

## WHOLE TRANSCRIPTOME ANALYSIS OF *PECTORALIS MAJOR* MUSCLE REVEALS DIFFERENCES IN CALCIUM SIGNALING PATHWAY BETWEEN WHITE STRIPING AFFECTED AND UNAFFECTED BROILERS

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Genetic selection for growth rate and feed efficiency has resulted in rapid muscle development in chickens. Modern broiler lines have shown high incidence of problems related to meat quality, such as the appearance of white striping in parallel to the direction of the meat fibers. However, little is known about the genetic mechanisms involved in this condition in poultry. Thus, this study aimed to characterize the genetic pathways involved in the manifestation of white striping in broilers by RNA sequencing of the *pectoralis major* muscle (PMM). RNA was extracted from 6 samples of PMM tissues (3 affected and 3 unaffected by white striping) collected from male broilers of a commercial line Cobb 500<sup>®</sup>, at 45 days of age. The whole transcriptome sequencing was conducted using Illumina HiSeq 2000 (2x100 bp). Libraries were prepared using the TruSeq<sup>™</sup> RNA Sample Prep Kit v2 following by paired-end sequencing. Sequence reads were mapped and analyzed using BWA MEM software. HTseq software and edgeR package were used to count and identify differentially expressed genes, based on the level of False Discovery Rate (FDR $\leq$ 0.01). Gene annotation was performed using KEGG pathway analysis and genes were categorized using DAVID database. The results revealed that 11,177 genes were expressed in the PMM from a total of 17,108 annotated genes in the chicken genome. Out of those, 1,041 genes were differentially expressed between affected and unaffected groups. Fifty-one percent of these genes (528) were upregulated in the affected chickens, while the remaining (513) were downregulated. Genes with defined biological function were clustered in 27 functional groups according to their most important molecular functions and allocated into 8 known metabolic pathways. Pathway analysis related these genes to biological functions and canonical pathways controlling the glycogenesis, regulation of actin cytoskeleton, pentose phosphate pathway, starch and sucrose metabolism, metabolism of alanine, aspartate and glutamate, calcium signaling pathway, natural killer cell mediated cytotoxicity, and focal adhesion. The most significant metabolic pathway differentially modulated between groups was glycogenesis. However, another interesting and significant pathway to be explored is the calcium signaling pathway, which has been previously associated with the occurrence of white striping. Increased levels of calcium were observed in white striping affected tissue. These results can help in the identification of genetic variants affecting the development of this disorder. This is the first comprehensive analysis of transcriptome and expression profiles related to the occurrence of white striping in commercial broilers. Furthermore, these findings may contribute to improve broiler meat quality, and to clarify the understanding of muscle myopathies, using chicken as an animal model.

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