

each of the individual cohort analyses; however, the use of a meta-analysis allowed the identification of genes across these cohorts that were associated with weight gain in beef steers. These genes will be important for further evaluation to elucidate and validate their functional roles in body weight gain in cattle. USDA is an equal opportunity provider and employer.

Key Words: Adipose, feed efficiency, growth, RNA-Seq

449 Effect of different nucleotides supplementation source on performance of newly weaned piglets

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Nucleotides are essential for cell division and when provided in the diet can be used to enhance growth and repair of tissues with fast cell turnover such as the intestine. The aim of this study was to evaluate the effect of different nucleotides supplementation source on performance in weaned piglets. The study was performed at University of Lavras, Minas Gerais, Brazil. In total, 108 piglets weaned at 24 d of age with an average weight of 6.6 ± 0.3 kg were randomly assigned to one of 3 diets: 1) Control (n=36), without nucleotides source; 2) Yeast extract (YE; n=36; Biotide Extra®, Biorigin, Brazil); 3) Autolyzed yeast (AY; n=36; Hicell®, Biorigin, Brazil). The diets were isoprotein, isoenergetic and isonucleotides (1000 ppm for the first 21 experimental days and 500 ppm for the last 21 experimental days). Each of the 3 treatments was fed 9 replicates (pens), with 4 piglets/pen, during 42 d. Animal performance was evaluated weekly. Data were analyzed by ANOVA using the PROC MIXED of SAS 9.1 with fixed dietary effect, time effect, interaction between diet and time. The piglets of control group had lower ($P < 0.05$) in performance between groups supplemented with nucleotides. In conclusion, the inclusion of exogenous nucleotides in the diets for weaned piglets improve animal performance and total replacement from yeast autolyzed to yeast extract it's an alternative that does not alter performance.

Key Words: Key words: Weaning, pigs, yeast extract

450 Impact of ergot alkaloid consumption during mid and late gestation on mammary development and lactation

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The consumption of ergot alkaloids found in endophyte-infected tall fescue [*Lolium arundinaceum* (Schreb.) Darbysh] reduces prolactin secretion and induces vasoconstriction. The objective of this study was to evaluate effects on maternal characteristics of parturition, mammary development, and lactation. Suffolk ewes (n = 60; 83.1kg) estimated to be carrying twins at d35 of gestation were stratified by genotype (AA, AG, GG; DRD2 SNP) to: endophyte-free tall fescue seed (E-; 0.0µg ergovaline + ergovalinine/g seed) or endophyte-infected tall fescue seed (E+; 4.14µg ergovaline + ergovalinine/g seed) during MID gestation (d 35–85) or LATE gestation (d 86–parturition). Endophyte-infected tall fescue seed provided 1772µg of ergovaline + ergovalinine/hd/d for E+ treatment while endophyte-free seed (0.0µg ergovaline + ergovalinine) was fed for E- treatment. This created four treatments: E-/E-, E-/E+, E+/E-, and E+/E+. Udder width, circumference, and teat measurements were collected at parturition. Milk tests were conducted on d1, 2, and 21 post-lambing to estimate milk production. Data were analyzed as a randomized block design with maternal genotype (AA, AG, GG), treatment (E-/E-, E-/E+, E+/E-, E+/E+), and interactions as fixed effects. There tended to be an interaction ($P = 0.10$) between treatment and time wherein ewes on E+/E- and E+/E+ had lighter bodyweights at d70 and E+/E+ ewes had lighter bodyweights at d98, 108, and 136 of gestation compared to E-/E- ewes. GG genotype ewes had larger ($P = 0.003$) udder widths compared to AA and AG ewes. Ewes receiving E+/E+ treatment had smaller ($P = 0.028$) udder circumferences, shorter ($P = 0.029$) teats, and a 64% reduction ($P = 0.029$) in milk production in the first two days post-lambing. Milk production at d21 post-lambing was reduced ($P = 0.002$) in E+/E- and E+/E+ treatments by 77% and 55%, respectively. Maternal consumption of ergot alkaloids during gestation has negative impacts on milk production.

Key Words: Sheep, fescue, lactation

451 Identification and characterization of euchromatic regions associated with gene expression and intramuscular fat in Nelore cattle.

