P310 The variance of gene expression in the porcine skeletal muscle changes in response to food intake. E. Mármol-Sánchez*[1], R. Quintanilla[2], TF Cardoso[3], J. Tibau[4], and M. Amills[1,5], *[1]Centre for Research in Agricultural Genomics (CRAG), CSIC-IRTA-UAB-UB, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain, [2]Animal Breeding and Genetics Program, Institute for Research and Technology in Food and Agriculture (IRTA), Torre Marimon, Caldes de Montbui, Spain, [3]CAPES Foundation, Ministry of Education of Brazil, Brasilia D. F., Brazil, [4]IRTA-Monells, Monells, Spain, [5]Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain.*

During the past few years, the analysis of RNA-seq data across different treatments has been mainly based on the contrast of expression means. Many studies have been conducted on diverse tissues and species, aiming to disentangle the complex responses at the gene level that different stimuli can trigger within the cell transcriptome. However, focusing on differences in gene expression means may have overlooked other valuable sources of biological information such as gene expression variance (GEV). We aimed to gain new insights into the relationship between nutrition and GEV by evaluating the dispersion of the expression of coding and non-coding genes in 48 Duroc pigs divided in 4 groups: pigs fed *ad libitum* and slaughtered under fasting conditions, pigs fed *ad libitum* and slaughtered 5 and 7 h after feeding, and pigs managed under restricted feeding during the first fattening phase and slaughtered under fasting conditions. *Gluteus medius* samples were collected and both RNA and small RNA fractions were subsequently sequenced. Novel long intergenic non-coding RNAs (lincRNAs) and natural antisense transcripts (NATs) were predicted by following the HISAT2-Stringtie pipeline and a combination of CPAT, CNCI, CPC2 and LncFinder softwares. Differences in GEV were assessed with the MDseq software. The Biological Coefficient of Variation (BCV) was calculated for each expressed protein-coding, long non-coding RNA and miRNA genes and differences across groups were evaluated. Highly expressed genes had more stable gene expression profiles than lowly expressed genes, which showed increased BCV values. Non-coding transcripts evidenced a reduced expression level compared with protein-coding genes and higher variance within analyzed groups. Genes having differential variance levels between conditions, *i.e.* differentially dispersed genes that, at the same time, did not show differences in mean expression, mostly belonged to DNA binding proteins and transcription factors (TFs), which mainly regulate the expression of many other transcripts by influencing the early steps of signaling pathways. These results might provide new hints to understand why the variance of gene expression changes across different experimental conditions.

Key Words: RNA-seq, nutrigenomics, gene expression

P311 Integration of phenomics, transcriptomics, epigenetics and glycomics to reveal the mechanism underlying the embryo-maternal interaction during implantation in pigs. F. Wang*, K. Han, J. Huang, D. Deng, W. Wang, and M. Yu, *Key Lab of Agricultural Animal Genetics, Breeding and Reproduction of Ministry of Education, College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, Hubei, China.*

The study was aimed to investigate the mechanism of embryo-maternal interaction in pigs which has not yet to be understood. First, by using digital slide scanning system, we performed systematical and large-scale examination on the morphological structure of porcine uterine lumen during implantation. Two phenotypic features involved in embryo implantation statuses were defined for the first time. Meanwhile, the 3-dimensional status of implanting embryo within uterus was imaged by taking advantage of a 3D reconstruction technology. Second, to obtain the in situ embryo-maternal interaction information at gestational d 12 and 15 (gd12 and gd15), we collected samples including conceptus and luminal epithelium from anti-mesometrial and mesometrial side adjacent to the conceptus, respectively, by using the laser capture microdissection technology. Then, we analyzed the RNA-seq and ATAC-seq data generated from these samples. The comparisons were as follows: (i) luminal epithelium at mesometrial vs anti-mesometrial side from gd12; (ii) luminal epithelium at mesometrial vs anti-mesometrial side from gd15; (iii) luminal epithelium of mesometrial side from gd12 vs those from gd15; (iv) luminal epithelium of anti-mesometrial side from gd12 vs those from gd15; (v) conceptuses from gd12 vs those from gd15. We found many differentially expressed genes and some regulatory pathways that may be associated with embryo-maternal interaction, for example, steroid hormone biosynthesis and metabolism pathway, retinoic acid signaling pathway, integrin-mediated signaling pathway. Third, the glycome of porcine endometrium was characterized for the first time and we found that sialylation of cell adhesion molecules has important roles in endometrium remodeling during implantation. Taken together, the integrative analyses of data described above revealed novel molecular pathways involved in implantation in pigs.

