



Gut microbiota and host interactions in chickens: a dynamic interplay with performance implications.

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Historically, health issues were addressed through the addition of antimicrobials such as antibiotics, ZnO, CuSO₄, or antibiotics for prophylactic and metaphylactic purposes. However, emergence of bacterial resistance and environmental pollution have prompted legislation which limits or bans the use of antibiotic growth promoters and ZnO. As a result, there is an increasing focus on studying the microbiota and its interaction with the host. The aim of the current study was to investigate differences in sex and environmental factors. To do this, two trials were performed in Belgium, where microbiota, gut permeability, and ileal gene expression in broiler chickens was tested.

Firstly, a small-scale broiler experiment with 144 male and 144 female Ross 308 chicks was performed. The broilers were divided into four pens and monitored until 21 days (d) according to breed specifications but with a diet rich in protein and non-starch polysaccharides (NSP) from wheat and rye. Ileal tissue and content samples were collected, and *in vivo* gut permeability was assessed using FITC-dextran-4kDa. Analysis included body weight, microbiota (V1-V9 16sRNA sequencing), gut permeability, and ileal gene expression (high-throughput qPCR analysis).

Secondly, a larger-scale broiler experiment was performed, monitoring two groups of male broilers for 5 weeks under *Enterococcus cecorum* challenge. Each group consisted out of 8 pens containing 20 birds each and monitored till day 35 and were consuming the same diet as in trial 1 (rich in protein and non-starch polysaccharides (NSP) from wheat and rye). Parameters were as in the first trial, with extra sampling at days 28/29 and 35.

In the first trial, differences in microbiota and gene expression could be observed between sexes soon after hatching. Microbiota, intestinal permeability and expression of nutrient-transport related genes showed differences at 21d, coinciding with the sex-related growth curve divergence. The results of the challenge trial demonstrate differences in metabolism and nutrient transport gene expression due to the infection, as well as severely diminished performance parameters.

In conclusion, sex differences should be considered from early life when optimizing health and performance, while *Enterococcus cecorum* infection results in differential gene expression of a range of genes. This may form the basis of further unravelling the complex dynamic interaction that gut health has with performance of the broiler flock.