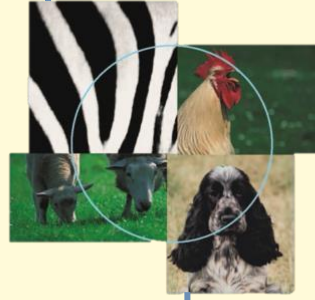


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5A3. Whole transcriptome analysis in broiler chicken fed mealworm meal

Nery J¹, Soglia D¹, Sartore S¹, Maione S¹, Stoppani N¹, Sacchi P¹, Bergero D¹, Bianchi C¹, Gai F², Gasco L³, Schiavone A^{1,2}

¹Department of Veterinary Sciences, University of Turin, ²Institute of Science of Food Production, National Research Council, Turin, ³Department of Agricultural, Forest and Food Sciences, University of Turin, Italy; E-mail: joana.nery@unito.it

Introduction: Over the last decades, increasing demand for cost-effective protein sources lead to global research of alternative food and feed sources [1,2]. The aim of this study was to assess the effect of dietary *Tenebrio molitor* meal supplementation on intestinal digestion and absorption of nutrients and the overall metabolism of carbon, nitrogenous and lipidic compounds in hepatic, intestinal and muscular tissues of broilers.

Animals, materials and methods: Ten replicates of day-old broiler chicks (Ross 708; 8 birds/pen) were divided into 2 groups and fed isonitrogenous and isoenergetic diets (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 day 52) containing either 0% (CT) or 15% (TM) mealworm meal. Two broilers/pen were slaughtered on day 53. Liver, jejunal, caecal and breast muscle samples were collected, pooled samples of each treatment and were analyzed for whole RNA-seq. Differential expression of genes (DEG) was carried out using the Cuffdiff. Functional analysis of gene expression was done using Reactome and KEGG database. Significant coding gene expression was defined for DEG below -1 and above 1. Fisher test corrected with the Bonferroni procedure was used and differences were considered significant at $p < 0.05$.

Results and discussion: Hepatic upregulation ($p < 0.001$) of primary bile acid biosynthesis (AKR1D1), steroid hormone biosynthesis (AKR1D1 and CYP1A1) and GLY, SER, THR, CYS and MET metabolism (BHMT) was observed in the TM compared to the CT groups. Birds fed the TM treatment presented upregulation of the jejunal ADH1B ($p < 0.001$) indicating increased glycolysis, gluconeogenesis, pyruvate metabolism along with fatty acid degradation, TYR metabolism and retinol metabolism. Jejunal upregulation of RBP2 ($p < 0.001$) in the TM compared to the CT group indicate higher vitamin digestion and absorption. Downregulation of genes involved in nitrogen metabolism (CA4, $p < 0.001$), pancreatic secretion (CCK, SLC26A3; $p < 0.001$) and protein digestion and absorption (CELA2A, $p < 0.01$) were found in the TM compared to the CT groups. The caecal samples of the TM group were downregulated for genes involved in carbon metabolism (PSPH, $p < 0.001$; AMT, $p < 0.05$), biosynthesis of amino acids (PSPH), GLY, SER and THR metabolism (PSPH, AMT), glyoxylate and dicarboxylate metabolism (AMT), oxidative phosphorylation (COX8A, $p < 0.001$), purine metabolism (HDDC3, $p < 0.05$), butanoate metabolism and VAL, LEU and ILE degradation (HMGC2, $p < 0.01$), glycerophospholipid metabolism, ether lipid metabolism, essential fatty acids metabolism, pancreatic secretion, fat digestion and absorption (PLA2G2E, $p < 0.05$). Upregulation of genes involved in caecal fat digestion and absorption (APOA4 and FABP1, $p < 0.001$), cholesterol metabolism and vitamin digestion and absorption (APOA4) was seen in the TM compared to the CT groups. Muscle downregulation of CHAC1 ($p < 0.001$) involved in glutathione metabolism and upregulation of PHGDH ($p < 0.001$) involved in carbon metabolism, biosynthesis of amino acids, GLY, SER, THR, CYS and MET metabolism was observed in the TM compared to the CT groups. The influence of *T. molitor* supplementation on protein metabolism in poultry [3] was previously reported.

Conclusion: Diet supplementation with *T. molitor* meal seems to stimulate hepatic gene expression of lipid and amino acid metabolism. It also influences intestinal glucose, fat and protein metabolism, and lipid, protein and vitamin digestion and absorption. Finally, *T. molitor* supplementation leads to the upregulation of protein metabolism in muscle.

References: [1] Elhassan et al. (2019) Foods 8(3):95; [2] Gasco et al. (2019) Animals (Basel) 9(4):170 ; [3] Soglia et al. (2022) Poultry 1(1), 14-29. Department of Veterinary Sciences Ethical Committee, Ref. 4, 23/06/14.