

Abstract citation ID: skae234.508

PSX-3 Transcriptional response to an alternative diet on liver, muscle, and rumen of beef cattle. Anna Carolina Fernandes¹, Antonio Reverter², Kate Keogh³, Pâmela Almeida Alexandre², Juliana Afonso⁴, Júlio César Pascale Palhares⁴, Tainã Figueiredo Cardoso⁴, Jéssica M. Moraes Malheiros⁵, Jennifer Jéssica Bruscadin⁶, Priscila Silva Neubern de Oliveira⁴, Gerson Barreto Mourão¹, Luciana Correia de Almeida Regitano⁴, Luiz Lehmann Coutinho¹, ¹*Luiz de Queiroz College of Agriculture | University of São Paulo (ESALQ/USP)*, ²*CSIRO | Commonwealth Scientific and Industrial Research Organisation - Animal Breeding and Genomics Group*, ³*Teagasc, Animal and Bioscience Research Department, Grange, Dunsany, Co. Meath, Ireland*; *CSIRO, Agriculture & Food, Queensland Bioscience Precinct, 306 Carmody Rd., St. Lucia, Brisbane, QLD 4067, Australia*, ⁴*Brazilian Agricultural Research Corporation - Embrapa Southeastern Livestock*, ⁵*Animal Science Institute (IZ) - Beef Cattle Research Center*, ⁶*Federal University of São Carlos - Center of Biological and Health Sciences*

Abstract: Feed cost represents a major economic determinant within cattle production, amounting to an estimated 75% of the total variable costs. Consequently, comprehensive approaches such as optimizing feed utilization through alternative feed sources, alongside the selection of feed-efficient animals, are of great significance. Here, we investigate the effect of two diets, traditional corn-grain fed and alternative by-product based, on 14 phenotypes related to feed, methane emission and production efficiency and on multi-tissue transcriptomics data from liver, muscle, and rumen wall, derived from Nellore bulls (n = 52), 26 on each diet. To this end, diets were contrasted at the level of phenotype, gene expression, and gene-phenotype network connectivity. As regards the phenotypic level, at a P -value < 0.05, significant differences were found in favor of the alternative diet for average daily weight gain at finishing, dry matter intake at finishing, methane emission, carcass yield and subcutaneous fat thickness at the rib-eye muscle area. In terms of the transcriptional level of the 14,776 genes expressed across the examined tissues, we found 487, 484, and 499 genes differentially expressed due to diet in liver, muscle, and rumen, respectively (P -value < 0.01). To

explore differentially connected phenotypes across both diet-based networks, we focused on the phenotypes with the largest change in average number of connections within diets and tissues, namely methane emission and carcass yield, highlighting, in particular, gene expression changes involving SREBF2, and revealing the largest differential connectivity in rumen and muscle, respectively. Similarly, from examination of differentially connected genes across diets, the top-ranked most differentially connected regulators within each tissue were MEOX1, PTTG1, and BASP1 in liver, muscle, and rumen, respectively. Changes in gene co-expression patterns suggest activation or suppression of specific biological processes and pathways in response to dietary interventions, consequently impacting the phenotype. The identification of genes that respond differently to diets and their associated phenotypic effects serves as a crucial steppingstone for further investigations, aiming to build upon our discoveries. Ultimately, such advancements hold the promise of improving animal welfare, productivity, and sustainability in livestock farming.

Keywords: beef cattle, gene co-expression networks, multi-tissue transcriptomics