Key Words: pig, embryo implantation, phenomics, RNA-seq, ATAC-seq

P312 Combining metabolomics and genomics to elucidate physiological processes related to tail damage score in pigs. E. Dervishi*[1], L. van der Zande[2], T. da Silva Valente[1], I. Reimert[3], P. Mathur[2], M. S. Lopes[2,4], E. F. Knol[2], and G. S. Plastow[1], *[1]University of Alberta, Edmonton, Alberta, Canada, [2]Topigs Norsvin Research Center, Beuningen, The Netherlands, [3]Wageningen University & Research, Wageningen, The Netherlands, [4]Topigs Norsvin, Curitiba, Paraná, Brazil.*

The purpose of this study was to identify important metabolites related to tail damage (TDAM) score and to identify genomic regions associated with variation in the metabolites. We used 181 Tempo × Topigs-20 animals divided over 2 batches balanced for gender and selected for positive (n = 81) or negative (n = 100) indirect genetic effect (IGE) for growth. Half of the pigs were housed in a barren environment, and the other half in an enriched environment. The tail scores were recorded at weaning and thereafter once a week (score 1 no visible tail damage, score 2 hair removed from the tail, score 3 bite marks and score 4 clearly visible wound). Blood samples collected at 8, 9 and 22 weeks of age were used to determine metabolic profiles at The Metabolomics Innovation Centre (University of Alberta). A total of 53 compounds were quantified. Statistical analyses were performed in R version 3.5 using a generalized mixed model with repeated measurements. A single step genome-wide association study (ssGWAS) was performed to identify genomic regions associated with significant metabolites for tail biting score. Preliminary results show that serum levels of glycerol and isopropanol were significantly associated with tail damage score. Animals with TDAM 2 had greater glycerol concentration in blood when compared with animals with TDAM 3 and 4 ($P < 0.05$). In addition, animals with TDAM 1 had lower isopropanol concentration when compared with animals with TDAM 2 and 3 ($P < 0.05$). GWAS identified 2 candidate regions located on chromosome 6 associated with glycerol and isopropanol (at 45Mb, and at 149Mb respectively). The candidate genes identified in these regions were *ZFP14*, *DOCK7*, *ANGPTL3*, *USP1* and *KANK4*. Angiopoietin like 3 is a secreted protein encoded by *ANGPTL3* that is involved in the regulation of lipid and glucose metabolism. This protein is present at high levels in the liver where it can bind to adipocytes to activate lipolysis, releasing free fatty acids and glycerol. These results suggest that animals with tail damage (propensity to being bitten) might have impaired lipolysis processes.

Key Words: pig behavior, tail damage, metabolomics, genomics

P313 Investigation of gene expression profiles for correlation between female reproductive hormones and estrous cycle in the ovary, oviduct, and endometrium in swine. W. Park*[1], B.-H. Choi[1], J.-M. Kim[3], J.-E. Park[1], H. Ka[4], K.-T. Lee[2], and D. Lim[1], *[1]Animal Genomics and Bioinformatics Division, National Institute of Animal Science, RDA,Wanju, Republic of Korea, [2]Animal Genetics and Breeding Division, National Institute of Animal Science, RDA, Wanju, Republic of Korea, [3]Department of Animal Science and Technology, Chung-Ang University, Anseong, Gyeonggi-do, Republic of Korea,*