POTENTIAL RELATIONSHIP OF THE PORCINE MUSCLE THANATOTRANSCRIPTOME TO PORK QUALITY

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I. OBJECTIVES

Genome-wide association studies for pork quality traits that are defined antemortem (i.e., fatty acid profile) tend to yield clear QTL associations, while studies for traits affected by postmortem metabolism (i.e., color) are less clear. Most gene expression studies for identification of meat quality candidate genes involve tissues collected at death, though studies have reported many genes to be upregulated postmortem (thanatotranscriptome). Anaerobic glycolysis is considered the primary postmortem metabolic pathway in the conversion of muscle to meat; however, oxygen remains in postmortem muscle for hours to support mitochondrial function. The objectives of this study were to determine changes in gene expression within the postmortem interval and relate these affected genes and pathways to QTL for pork quality.

II. MATERIALS AND METHODS

Gilts ($n = 5$; 262 to 325 d of age) were harvested using electrical stunning and conventional chilling. *Longissimus lumborum* muscle samples were removed at 0, 24, and 48 h postmortem. Samples for the 24- and 48-h time periods were chilled as part of the carcass. From each sample, RNA-seq libraries were prepared. An average of 58.5 million paired-end reads were collected from each library, mapped to Sscrofa 11.1 assembly, and differential gene expression was determined using DESeq2. Genes were considered differentially expressed with a false discovery rate-corrected $P \leq 0.05$. Differentially expressed genes were compared to existing QTL for pork quality traits.

III. RESULTS

Compared to 0-h samples, 4 and 1,943 genes were more highly expressed and 132 and 2,280 were more lowly expressed at 24 and 48 h, respectively ($P < 0.05$), with log2 fold changes ranging from −7.15 to 2.55 compared to 0 h. The most overrepresented pathways included ribosomal protein, protein translation, oxidative phosphorylation, and cytochrome-C oxidase activity ($P < 0.05$). Genes coding for mitochondrial complexes I (34 of 44), II (3 of 4), III (2 of 10), IV (19 of 9), and V (11 of 20) were more highly expressed ($P < 0.05$) at 48 h postmortem than at death. These differentially expressed genes are primarily involved in electron transport, the TCA cycle, and ATP synthesis. Differentially expressed genes ($P < 0.05$) also included ribosomal proteins (85 of 109) as well as mitochondrial ribosomal proteins (40 of 77), suggesting an increase of translational capacity. Enzyme-linked immunosorbent assay for 3 proteins (HSPA6, CCL21, and EPB42) with gene expression fold changes of 5.1, 2.94, and 4.4 at 48 h showed protein content changes ($P < 0.05$) of 88.01%, 42.19%, and −37.17% at 48 h, respectively. One hundred and twenty more highly expressed genes ($P < 0.05$) at 48 h postmortem were located within QTL associations for color, pH, water-holding capacity, and tenderness.

IV. CONCLUSION

These results imply that gene expression and protein translation continue to occur in postmortem muscle. Increased gene expression resulted in protein synthesis. This contrasts with the current dogma that gene expression ends at death. The overlap of genes expressed postmortem with genes previously associated with pork quality traits indicate that postmortem gene expression could impact meat quality.

Keywords: gene expression, pork, postmortem change, quality, thanatotranscriptome