NDF range had an impact on the enrichment of gene sets, steers were separated into two groups, one with a diet >40% NDF (n = 611) and one with NDF content <40% (n = 276). Significant SNPs ($P < 0.05$) within the average haplotype block length for the population (8.5 kb) that were associated with RFI by genome-wide association analysis for RFI were used as a proxy for each of 19,723 annotated genes from the UMD3.1 genome assembly. Gene sets from five databases were used for the GSEA-SNP: Panther (n = 165), Kyoto Encyclopedia of Genes and Genomes (KEGG; n = 186), Biocarta (n = 217), Reactome (n = 674), and Gene Ontology (GO; n = 3,147). The null distribution for testing the normalized enrichment score was estimated with GenABEL (R package) and 10,000 permutations. Enriched gene sets (NES > 3.0) and their LEG associated with RFI were identified. Mean DMI and RFI for the steers fed a diet with >40% NDF was 10.67 kg ± 1.36 and -0.39 ± 0.05 and 10.08 kg ± 1.30 and 0.44 ± 0.07 for the <40% NDF. Enriched gene sets for steers fed <40% NDF were GO Behavior (GO:0007610) with 128 LEG and GO Ras Protein Signal Transduction (GO:0007265) with 136 LEG. Four LEG genes were common across the Behavior (GO:0007610) and Ras Protein Signal Transduction (GO:0007265) pathways indicating their importance to the RFI trait. Four gene sets were enriched for steers fed >40% NDF: KEGG Glycerophospholipid Metabolism (map00564) with 65 LEG, GO Ubiquitin Ligase Complex (GO:00001051) with 54 LEG, Reactome Synthesis of Phosphatidic Acid (R-HSA-1483166) with 25 LEG and the Panther Opioid Proopiomelanocortin pathway (P05917) with 18 LEG. The GSEA-SNP analysis based on dietary NDF level resulted in no common gene sets. Steers fed diets containing higher NDF levels had enriched gene sets for lipid metabolism and feed intake while those steers fed diets containing lower NDF levels were enriched for protein transduction and general behavior genes. The diet fed during the determination of RFI had an impact on the gene sets and LEG genes, suggesting differences in metabolic pathways associated with the trait.

Key Words: RFI, Gene Set Enrichment, Beef
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588 Gastrointestinal tract gene expression in ewes under feed restriction. A. I. Trujillo*[1], C. Febrer[1], A. Casal[1], V. de Brun[2], A. L. Astessiano Dickson[1], M. Carriquiry[1], and J. A. Abecia[3], *[1]Facultad de Agronomia, Universidad de la Republica, Montevideo, Uruguay, [2]Facultad de Veterinaria, Universidad de la Republica, Montevideo, Uruguay, [3]IUCA. Universidad de Zaragoza., Zaragoza, Spain.*

The gastrointestinal tract is known to adapt itself to changes in feed conditions and is the source of various signals that regulate feed intake and energy homeostasis. Therefore, the objective of this study was to assess the effect of a feed restriction period in the mRNA expression of target genes related to feed intake. The study was conducted in a randomized block design with 5 temporal replications (n = 4 or 3 per treatment and replication) in which thirty-five Rasa Aragonesa ewes (BW = 67.1 ± 8.6 kg and BCS = 3.0 ± 0.5) were assigned to two nutritional treatments (3.15 vs 1.05 Mcal per day/1.5 vs 0.5 times the daily requirements for maintenance; Control and Low, respectively) during 30 days. At the end of this period ewes were slaughtered and a total of 12 samples from abomasum and 12 samples from small intestine (6 ewes per treatment selected by embryo presence) were collected. Relative mRNA expression of glucagon-like peptides 1 and 2 (*GLP1*, *GLP2*) and their receptors (*GLP1R, GLP2R*), neuropeptide Y2 receptor (*NPY2R*), ghrelin, insulin-like growth factor-1 (*IGF1*) and its receptor (*IGF1R*) were determined in abomasum while mRNA expression of *IGF1*, *IGF1R*, cholecystokinin (*CCK*), protein kinase AMP-activated-beta 1 (*AMPKB1*), neuropeptide Y1 and Y2 receptors (*NPY1R, NPY2R*), peptide YY (*PYY*), insulin receptor (*INSR*) and ghrelin were determined in the small intestine. The mRNA abundance of target genes was assessed by qPCR using SYBR-Green and normalized by the expression of 3 reference genes. Data were analyzed using a mixed model including nutritional treatment as a fixed effect and block as a random effect. Abomasal expression of *GLP1* mRNA (1.57 vs -1.03 ± 0.45; $P = 0.004$) and *GLP2* mRNA (0.25 vs -1.39 ± 0.37; $P = 0.014$) were greater in Control than Low ewes. Expression of *IGF1R* mRNA in small intestine was greater in Control than Low ewes (-2.01 vs -2.93 ± 0.26; $P = 0.0375$). No other measured genes in abomasum or small intestine showed a differential expression between Control and Low ewes ($P > 0.05$). Results suggest that ewes fed 1.5 times maintenance requirement presented greater expression of genes related to feed intake regulation. The greater expression of *IGF1R* mRNA in small intestine in these ewes may be associated with greater IGF-1 availability in this tissue, while the greater gene expression of *GLP1* and *GLP2* mRNA at abomasal tissue need further investigation.

Key Words: nutritional status, Rasa Aragonesa ewes, mRNA expression
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589 Heat-induced changes in protein molecular structure associated with rumen degradation of oat grains in dairy cows detecting by vibrational molecular spectroscopy. L. Louzada Prates*, and P. Yu, *Department of Animal and Poultry Science, College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, SK, Canada.*

Heat processing may simultaneously affect protein rumen degradation and protein intestinal digestion by altering molecular protein structure in seeds. Attenuated Total Reflectance Fourier transform vibrational molecular spectroscopy (ATR-Ft/VMS) is a novel technique that reveals molecular structural features, increasing the understanding of feed structures at cellular level and new level of analytical information. The