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In eukaryotes, DNA is organized along with histones in nucleoprotein complexes known as chromatin, which has nucleosomes as their fundamental unit. Chromatin

exists in two forms: euchromatin, corresponding to a lightly condensed structure and an easily transcribed region, and heterochromatin, a highly condensed and transcriptionally silent region. Therefore, the chromatin compaction degree interferes with regulation of gene expression, and nucleosomes act as gene silencers. In this context, using Assay for Transposase-Accessible Chromatin technique (ATAC-seq), the aims of the present study were to identify, map and characterize euchromatin regions in *Longissimus dorsi* muscle of Nellore cattle to understand if these regions are associated with gene expression and intramuscular fat content. Different transposase-treated nuclei concentrations were tested: 50 thousand, 75 thousand and 100 thousand, and their nucleosomal periodicity was analyzed to check the efficiency of ATAC-seq enzymatic activity. From these, 6,811, 11,121, and 11,473 euchromatin peaks were respectively found by using Model-based Analysis of ChIP-Seq (MACS2). A total of 6,212 open chromatin regions were coincident among the three nuclei concentrations, and this data was used in subsequent analyzes. Enrichment analysis performed using package RegioneR in R, considering significance of $p < 0.05$, revealed over-representation of peaks in 1) transcription start sites of genes expressed in skeletal muscle; 2) differentially expressed genes (GDE) associated with intramuscular fat content; 3) expression quantitative trait loci (eQTL) identified in skeletal muscle tissue. Our results indicate that skeletal muscle regulatory regions identified by ATAC-seq are involved in the control of gene expression and intramuscular fat content in cattle.

Key Words: ATAC-seq, Gene expression, *Bos indicus*

- 452** **Supplementation of *Saccharomyces cerevisiae* boulardii and an antibiotic growth promoter affects bacterial composition of the gastrointestinal tract of calves during the pre- and post-weaning periods.** B. Fomenky¹, D. Do¹, G. Talbot², N. Bissonnette², M. Lessard², Y. Chouinard³, E. Ibeagha-Awemu¹, ¹*Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*, ²*Agriculture et Agroalimentaire Canada / Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*, ³*Université laval, Sainte-Foy, QC, Canada*

The gastrointestinal tract (GIT) microbiota has attracted much attention due to its impact on animal health and productivity. This study characterized the GIT bacterial communities of calves (8/treatment) supplemented with *Saccharomyces cerevisiae* boulardii CNCM1-1079 (SCB) (7.5x10⁸CFU/L milk replacer

+ 3x10⁹CFU/kg feed) or an antibiotic (ATB) (chlortetracycline (528mg/L)/neomycin (357mg/L) pre-weaning and chlortetracycline (55mg/kg) post-weaning) or not supplemented (CTL). Twelve calves (4/treatment) were euthanized on day33 (pre-weaning) and another 12 (4/treatment) on day96 (post-weaning) for collection of digesta from rumen (RuD), ileum (IID) and colon (CoD), and mucosa from ileum (IIM) and colon (CoM). Extracted DNA was subjected to amplicon sequencing of the V3–V4 region of the 16S rRNA gene (Illumina MiSeq) followed by bioinformatics with QIIME pipeline. Abundance at genus level was compared between treatments using DESeq2. Functional analyses of inferred genes were performed using PICRUSt software. Pre-weaning, SCB and ATB significantly reduced ($p.FDR \leq 5.97E-03$) *Streptococcus* abundance in CoM meanwhile SCB reduced *Tyzzereella_4* ($p.FDR = 4.27E-09$) in IIM compared to CTL. Post-weaning, SCB increased ($p.FDR \leq 7.01E-04$) *Fibrobacter* and *Roseburia* while ATB increased ($p.FDR \leq 5.15E-03$) *Dorea* and *Aneorovibrio* compared to CTL. SCB treatment significantly ($p < 0.05$) influenced six pathways in IIM and five pathways in RuD during pre-weaning. ATB treatment significantly changed the abundance of thyroid hormone signaling and lipid metabolism pathways in IID, cAMP signaling in CoM and RIG-I-like receptor signaling, D-arginine/D-ornithine metabolism and butanoate metabolism pathways in IIM. ATB and SCB affected the bacterial communities of IIM, IID, CoM, and RuD. In addition, SCB and ATB treatment shared common mechanisms like bile secretion in IIM, steroid biosynthesis, and cAMP signaling in RuD. However, SCB affected more GIT sites and pathways compared to ATB. This study indicates that SCB and ATB mostly influenced different bacterial communities in different GIT sites during the pre- or post-weaning periods. Thus, SCB deserves attention as a probable alternative to antibiotics growth promoter.

Key Words: Gastro-intestinal tract, *Saccharomyces cerevisiae*, antibiotics, calf, microbiota, 16S rRNA gene

- 453** **Biological responses to non-coated and coated steroidal implants containing equal doses and ratios of trenbolone acetate and estradiol benzoate in beef steers.** Z. Smith¹, J. Baggerman², J. Kim¹, K. Wellmann¹, B. Johnson¹, ¹*Texas Tech University, Lubbock, TX, United States*, ²*Huntington University, Huntington, IN, United States*

Predominately Angus steers ($n = 24$; initial BW = 435 ± 28.3 kg) were used to evaluate non-coated