

POSTER - RNA AND TRANSCRIPTOMICS

**DIFFERENTIAL GENE EXPRESSION IN SKELETAL MUSCLE OF PIGS
WITH EXTREME VALUES OF OLEIC ACID CONTENT**

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The meat's fatty acid composition is directly linked with pork quality, eating experience, and nutritional value for human health. Monounsaturated oleic acid (OA, C18:1) is a fatty acid associated with a lower risk of human metabolic diseases, including inflammation and obesity. The proportion of OA in intramuscular fat (IMF) is highly influenced by the animals' diet and genetic background, and it can modulate the gene expression level in different tissues. Considering the importance of OA for human health and its relationship with metabolic processes, the main objectives of this study were to investigate the differences in the gene expression level in the skeletal muscle of pigs the Large

White line that deposited extreme levels of OA in IMF when fed a basal diet supplemented with canola oil (CO), soybean oil (SOY), or fish oil (FO) and identify metabolic pathways and gene networks involved in the metabolic processes identified. This study was approved by the Animal Care and Use Committee of Luiz de Queiroz College of Agriculture (ESALQ/USP). Among 54 Large White immunocastrated male pigs, 9 and 11 presented low and high OA content in IMF, respectively, based on the adjusted phenotypic values by a linear model in the R software. The Tukey test was used to identify significant differences between treatments at a significance level of 5%. RNA-Seq data from the selected animals were used to identify differentially expressed genes (DEG) in the skeletal muscle of pigs. The quality of the raw RNA-Seq reads was evaluated using the FastQC v.0.11.8 software. The reads were filtered using Trim Galore v.0.6.5 software and aligned to the Sus Scrofa 11.1 reference genome available on the Ensembl database. The mRNA abundance for all annotated genes was calculated using the STAR v.2.7.6a package and gene expression levels were normalized using the R package DESeq2. The results obtained through the statistical mean test performed between the high and low OA groups showed significant differences ($p < 0.05$). A total of 142 DEG (\log_2 -FC difference = 1 or = - 1; FDR-corrected p-value < 0.1) were identified between the group of animals with low and high OA deposition in IMF. Of these, 69 DEG were down-regulated and 73 were up-regulated. Among the up-regulated genes, SLC9A3 (\log_2 FC +2.55), NCEH1 (\log_2 FC +1.88), and EPHX1 (\log_2 FC +1.78) are key candidate genes related to the bile secretion pathway. On the other hand, the adipocyte lipolysis regulation pathway was enriched with down-regulated genes, including GNAI1 (\log_2 FC -1.63), PLIN1 (\log_2 FC -3.90), and IRS3 (\log_2 FC -3.99). These findings provide important insights into the mechanisms involved in OA deposition in pork meat and may contribute to the development of nutritional strategies to improve meat quality.