gene expression in periruminant holstein bull calves fed a fermentation extract of *Aspergillus oryzae*.
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A fermentation extract of *Aspergillus oryzae* has previously been utilized as a direct fed microbial (DFM) to promote starter intake and feed efficiency in calves. Potential effects of this DFM on rumen epithelial gene expression are unknown, and may help explain some benefits of supplementation. The objective was to determine if age and dietary inclusion of an extract of *A. oryzae* alter relative abundance of select rumen epithelial genes in periruminant Holstein bull calves. The genes investigated encode proteins that specialize in: VFA transport (*MCT1*, *MCT2*, *MCT4*), intracellular regulation of pH (*NHE1, NHE2, NHE3, DRA, PAT1*), and epithelial barrier function (*GJA1, CLDN1*). Individual calves (n = 52) were randomly assigned to a slaughter age, 4 wk (n = 16) or 8 wk (n = 36), and treatment, control (CON; n = 27) or direct fed microbial (DFM; n = 25). Calves were housed with no bedding and fed individually. Liquid DFM was delivered in milk replacer (2 g per day) for the first 4 wk of the trial; solid DFM (2 g per day) was top-dressed on grain thereafter. Calves were fed nonmedicated milk replacer twice daily (22.0% CP, 20.0% fat DM basis; 680 g/d) and had ad libitum access to texturized grain (20% CP, 2.0% fat) and water. At slaughter, rumen tissue was obtained from the cranial ventral region of each calf; the epithelial portion was separated and preserved for later RNA extraction and cDNA synthesis. cDNA was used in quantitative reverse transcription PCR assays. *UXT, RPS9, RPS15, and RPS26* were endogenous control genes. All transcripts were detectable in all calves. Relative mRNA abundance of *NHE3* was shown to decrease with age (P < 0.05); no other genes were affected by age or treatment. In summary, dietary inclusion (2 g/d) of an extract of *A. oryzae* did not result in altered rumen epithelial gene expression when supplemented animals were compared with cohorts not fed DFM. More differences were expected due to age, as selected genes are related to metabolic development of the rumen, but it is important to point out that gene level data do not always correlate with protein abundance. Further, it is possible that the dose used here was not high enough to elicit treatment effects. Regardless, we provide new data about ruminal gene expression in periruminant dairy calves.

Key Words: dairy calf, rumen, gene expression

0372 Performance and rumen development of artificially reared calves to dietary butyrate supplementation. A. K. Kelly[1], J. V. O'Doherty[1], D. A. Kenny[2], T. M. Boland[3], and K. M. Pierce*[3], *[1]School of Agriculture and Food Science, University College Dublin, Dublin, Ireland, [2]Teagasc Grange, Meath, Ireland, [3]School of Agriculture and Food Science, University College Dublin, Dublin 4, Ireland*.

Recently, there has been increased interest in the potential of certain diet-derived chemicals to enhance immune response, gastrointestinal health, and growth potential of young livestock. Of those evaluated thus far, the short-chain fatty acid butyrate has shown significant potential as an antipathogenic immune stimulant. The aim of this study was to determine the effect of sodium butyrate supplementation on calf performance, intestinal development, and volatile fatty acids profiles in preweaned calves. Forty-four Holstein Fresian male calves with a mean age of 13 ± 5 d were divided into 2 equal groups and fed milk replacer supplemented with 4 g of coated sodium butyrate (SB)/d or with no-coated sodium butyrate (CON). Calves were allocated to a standard 56 d calf rearing requiem: Milk offered at 6 L/d (125 g/L) for 10 to 49 d and weaning over 7 d (49 to 56 d) by gradually reducing the allowance. Concentrate and water was offered to calves on an ad libitum basis thoughout the trial period. Milk replacer and concentrate intake was recorded daily using a computerized calf rearing system (Forster Technik, Germany). Bodyweight was measured weekly. Respiration rate, rectal temperature, and fecal scores were recorded daily. At weaning (d 56), 8 animals from each treatment (SB vs. CON) were euthanized. Rumen digesta and tissue was harvested for VFA and rumen development analysis. Calves supplemented with SB tended ($P = 0.08$) to have higher preweaning growth rates compared with CON (0.69 vs. 0.59 kg/d). At weaning, SB calves (80.2 kg) were 3.2 kg heavier than the CON group (76.9 kg), with bodyweight difference detected from d 42 to weaning. Bodyweight differences between treatments were not evident before this ($P > 0.10$). Total DMI was not different between dietary treatments, but preweaning SB supplementation tended ($P = 0.08$) to improve feed conversion rate of the calves. There were no significant differences on rectal temperature, respiration rate, and fecal score between the treatments. Rumen papillae length, width, and perimeter were not affected by SB supplementation of milk replacer. Similarly, rumen concentrations of total VFAs were not altered by dietary treatments. In conclusion, the supplementation of milk replacer with coated sodium butyrate could improve preweaning performance of dairy calves.

