

RNA-Seq data provide new insights into the molecular regulation of breast muscle glycogen reserves, a key factor in muscle function and meat quality in chickens

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Abstract:

Understanding the molecular mechanisms underlying muscle glycogen reserves in chickens is crucial due to their major impact on muscle ultimate pH and meat quality. The Pectoralis major muscles of two chicken lines, divergently selected for ultimate pH (pHu+ and pHu-), represent a unique model for exploring these mechanisms.

This study aimed to (i) perform RNA-Seq analysis of breast muscle from the 15th generation of these lines to characterize gene expression divergence, and (ii) investigate molecular interactions between digestive and muscular tissues through co-expression network analysis.

RNA sequencing was performed on breast muscle and jejunum tissues from 4-week-old chickens of both lines. Differential gene expression analysis revealed transcriptomic differences in the breast muscle between the two lines. Weighted Gene Co-expression Network Analysis (WGCNA) was used to identify modules of co-expressed genes across tissues and to explore associations with muscle glycogen content and digestive traits.

In total, 2,676 differentially expressed genes ($\text{Padj} \leq 0.05$) were identified in the breast muscle. The pHu- line exhibited activation of pathways involved in energy production from various substrates and in the development of blood and lymphatic tissues. In contrast, the pHu+ line showed enrichment in processes related to muscle remodeling, immune response, inflammation, and mitochondrial dysfunction patterns similar to those observed in wooden breast pathology. WGCNA identified 64 co-expression modules, among which a key module composed of 70% of genes expressed in muscle and 30% in jejunum was correlated with muscle glycogen content and intestinal health indicators. This module was enriched in functions related to nerve signaling and oxygen transport.

This study highlights specific molecular signatures associated with divergent muscle glycogen reserves in chicken lines and provides new insights into gut–muscle interactions. Several differentially expressed genes co-localized with QTLs, selection signatures, or had previously been associated with wooden breast, thus offering promising markers for further investigation.

Keywords: Chicken, Muscle, Gut, RNA-Seq and Glycogen