INSIGHT INTO THE CELLULAR MECHANISM OF PHYTOGENIC COMPOUNDS VIA TRANSCRIPTOMICS APPROACH

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Plant-derived feed additives are considered as good alternatives to in-feed antibiotics, showing beneficial effects on the palatability of feed, growth of animals, and their gut development and health. However, the mechanisms underlying their functions are still largely unclear. The emergence of Next Generation Sequencing can lead the way to optimize animal nutrition, with RNA sequencing being an important tool in the elucidation of mode of action. The chicken genome has been updated end of 2016 (Galgal5), reaching now 25,000 annotated genes, and therefore, increasing the information gain during transcriptomics analysis. Two broiler chicken trials were conducted separately, in which birds were fed either basal feed or feed supplemented with phytogenic compounds. For each trial, the small intestine was sampled at day 35, and RNA was extracted from five birds per diet, and sent for RNA-Seq (Illumina HiSeq, PE data, 30M reads, 150 bp). The transcriptome was analyzed via mapping of the reads in STAR with Galgal5, quantification with HTSeq count and normalization in edgeR. This resulted in the identification of 73 differentially expressed genes (DEGs) between control and phytogenic groups (cut-off 2 and FDR with p<0.05). The pathways enriched with these DEGs were determined in IPA, and were mostly related to immunological processes, e.g. IL-22 or STAT3 signaling. To validate these findings on immunomodulatory effects in a disease model, chickens were orally challenged with an overdose of coccidial vaccine, and the typical lesions observed in the ceca of challenged birds were significantly reduced in the birds fed the phytogenic formulation.