The Influence of Previous Plane of Nutrition on Grain or Grass-fed Finished Steers: Water-Related Gene Expression in the Kidney. Aghata Elins Moreira da Silva, Arturo Macias Franco, Felipe Henrique De Moura, Bradley S. Ferguson, Mozart Fonseca, \textsuperscript{1}University of Nevada, Reno

Abstract: The extenuating stressors inherent to various beef cattle backgrounding systems in the U.S. may imprint different nutritional carryover effects of earlier stages of life onto the finishing phase. Therefore, the objective of this study was to evaluate the effects of previous plane of nutrition (PPN) onto water-related gene expression in the kidney of grain or grass finished steers. Twenty-four crossbred Angus steers were randomly distributed into either low or adequate PPN during the background phase. After 85d of backgrounding, animals were moved onto a 105-d finishing phase blocked by their PPN. The grass-finished group received only alfalfa hay, whereas the grain-finished group received a high grain diet (80% whole corn and 20% alfalfa hay). By the end of the finishing phase, animals were harvested and kidney samples were collected. Changes in gene expression of Aquaporins (AQP) -2, -3, -4, -7, ATP1A1, ATP1B1, SGK1, and CLIC1 from kidney tissue were assayed via real-time qPCR; and the 18S rRNA was used as an endogenous control. One-way ANOVA followed by Tukey post hoc analysis were conducted. When comparing grain versus grass-finished according to their PPN, ATP1B1 ($P = 0.0290$) was the only gene significantly different, with animals coming from a low PPN finished on grass having greater expression than for the grain-finished. However, within animals backgrounded at a low PPN, AQP3 ($P = 0.0289$), AQP7 ($P = 0.0260$), ATP1B1 ($P = 0.0239$), and SGK1 ($P = 0.0411$) were upregulated for the grass-finished animals. No differences were found for the other genes analyzed. These results suggest that PPN can impact water-related gene expression in the kidney of finishing steers; the greatest impact for water-related gene expression occurred in animals from a low PPN that were fed different finishing systems, where grass-fed animals had a greater gene expression compared with grain-fed animals.

Keywords: aquaporins, finishing systems, kidney

Candidate Plasma Biomarkers Associated with Residual Feed Intake in Beef Steers. Godstime A. Taiwo, Modoluwanu Idowu, Shelby Collins, Taylor S. Sidney, Matthew E. Wilson, Andres a. Pech-Cervantes, Ibukun M. Ogunade, \textsuperscript{1}West Virginia University, \textsuperscript{2}Fort Valley State University

Abstract: We applied chemical group-based metabolomics to identify blood metabolic signatures associated with residual feed intake in beef cattle. A group of 56 crossbred growing beef steers (average BW = 261 ± 18.5 kg) were adapted to a high-forage total mixed ration in a confinement dry lot equipped with GrowSafe intake nodes for period of 49 d to determine their residual feed intake (RFI) classification. After RFI determination, weekly blood samples were collected three times from beef steers with the least RFI [most efficient (HFE); n = 8; RFI = - 1.93 kg/d] and greatest RFI [least efficient (LFE); n = 8; 2.01 kg/d]. Plasma was prepared by centrifugation and composited for each steer. Metabolome analysis was conducted using a chemical isotope labeling (CIL)/liquid chromatography–mass spectrometry. Analyzed metabolites included those containing amine/phenol-, carboxylic acid-, and carbonyl-chemical groups, which are metabolites associated with metabolism of amino acids, fatty acids, and carbohydrates, respectively. A total number of 495 amine/phenol-containing metabolites were detected and identified; pathway analysis of all these metabolites showed that arginine biosynthesis and histidine metabolism were enriched ($P < 0.10$) in HFE, relative to LFE steers. Biomarker analysis of the amine/phenol-metabolome identified methionine, 5-aminopentanoic acid, 2-aminohexanedioic acid, and 4-chlorolysine as candidate biomarkers of RFI [false discovery rate ≤ 0.05; Area Under the Curve (AUC) > 0.90]. A total of 118 and 330 metabolites containing carboxyl- and carboxylic acid-chemical groups, respectively, were detected and identified; no metabolic pathways associated with these metabolites were altered and only one candidate biomarker (methionine sulfoxide) was identified. These results identified five candidate metabolite biomarkers of RFI in beef cattle which are mostly associated with amino acid metabolism. Further validation using a larger cohort of beef cattle of different genetic pedigree is required to confirm these findings.

Keywords: amino acid, metabolism, metabolome