MT297 Co-expression network analysis identifies genes associated with meat tenderness. W. Diniz*[1], A. Cesar[2], L. Geistlinger[3], P. Tizioto[2], P. Oliveira[3], J. Afonso[1], M. Rocha[1], A. Lima[1], C. Buss[1], L. Coutinho[2], and L. Regitano[3], [1]*Departament of Genetic and Evolution, Federal University of São Carlos, São Carlos, São Paulo, Brazil;* [2]*Department of Animal Science, University of São Paulo/ESALQ, Piracicaba, São Paulo, Brazil;* [3]*Embrapa Pecuária Sudeste, São Carlos, São Paulo, Brazil.*

Tenderness is an important trait of meat quality and is known to be influenced by several factors including genetic composition. Although various studies have reported gene expression differences between tough and tender meat, it has been rarely analysed to which extent this can be attributed to interaction among genes and coordinated activation or repression of specific pathways. To identify candidate gene networks associated with meat tenderness, we performed weighted gene co-expression network analysis (WGCNA) in a Nelore cattle population of 129 steers. Gene expression was measured with RNA-seq in *Longissimus dorsi* muscle samples and genomic estimated breeding values for shear force (GEBV-SF) were used as a quantitative trait for meat tenderness. From the co-expression modules detected by WGCNA, we found two modules to be significantly negatively correlated with GEBV-SF. Genes in these modules are involved in muscle fibre composition, muscle contraction, and cell morphology. Proteolytic processes, known to play a key role in meat tenderness variation, were found significantly enriched for the genes presented in the associated modules. We also found tenderness markers such as *CAPNS1*, *MAP2K5*, *MYOZ1*, *TNNT3*, and *HMGA1* contained in the detected modules. We further observed *EIF3L* as a hub gene, which has been previously reported as involved in formation of primary myoblasts and differentiation of muscle fibres but not described as related to shear force. The detected co-expression modules in this study provide evidence for substantial interplay between genes in processes influencing meat tenderness. Further studies will be required to elucidate the underlying regulatory mechanisms of the observed co-expression networks. This project was supported by FAPESP (12/23638–8, 15/09158–1).

Key Words: cattle and related species, gene expression, network analysis, RNA-seq, systems biology

MT298 Comparative genome-wide methylation analysis of longissimus dorsi muscles between Japanese Wagyu and Chinese Red Steppes cattle. X. Fang[1], Z. Zhao[1], G. Li[2], X. Yu[3], Z. Wei[2], H. Yu[1], and R. Yang*[1], [1]*College of Animal Science, Jilin University, Changchun, Jilin Province, China;* [2]*The Key Laboratory of National Education Ministry for Mammalian Reproductive Biology and Biotechnology, Inner Mongolia University, Hohhot, Inner Mongolia Autonomous Region, China;* [3]*Department of Biological Sciences, Clemson University, Clemson, SC, USA.*

DNA methylation is an important epigenetic mechanism involved in many biological processes including muscle development and lipometabolism. DNA methylation can affect meat quality traits and fat deposition traits by regulating the expression of genes important for myoblast proliferation and adipocyte differentiation. Significant differences in meat quality traits have been reported between Japanese Wagyu and Chinese Red Steppes cattle, which presented a unique model for analysing the effects of DNA methylation on these economically important meat quality traits. In the present study, we sequenced the whole genome DNA methylation in the longissimus muscle of these two cattle breeds to detect whether DNA methylation plays a role in determining the fat deposition and meat quality traits of beef battle by whole genome bisulfite sequencing (WGBS) method. A high quality methylation map of two cattle breeds was obtained in this study. 23150 differentially methylated regions (DMRs) were identified which were located in 8596 genes enriched in 9922 GO terms, of which 1046 GO terms were significantly enriched ($P < 0.05$) including lipid translocation (GO:0034204) and lipid transport (GO:0015914). KEGG analysis showed that the DMR related genes were distributed among 276 pathways. Correlation analysis found that 331 DMRs were negatively correlated with expression levels of differentially expressed genes (DEGs) with 21 DMRs located in promoter regions. Interestingly, DNA methylation of ZBED-6, IGF-2R, IGFBP-5 and GJC1 showed significant difference across breeds, and five CpG were significantly correlated with RNA expression. This study identified novel candidate DMRs and DEGs correlated with muscle development and lipometabolism, which will be provides a thorough understanding of meat quality traits variation in beef cattle from an epigenetic perspective.

Key Words: cattle, epigenomics, genome sequencing, candidate gene, meat production

MT299 Scanning of selection signature provides a glimpse into important economic traits in goats (*Capra hircus*). D. Guan*, N. Luo, X. Tan, Z. Zhao, Y. Huang, R. Na, J. Zhang, and Y. Zhao, *College of Animal Science and Technology, Southwest University, Chongqing, China.*

Goats (*Capra hircus*) are one of the oldest domesticated species, which are distributed over all types of ecological areas with more concentrated in the tropics, dry zones and developing countries and have been used for their milk, meat, hair and skins over much of the world. However, the genetic components underlying these phenotypic traits remain largely unknown. We collected a total of 12 blood samples of unrelated individuals from Dazu black female goats (DBG, $n = 6$) and Inner Mongolia cashmere female goats (IMCG, $n = 6$). Genomic DNA was extracted and sequenced. We performed SNP calling on a population scale for two groups. Selective sweep analyses were performed by calculating heterozygosity (Hp) and population differentiation (Fst). The study presented here has generated 192.747G raw data and identified more than 5.03 million SNPs and 334,151 Indels. In addition, we identified 155 and 294 candidate regions harboring 86 and 97 genes based on allele frequency differences in DBG and IMCG, respectively. Populations differentiation reflected by Fst values detected 368 putative selective sweep regions including 164 genes. The top 1% regions of both low heterozygosity and high genetic differentiation contained 239 (135 genes) and 176 (106 genes) candidate regions in DBG and IMCG, respectively. These genes were related to reproduction and production traits, such as 'neurohypophyseal hormone activity' and 'adipocytokine signaling pathway'. The works performed here provided an important resource for future goat breeding.

Key Words: *Capra hircus*, whole genome sequencing, selective signature, heterozygosity (Hp), population differentiation (Fst)

MT300 Transcriptome analyses reveal reduced hepatic lipid synthesis and accumulation in more efficient beef cattle. R. Mukiibi*[1], M. Vinsky[2], C. Fitzsimmons[1,2], S. M. Waters[3], P. Stothard[1], and C. LI[1,2], [1]*Department of Agriculture, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada;* [2]*Agriculture and Agri-Food Canada, Lacombe Research and Development Centre, Lacombe, Alberta, Canada;* [3]*Animal and Bioscience Research Department, Teagasc, Grange, Dunsany, County Meath, Ireland.*

The specific genes and variants underlying the genetic control of residual feed intake (RFI) in beef cattle are largely unknown. In the present study, we aimed to identify genes associated with RFI using whole transcriptome analyses in three Canadian beef cattle breeds raised under similar environments. Liver samples were collected at slaughter from high ($n = 6$) and low ($n = 6$) RFI phenotype steers of Angus, Charolais, and Kinsella composite (KC) breeds. RNA was extracted and gene expression profiles obtained by mRNA sequencing (RNA-seq) using Illumina HiSeq sequencing technology yielding an average of 36 million reads with a mean