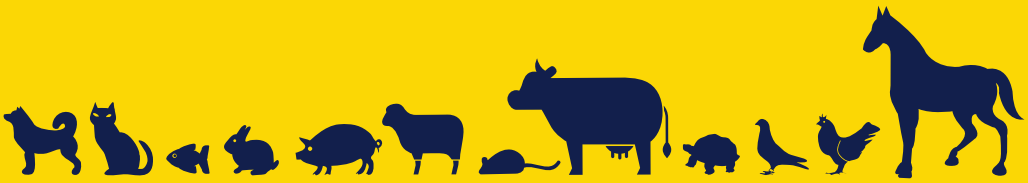
ESVCN

European Society of
Veterinary & Comparative
Nutrition

CONGRESS PROCEEDINGS

23rd Congress of the European Society of Veterinary and Comparative Nutrition



University of Torino - Italy | September 18th - 20th 2019

UNIVERSITÀ
DEGLI STUDI
DI TORINO

Animal Nutrition Unit
Dept. of Veterinary Sciences

uniss
UNIVERSITÀ DEGLI STUDI DI SASSARI

Co-organizer:
Animal Nutrition Unit
Dept. of Veterinary Medicine

Immune responses gene expression in broiler chickens fed mealworm meal

Nery J[1], Soglia D[1], Sartore S[1], Maione S[1], Viola I[1], Dabbou S[1], Sacchi P[1], Rasero R[1], Bergero D[1], Bianchi C[1], Gai F[2], Renna M[3], Gasco L[2,3], Schiavone A[1]
[1]Department of Veterinary Sciences, University of Turin, Italy; [2]Institute of Science of Food Production, National Research Council, Turin, Italy; [3]Department of Agricultural, Forest and Food Sciences, University of Turin, Italy. e-mail: achille.schiavone@unito.it

Introduction. Over the last decade several studies were done to assess the nutritional composition and effects of partial substitution of traditional protein sources with insect meal in animal health. The aim of this study was to assess the effect of dietary *Tenebrio molitor* (TM) meal supplementation on immune and cellular responses to external stimuli of intestinal mucosa and liver in poultry.

Animals, material and methods. One-day old broiler chicks (Ross 708) were raised in 10 pens (8 birds/pen), and were divided in 2 groups. Two isonitrogenous and isoenergetic feeding plans were used (12.9 MJ ME/kg and 23.5% CP from day 1 until day 12; 13.3 MJ ME/kg and 21.3% CP from day 12 until day 25; and 13.5 MJ ME/kg and 19.6% CP from day 25 until slaughter) containing either 0% (CT) or 15% (TM) mealworm meal (52.4% CP, 28.0% EE and 8.8% ash as fed). Two broilers/pen were slaughtered at 53 days of age. Liver, jejunum, and caecum samples were collected and stored in RNA Later solution (Ambion) at -80°C pending analysis. Pooled samples of each treatment were analyzed for RNA-seq using Illumina NGS analyzer. Differential expression of genes (DEG) was carried out using Cuffdiff test. Fisher test corrected with Bonferroni procedure [1] was used for statistical analysis of RNA sequencing data. Significant differences were considered for $p<0.05$.

Results and discussion. In a previous study the performance traits were reported [2]. Briefly FCR was higher ($p<0.01$) in TM than in CT group. The most important metabolic pathways with DEG between dietary treatments were liver and caecum innate immune responses, and cellular responses to stress and to metal ions. The DEG of most significant genes is presented in Table 1.

Table 1. DEG in birds fed TM compared with CT group (log2[fold change]).

Gene	Liver	Caecum	Observations, in birds fed TM[#]
AHSG	1.154***	-	Upregulation of proteins involved in endocytosis
CL2	1.034***	-	Upregulation of RNA catalysis
GPX3	-	-0.693***	Upregulation of intestinal antioxidant protective role
GPX2	-	0.141*	
PRDX1	-	0.143***	
H4-I	-	-1.084***	Downregulation of chromatin compaction
HMGA1	1.037*	-0.657***	Dysregulation of gene transcription
HPS5	-1.617***	-	Upregulation of organelle biogenesis (melanosomes, platelet dense granules, and lysosomes)
UBB	0.577***	0.053***	Upregulation of cellular protein targeting for degradation
TTR	0.837***	-1.499*	Dysregulation of thyroid hormone and retinol transport
VTN	0.402***	1.943***	Upregulation of cell adhesion and spreading, inhibition of membrane damaging

*$p<0.05$; **$p<0.01$; ***$p<0.001$.

Conclusion. Results suggest increased antioxidant defense, downregulation of gene transcription and upregulation of genes involved in cell adhesion in the caecum in TM compared to CT group. Liver gene expression was mostly related with genes coding for protein degradation and synthesis, which were generally upregulated in TM group.

References: [1] Xu et al. (2012) BMC Genomics. 13 (Suppl 8):S2; [2] Biasato et al. (2018) Poult. Sci. 97: 540-548.