Key Words: butyrate, dairy calf, rumen development

0373 Nongenomic effects of trenbolone acetate on bovine satellite cell proliferation. K. J. Thornton*, E. Kamanga-Sollo, M. E. White, and W. R. Dayton, *University of Minnesota, Saint Paul.*

Androgen treatment improves skeletal muscle growth in a number of species; however, the mechanism responsible for this improved muscle growth has not been fully elucidated. Trenbolone acetate (TBA), a testosterone analog that does not undergo aromatization to estradiol, has been shown to increase proliferation and protein synthesis rates and decrease protein degradation rate in bovine satellite cell (BSC) cultures. This is particularly significant because satellite cells are the source of nuclei needed to support postnatal muscle fiber hypertrophy and are thus crucial in determining the rate and extent of muscle growth, although the mechanism responsible for these effects of TBA on BSC has not been fully determined. The classical genomic actions of testosterone in which the androgen receptor acts as a ligand inducible transcription factor modulating target gene transcription has been well characterized. However, our recent studies have indicated that TBA may also initiate a quicker, nongenomic response that involves release of membrane-bound heparin-binding epidermal growth factor-like growth factor (hbEGF), which then binds to and activates the epidermal growth factor receptor (EGFR). To determine whether this nongenomic pathway is involved in TBA-stimulated BSC proliferation, we analyzed the effects of treating BSC with AG1478, a specific EGFR tyrosine kinase inhibitor, and CRM197, a specific inhibitor of hbEGF, on TBA-stimulated proliferation rate (3H-thymidine incorporation). As expected, BSC cultures treated with 10 nm TBA showed significantly ($P < 0.05$) increased proliferation rate when compared with control cultures. Additionally, treatment with 5 ng hbEGF/mL stimulated proliferation in BSC cultures ($P < 0.05$). Treatment with AG1478 significantly ($P < 0.05$) suppressed TBA-induced increases in proliferation. Additionally, in the presence of CRM197, TBA induced increases in proliferation were significantly ($P < 0.05$) decreased. These data indicate that hbEGF and the EGFR may play a role in TBA-mediated increases in BSC proliferation. Further, these findings demonstrate that testosterone and/or TBA may stimulate increases in skeletal muscle growth utilizing a nongenomic mechanism.

Key Words: epidermal growth factor receptor, satellite cells, trenbolone acetate

0374 Effects of recombinant bovine somatotropin on performance and biological activity of skeletal muscle over the finishing phase of feedlot heifers.
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Our objective was to determine if recombinant bovine somatotropin (rBST) enhanced performance and biological activity in skeletal muscle over the finishing phase of feedlot heifers. Heifers (n = 16; initial BW = 457 ± 3 kg) were randomly assigned to pens (4 pens/treatment; 2 heifers/pen) and treatment: (1) no rBST (control); (2) 500 mg/animal of sometribove zinc at d 0 and 14 (rBST; Posilac, Elanco Animal Health). Upon arrival, heifers were acclimated for 14 d. *Longissimus* muscle biopsies for gene expression and protein abundance were performed on d 0, 14, 28, 42, and 56. On d 88 (102 d on feed) heifers were harvested and carcass data were collected. Average daily gain, DMI, and G:F were not affected by treatment ($P > 0.05$). There was no change in final BW, HCW, or dressing percentage (DP; $P > 0.05$); however, there was a tendency for control cattle to have greater marbling and decreased KPH ($P \leq 0.08$). Loin muscle area, fat thickness, and yield grade did not differ ($P > 0.05$). Using quantitative reverse transcription PCR, genes of interest were quantified: AMPKα, β_1AR, β_2AR, β_3AR, MHC-I, MHC-IIA, MHC-IIX, IGF-I, GPR43, GPR41, Glut4, SCD, CEBPβ, and PPARγ. The rBST cattle had the greatest quantity of AMPKα mRNA ($P < 0.05$) on d 0. There was a day effect on MHC-IIA, MHC-IIX, β_2AR, PPARγ, and SCD ($P < 0.05$). All cattle had the greatest concentration of MHC-IIA mRNA on d 56 and the greatest concentration of MHC-IIX mRNA on d 14, 28, and 42 ($P < 0.05$). Concentration of β_2AR mRNA were the greatest on d 56 ($P < 0.05$), while the greatest concentration of PPARγ and SCD mRNA were on d 0 and 56 ($P < 0.05$). No differences ($P > 0.05$) were observed in mRNA between treatments for MHC-I, β_3AR, GPR41, or Glut4. Protein quantification was performed utilizing western blotting procedures to assess the abundance of β_1AR, β_2AR, and β_3AR. There was a day effect on protein abundance ($P < 0.05$). The βAR were quantified at their greatest abundance on d 0 for β_1AR, d 0 and 42 for β_2AR, and d 0 and 28 for β_3AR ($P < 0.05$). These data indicate that as days on feed increase, the effects of skeletal muscle biological activity may not be solely dependent on rBST administration. However, further investigation is needed to elucidate interactions that effect muscle metabolism during the finishing period.

