



Functional genomics of the digestive function in broilers

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Functional genomics of the digestive function in broilers

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While poultry breeding strategies have so far favored highly performing animals, the sustainability of poultry farming relies on the development of production systems incorporating more various feedstuffs. This implies to integrate adaptation to feed in breeding programs, such as digestive efficiency of feedstuffs with lower values. The aim of the ADIGEN project was to improve the understanding of genes involved in digestive function by characterizing the transcriptome of different compartments of the gastrointestinal tract: the junction between proventriculus and gizzard, the gizzard, the gastroduodenal junction, and the jejunum.

Total RNA from the 4 tissues were sequenced on HiSeq2500 for six individuals from a F2 cross between two broiler lines divergently selected for digestive efficiency (D+ / D-) on a Rialto wheat based-diet. Reads were aligned against the chicken genome (Galgal4 version) with TopHat and then quantified with featureCounts. Biostatistical analysis was performed with EdgeR and a total of 11216 differentially expressed transcripts (representing 9155 genes) between at least two tissues was characterized. In total, eight groups of genes with markedly different expression profiles were identified. The greatest differences in expression were related to the expression in the jejunum, which is a particular tissue compared to the other three, as its main function is the absorption of nutrients. Nevertheless, we also detected a cluster of genes overexpressed in the two junctions (proventriculus to gizzard and gizzard to duodenum), which included among others, different genes involved in muscle contraction. The functional analysis of the expression clusters by "Gene Ontology" showed a significant enrichment of the immune function and the catabolism of small molecules in the jejunum, which is in agreement with the literature. In a more original way, we observed an enrichment for genes involved in protein synthesis in the gizzard and the gastro-duodenal junction, compared to the other compartments.

This analysis allows us to draw the first molecular portrait of the different compartments of the digestive tract, which will serve as a basis for future studies on the genetic and physiological control of the animal response to feed variations.

Keywords: digestive efficiency; broiler; transcriptomics