
0341 miRNAs related to fatty acids composition in Nellore cattle. P. S. N. Oliveira^{*1}, A. S. M. Cesar², G. B. Oliveira², P. C. Tizioto¹, M. D. Poleti², W. J. S. Diniz³, A. O. D. Lima³, J. M. Reecy⁴, L. L. Coutinho², and L. C. A. Regitano⁵, ¹Embrapa Southeast Livestock, São Carlos, Brazil, ²Animal Biotechnology Laboratory-ESALQ, University of São Paulo, Piracicaba, Brazil, ³Federal University of São Carlos, Brazil, ⁴Iowa State University, Ames, ⁵Embrapa Southeast Livestock, São Carlos, Brazil.

Fatty acid (FAs) content is an important trait that can influence the sensorial and nutritional value of meat and play a significant role in biological processes such as adipogenesis. In beef cattle, adipogenesis as well as several other biological processes have been reported that could be regulated by miRNAs. The goal of this study was identify differentially expressed (DE) miRNAs and biological processes associated with FA content between the groups Nellore steers that showed extreme genomic breeding values (GEBV) for oleic acid (OA) and conjugated linoleic acid cis9 trans11 (CLAc9t11). In this study, small RNA libraries from Longissimus dorsi (LD) muscle tissue from a group of 28 (top 14 animals with highest GEBV distribution (H) and bottom 14 with lowest GEBV distribution (L) for OA and CLAc9t11 content) were sequenced on a MiSeq using the Miseq Reagent Kit V3 150 cycles. After quality control, the miRDeep2 software was used to identify and quantify novel and known miRNAs using *Bos taurus* UMD3.1 as reference genome. Differentially expressed (FDR = 10%) miRNAs were identified by DESeq2 R package and potential regulatory target transcripts were predicted by TargetScan software. The bta-miR-126-5p (padj = 0.0987) and bta-miR-2419-5p (padj = 0.0041) were DE for OA and CLA, respectively. The genes *CDS2*, *FAR2*, *DIP2B*, *NAB1*, *EPT1*, *UBE2E3*, *PRKAG2* and *CAV3* were identified as target genes of these DE miRNAs, which were identified as DE in a previously RNaseq study. These genes are related to some biological process for fatty acids composition; like phospholipid and lipid metabolism, skeletal system development, proteolysis and insulin signaling pathway. This study helps to better understand of the biological mechanisms that control intramuscular fat deposition and composition, and could positively benefit beef production by supplying the product that the consumer wants.

Key Words: *Bos indicus*, adipogenesis, gene regulation

0342 Expression levels of the bovine SCD gene are significantly associated with fatty acid composition of cattle. H. Chung^{*}, *National Institute of Animal Science, Wanju, Korea (The Republic of).*

The experiment shows that a long-term administration of low and high-energy diets may not functionally either increase or decrease SFA and UFA. The interesting finding was that

variation for proportions of all FAC in the low-energy diet group were higher than that of the high-energy diet group except Linoleic acid (18:2n6) and PUFA. According to the variance analysis, the proportions of FAC in the low group tended to have an approximate normal distribution while the high group showed a skewed pattern. Expression analysis of stearoyl-CoA desaturase (SCD) revealed at least twofold high expression levels in the high-diet group, and especially, the SCD4 and SCD6 segments detected more than 10 folds high expressions, whereas none of the SCD segments had high expression values in the low-diet group. The results indicate that long-term feeding with high energy levels of diets lead high expression levels of the SCD gene. However, excessive proportions of nutritional materials limited metabolic availabilities or restricted functional systems for the ruminal biohydrogenation between FA. Therefore, the present results deliver a critical issue to the public that manipulations of FAC with high nutritional levels in diets may be oriented toward increases of expression levels of SCD, but not activities of other genes that functional elongate and desaturase FA.

Key Words: expression, SCD, FAC

0343 Profiling microRNA expression in longissimus dorsi muscle of F2 pigs from the Michigan State University Duroc x Pietrain resource population.

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MicroRNAs (miRNAs) are a class of small, non-coding RNAs shown to regulate gene expression post-transcriptionally through complementary binding with an approximately 7 nt “seed” sequence in the 3’UTR of target mRNAs. MiRNAs have been shown to regulate numerous complex biological processes across tissue types, including fetal and postnatal skeletal muscle in pigs. While miRNAs have been characterized for these developmental stages, a more comprehensive understanding of the effects of miRNA regulation in market-age pigs is needed. The objective of this study was to profile the expression of miRNAs in the Longissimus dorsi (LD) muscle of 174 F2 pigs (~5.5 mo of age) from the MSU Duroc x Pietrain Resource Population. Total RNA was extracted from LD samples using the QIAGEN miRNeasy Mini Kit, and library preparation for sequencing was conducted utilizing the Bio Scientific NEXTflex Small RNA Sequencing Kit (v2) with one cDNA library prepared per sample. The 174 libraries were multiplexed and sequenced on an Illumina HiSeq 2500 platform in 1x50 bp format. Raw sequence reads (fastq format) were trimmed for adaptor sequences, size- and quality-filtered, and PCR duplicates were removed. After processing, 232,826,977