Key Words: β-adrenergic receptor, myosin heavy chain, recombinant bovine somatotropin

0375 Identification of potential serum biomarkers for feed efficiency in young pigs.
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Identification of biomarkers for feed efficiency is important for increasing overall productivity of animal production. Early indicators of feed efficiency would be of particular value. The purpose of this project was to establish serum biomarkers for feed efficiency in young pigs. Serum was collected from 5-wk-old pigs from generation 8 of the Iowa State Residual Feed Intake (RFI) project. The pigs were then finished on either a high energy, low fiber diet or low energy, high fiber diet. The RFI was calculated using feed intake data from FIRE Performance Testing System (Osborne Industries, Osborne, KS). Serum protein samples were analyzed using 2D Difference in Gel Electrophoresis (2D-DIGE). Separate 2D-DIGE experiments were carried for each diet using pigs from the more efficient low RFI line (n = 8) or the less efficient high RFI line (n = 8). Selected proteins were identified through mass spectrometry. Both 2D-DIGE comparisons yielded several potential protein biomarkers for feed efficiency including gelsolin, vitronectin, serpinA3–6, and serpinA3–8. Gelsolin and vitronectin were significantly increased (13 to 57%) in abundance in the low RFI line. SerpinA3–6 and A3–8 were identified in 14 protein spots, and the protein abundance in most of these SerpinA3–6 or A3–8 spots was > 100% higher in the low RFI line as compared with the high RFI line pigs. These differences were consistent between the diet comparisons. SerpinA3 is a serine protease inhibitor that has promise as a biomarker to many disease states. In young pigs, an increase in serine protease inhibition could result in lower protein turnover. A decrease in protein turnover indicates less metabolic energy is being used for cellular repair and replacement. These data indicate further investigation is needed into serpinA3 as a biomarker for feed efficiency. This project was supported by Agriculture and Food Research Initiative Competitive Grant no. 2011–68004–30336 from the USDA National Institute of Food and Agriculture.

Key Words: 2D-DIGE, residual feed intake, SerpinA3

0376 Enhanced protein accretion and vital organ growth with intermittent bolus compared with continuous feeding in neonatal pigs.

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Enhancing the efficiency of protein utilization through dietary interventions may provide new avenues for improving profitability in farm animals. In addition, neonatal pigs can serve as dual-use models for nutrition research in animal agriculture and biomedical fields. Recently, we showed that intermittent compared with continuous feeding enhances lean tissue accretion by increasing muscle protein synthesis in neonatal pigs. The aim of this study was to determine if these feeding modalities affect vital organ protein accretion and growth. Neonatal pigs (n = 6/treatment, 6 d old) were fed the same diet in equivalent amounts continuously (CON) or intermittently (INT; meal every 4 h) for 21 d. Plasma branched-chain AA and insulin and fractional protein synthesis rates in liver, kidney, jejunum, and ileum were determined on the last day of feeding. Fractional rate of protein synthesis in organs was measured using the flooding dose method, and activation of translation initiation factors was determined by PAGE. Weight gain was greater ($P < 0.05$) for INT than for CON pigs and resulted in heavier body weights from 9 d of feeding onward. Arterial branched-chain AA and insulin concentrations measured on the last day of feeding were greater for INT after the meal than for CON pigs ($P < 0.05$). Phosphorylation of ribosomal protein S6 kinase were higher in ileum and liver in INT compared with CON fed pigs, indicating increased translation initiation signaling ($P < 0.05$). The proportion of rpS8 mRNA associated with polysomes in liver was greater in the INT compared with CON fed group ($P < 0.05$). Protein synthesis increased by 14% in jejunum, 48% in ileum, and 22% in liver ($P < 0.05$), while for the kidneys the increase was only modest. Jejunum, ileum, liver, and kidneys were 41, 36, 73, and 55% heavier for pigs in the INT as compared with the CON group ($P < 0.05$). These results suggest that intermittent feeding, as compared with continuous feeding, enhances protein accretion in vital organ growth by up-regulating protein synthesis. Supported by NIH AR444474 and USDA/ARS 6250–51000–055.

Key Words: branched-chain amino acids, protein synthesis, insulin