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RNA-Seq to Identify Genes Involved with Femoral Head Necrosis in Broilers

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Room:

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Genetic improvement for faster growing chickens have negatively impacted the locomotor and metabolic functions, causing economic losses to producers and to the industry, in addition to affecting animal welfare. Several strategies have been used to reduce the prevalence of bone related problems in the poultry industry; however they were not effective, since the incidence has increased. Femoral head necrosis (FHN) is a frequent condition associated with lameness in broilers, nevertheless not much is known about the genetics involved with this pathology. Therefore, the objective of this study was to investigate the femur transcriptome of broilers from the same flock with 21 days of age to identify genes involved with this condition. For this, the mRNA from femur growth plate of 3 broilers with FHN and 3 healthy chickens was extracted using TRIZOL and sequenced with the Illumina HiSeq (15 M reads per sample, 2x100bp). After data cleaning, 97% of the reads were mapped to the chicken reference genome (Galgal4), which contains 17,108 genes (Ensembl release 75). EdgeR software was used to analyze gene expression data and identified 11,748 genes being expressed in femur samples. Out of those, 167 were differentially expressed between healthy and affected groups (FDR<0.05). Using DAVID, we have identified 142 genes participating in 16 different clusters of biological process, including extracellular region (p<7.3E-11), collagen triple helix repeat (p<3.9E-6) and proteinaceous extracellular matrix (p<5.5E-6). Our results indicate a significant difference in the expression of 167 genes related to FHN in broilers with 21 days of age.

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