They can regulate precise physiological processes and be altered during disease-states. We set out to understand their importance in rainbow trout, a carnivorous fish that develops severe enteritis when fishmeal in their diets is replaced with sustainable plant-based proteins. Through years of selective breeding, our group has developed an enteritis-free model rainbow trout strain that thrives on a 100% fishmeal-free diet. As dietary substitution is known to effect hepatic metabolism, commercial (susceptible to enteritis development) and selected (no enteritis) trout strains were fed replacement diets for several months, and then livers ($n$ = 20) were sampled and prepped for strand-specific Illumina HiSeq. Reads (~25M/liver) were clustered with Trinity. Transcripts were subjected to Annocript pipeline using BLASTn, BLASTx and rpsBLAST in searches of gene identification, gene ontology, open reading frame and conserved domain matches. Data was compiled with strand-information, a protein-coding-potential algorithm applied and non-coding probabilities calculated. To date, we identified 911 and 778 putative lncRNAs ( > 0.95 Pr) between commercial and selected trout, respectively. Similar to human GENCODE, the majority ( > 60%) identified were intergenic. Interestingly, exonic lncRNAs enriched in symptomatic fish include potential regulators of bile acid transporters and apolipoproteins, also observed in mammalian gastrointestinal disorders. With the trout genome in early stages of description, these data will be useful additions as we prepare for functional studies. Ongoing work includes addition of individuals, tissues and treatments to the map while confirmation experiments and full-length assessments are in preparation.

**Key Words:** noncoding RNA, trout, salmonid, enteritis, nutrition, diet, aquaculture

**P3032 Association of skeletal muscle transcripts with fatty acid content in Nellore cattle.**

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Fatty acids have been implicated in a variety of different biological processes — for example, activation of transcription factor. In this study, we utilized *Longissimus* muscle (skeletal muscle) with extreme fatty acid (FA) content to evaluate the association of different fatty acids and gene expression. The transcriptome and fatty acid profile of skeletal muscle from 200 Nellore steers was obtained by RNA-seq using Illumina platform (HiSeq 2500) and gas chromatography, respectively. Thirty animals with high (H) and 30 with low (L) skeletal muscle FA content were selected for this study for each fatty acid evaluated. The FAs used herein were oleic acid (OA), palmitic acid (PA), stearic acid (SA), linoleic acid (LA), conjugated linoleic acid *cis*9-tran11 (CLA-c9t11), eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA), which were chosen based on their importance in many biological processes. These animals did not differ in their intramuscular fat content (IMF) or backfat thickness. Tophat2, HTSeq and DESeq2 programs and R packages were utilized to performed differential expression analysis between H and L groups. No differentially expressed genes (DEGs, FDR 10%) were identified for LA or SA; only a few DEGs were identified for EPA (5), DHA (4 DEGs) and PA (123 DEGs); while a large number of DEGs were identified for OA (1134) and CLA-c9t11 (872). Functional annotation and enrichment from OA DEGs identified important genes and canonical pathways such as *SCD*, *PLIN5*, LDL-cholesterol, *CPT1* and *PPAR,* related to oxidative phosphorylation, insulin receptor signaling, docosahexaenoic acid (DHA) signaling and oleate biosynthesis. Enrichment analysis of CLA-c9t11 DEGs identified one KEGG pathway, Ribosome (BH-adj = 1.2e-02), and several molecular functions such as nucleotide binding (BH-adj = 1.7e-03), ATP binding (BH-adj = 2.2e-02) and structural constituent of ribosome (BH-adj = 2.4e-02). In this study, animals of common nutrition, sex and similar age with no statistical difference in IMF and backfat thickness had many DEGs due to variation in OA and CLA-c9t11 content. These results indicate that only a couple of fatty acids appear to have potential biological activity, by either direct or indirect effects, on skeletal muscle and possibly other tissues in Nellore beef cattle.

**Key Words:** conjugated linoleic acid, oleic acid, RNA-seq, differentially expressed genes