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Comparison of the digestive microbiota between two divergent lines of chickens selected based on apparent metabolisable energy. B Konsak^a, S Guardia^a, M. Leconte^a, C Moreau-Vauzelle^b, C Dupont^b, J. Doré^c, F. Levenez^c, S Mignon-Grasteau^a, I Gabriel^a. ^aINRA, UR83 Recherches Avicoles, F-37380 Nouzilly, France, ^bINRA, UE 1206, UEASM, Élevage alternatif et santé des monogastriques, Domaine du Magneraud, F-17700 Saint-Pierre-d'Amilly, France, ^cINRA, UMR1319 Micalis, F-78352 Jouy En Josas, France.

Digestive microbiota can be affected by extrinsic factors, such as rearing environment and feed including feed additives, but also intrinsic factors such as genetic of individual due to host and digestive microbiota interactions¹. Particularly, genetic selection of animals on their digestive capacity, leading to a change of compounds non-digested by the host and hence available substrates for the digestive microbiota, may lead to changes of this microbiota.

During this work, digestive microbiota of two divergent chicken strains selected during 9 generations on their apparent metabolisable energy (EMAn), EMAn+ and EMAn-², was compared. Microbiota was studied in two digestive segments, the small intestine (site of host digestion), more precisely the ileum, and the caeca (major site of microbiota development). Analyses were performed both on the digestive contents and on the mucosa. Approaches were qualitative (fingerprint, TTGE), and quantitative (qPCR).

The results showed that these animals with different growth performance and development of their digestive organs have different digestive microbiota. Thus, a slightly different microbiota fingerprint between strains was observed in ileal digestive content, along with a clear difference in the both the contents and mucosa of the caeca. The analysis by qPCR did not shown significant difference in total bacteria, but differences appeared for some major groups. Thus EMAn+ chickens showed in ileal content higher in *C. coccooides* and lower in *E. coli*. In caecal content, these birds showed lower *Lactobacillus*, and particularly *L. salivarius*, and also lower *E.coli*. In contrast, the *C. leptum* group was higher. In the ileal mucosa, lower *L. salivarius* were observed, and in caecal mucosa, lower total *Lactobacillus*, as well as *L. salivarius* and *L. crispatus*, but higher *E.coli* numbers. Thus this genetic selection on AMEn led to a clear change in digestive microbiota.

1 Gabriel, I., et al. (2006). Microflora of the digestive tract: critical factors and consequences for poultry. World's Poul. Sci. J. 62, 499-511.

2 Mignon-Grasteau, S., et al. (2004). Heritability of digestibilities and divergent selection for digestion ability in growing chicks fed a wheat diet. Poul. Sci. 83, 860-867.