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Diet-Induced Dysbiosis of the Intestinal Microbiota in Broiler Chickens

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The Problem

Deficiencies in intestinal health are associated with shifts in the composition of the intestinal microbiome (dysbiosis), leakage of the mucosal barrier and/or inflammation. The aim of this study was to develop an experimental feed-based dysbiosis challenge model.

How we investigated or researched the problem

Male broiler chickens (Ross 308) were fed either a control diet or a dysbiosis challenge diet (5 pens/group, 18 birds/pen). The composition of the dysbiosis diet was characterized by an increased level of sunflower meal and the inclusion of rye and rapeseed meal, resulting in a high dietary level of non-starch polysaccharides (NSP). Furthermore the level of essential amino acids was decreased by 10% and the level of dietary fat of animal origin (poultry) was increased compared to the control diet. Sampling was performed at day 13, 26 and 39. Intestinal microbiome profiling was performed by next-generation sequencing of 16S ribosomal DNA. mRNA expression of expression of genes involved in the mitogen-activated protein kinase pathway was evaluated by qRT-PCR.

Results

Broiler performance parameters were significantly negatively affected in chickens fed the dysbiosis challenge diet compared to the control diet. Alpha diversity of the ileal and caecal microbiota was not influenced by diet. In contrast, beta diversity of the ileal and caecal microbiota was significantly influenced by diet. An increased abundance of the family of *Enterobacteriaceae* was observed in the ileum of chickens of 13d old fed the dysbiosis challenge diet. At the age of 26 and 39d a significantly increased abundance of the genera *Bifidobacterium*, *Turicibacter* and *Sellimonas* was observed in the caecum, while the abundance of the genera *Akkermansia* and *Faecalitalea* was decreased. A remarkable increased abundance of the family of *Streptococcaceae* was demonstrated in the caecum of chickens fed the challenge group compared to the control group at d39, 14.67±6.55% versus 6.34±6.14%, respectively. Only some minor effects on the families of the *Ruminococcaceae* and *Lachnospiraceae* were observed. A significant increased mRNA expression of tumor necrosis factor (TNF) α was observed in the caecum of chickens fed the challenge diet (39d), and mRNA expression of *Toll-like receptor 2 β* and *4* (26d) was decreased.

Implications / Conclusions

A feed-based dysbiosis challenge model was being developed characterized by an increased ileal level of lipopolysaccharide (LPS) containing *Enterobacteriaceae* in young chicks. Decreased TLR *2 β* and *4* might correlate with intestinal cell protection against dysregulated pro-inflammatory gene expression in response to LPS. In older chicks, a microbiota shift similar as in certain cases of inflammatory bowel disease was observed, suggestive for an altered short-chain fatty acid profile towards lactate overproduction.