

**Impact of a genetic selection led on digestive efficiency on gut microbiota composition in broiler chicken.  
Impact d'une sélection génétique sur l'efficacité digestive sur le microbiote intestinal de poulet**

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Afin de comprendre l'influence complexe du microbiote intestinal sur l'efficacité digestive et la santé chez le poulet de chair, nous avons exploité une population F8 de 200 animaux dérivés d'un croisement entre deux lignées de poulet divergentes sélectionnées pour leur efficacité digestive avec un régime à base de blé. Des travaux précédents ciblant par Q-PCR les principaux groupes bactériens ont montré que la composition du microbiote caecal diffère entre les deux lignées. Nous avons sélectionné deux groupes de 20 animaux à partir de ces lignées

In order to understand the complex influence of intestinal microbiota on digestive efficiency and health in broiler, we took advantage of a F8 advanced intercross line progeny of 200 animals derived from a cross between two broiler chicken lines (D+/D-) divergently selected for their digestive efficiency on a wheat based diet. Previous work targeting specifically major groups of bacterias showed that caecal microbiota composition differs between D+/D- lines. We selected 2 groups of 20 animals with extreme digestive efficiencies at 23 days from this progeny. The AMEn values were 2558 and 3190 kcal.kg<sup>-1</sup> dry matter in the low and high efficiency groups, respectively. We assessed the microbiota composition in ileum, jejunum and caeca using a 16S rRNA gene sequencing approach. Relative abundances of the bacterial operational taxonomic units (OTUs) in each sample and their phylogenetic classification were obtained using the QIIME pipeline. Richness,  $\alpha$ - and  $\beta$ -diversity indices and comparisons of compositions in OTU were obtained with the phyloseq and metagenomeSeq R packages. As expected, caeca contained the richest and more diverse microbiota. We identified significant differences in OTU composition between the different intestinal segments, the more abundant order being Clostridiales for the caeca and Lactobacillales for ileum and jejunum. We observed significant differences in OTU abundances between the high/low digestibility groups of animals in each segment, thus confirming and enriching previous results. We identified 84 differentially abundant OTUs in caeca, with for instance 3 OTUs corresponding to *Butyricoccus pullicaecorum*, which is known as a butyrate producing bacteria with potential probiotic effects. We identified specific microbiota signatures in the gut of chickens harbouring poor/high digestibilities. We are currently investigating the correlations between individual variations in gut microbiota, digestive efficiency and physiology and innate immune status, in order to better describe the complex interplay between these physiological pathways.