**Lipid metabolism gene expression in broiler chickens fed mealworm meal**

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**Introduction:** Research on the use of insect meal in animal [1,2] and human [3,4] nutrition is growing over the last decade due to the scarcity of protein sources. The aim of this study was to assess the effect of dietary *Tenebrio molitor* (TM) meal supplementation on lipid metabolism of intestinal mucosa and liver in broiler chicken.

**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. Birds were fed 2 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 53) containing either 0% (CT) or 15% (TM) mealworm meal [1](52.4% CP, 28.0% EE as is, 20.19% TFA, 4.94% SFA, 8.01% MUFA, 7.24% PUFA on DM basis; chitin [1] 46.2 g/kg as is). At 53 days of age, 2 broilers/pen were slaughtered. Liver, jejunum, and caecum samples were collected, rinsed in saline solution and stored in RNA Later solution at -80°C pending analysis. Pooled samples per treatment were analyzed for RNA-seq using Illumina NGS analyzer. Differential expression of genes (DEG) was carried out using Cuffdiff. Fisher test corrected with Bonferroni procedure [5] was used for statistical analysis of RNA sequencing data. Significant differences were considered for p < 0.05.

**Results and discussion:** Performance traits were previously presented [1]. Briefly, FCR (p < 0.01) was higher in TM compared with CT group. The most important metabolic pathways with DEG between dietary treatments (table 1) were regulation of lipid metabolism by peroxisome proliferator-activated receptor alpha, fatty acid metabolism, triglyceride metabolism and ketone body metabolism.

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Gene | Liver | Jejunum | Caecum | Observations, in birds fed TM# |
| APOA1 | 0.59\*\*\* | -0.27\*\*\* | - | Higher liver and lower jejunum HDL-cholesterol transport |
| FABP1 | 0.48\*\*\* | - | -1.90\*\*\* | Higher liver LCFA uptake, transport and metabolism, and TG catabolism and lower caecum LCFA transport |
| CYP1A1 | 2.25\*\*\* | - | - | Higher lipid synthesis  |
| PLIN2 | -1.33\*\*\* | - | - | Lower lipid accumulation |
| HMGCS1 | -0.19\*\*\* | - | - | - |
| HMGCS2 | - | - | -2.00\*\* | Lower ketogenesis |
| FABP6 | - | -0.36\*\*\* | - | Lower LCFA transport and metabolism |
| FABP3 | - | - | 0.43\* | Higher LCFA transport and metabolism |

\*p < 0.05; \*\*p < 0.01; \*\*\*p < 0.001; #HDL, high density lipoprotein; TG, triglyceride; LCFA, long-chain fatty acid.

**Conclusion:** Gene expression involved in lipid metabolism could indicate an hepatic anabolic state together with decreased lipid accumulation, and lower transport in distal segments of the intestinal tract of broilers fed TM meal compared with CT diet. Therefore TM diets could lead to increased fat deposition in peripheral tissues while preventing hepatic fat accumulation in broilers.

**References**: [1] Biasato et al. (2018) Poult. Sci. 97: 540-8; [2] De Marco et al. (2015) Anim. Feed Sci. Technol. 209, 211-8; [3] Payne et al. 2016, Eur J Clin Nutr 70, 285-91; [4] Stoops et al. 2016 Food Microbiol 53, 122-7; [5] Xu et al., 2012, BMC Genomics 13:S2.