

## Comparison of the digestive microbiota between two divergent lines of chickens selected based on digestive capacity

Barbara Konsak<sup>a</sup>, Sarah Guardia<sup>a</sup>, Maryse Leconte<sup>a</sup>, Carole Moreau-Vauzelle<sup>b</sup>, Christel Dupont<sup>b</sup>, Sandrine Mignon-Grasteau<sup>a</sup>, Irène Gabriel<sup>a,\*</sup>

<sup>a</sup>INRA, UR83 Recherches Avicoles, Nouzilly, F-37380 France

<sup>b</sup>INRA, UE 1206, UEASM, Surgères, 17700 France

\*Irene.Gabriel@tours.inra.fr

### Abstract

Gastrointestinal microbiota exists in symbiosis with the host and is implicated in numerous functions such as protection against harmful organisms, development and functionality of the digestive tract and its immune system, digestion of non digestible feed compounds and animal metabolism [1]. All these physiological effects influence animal performance. Digestive microbiota can be modified by factors such as diet, including feed additives (prebiotics, plant extracts, etc...), or the rearing environment [2-5]. Factors intrinsic to the animal may also be involved, such as the genetics of the individual. In particular, genetic selection of animals with varying digestive capacities may result in a change in the undigested feed components available as substrates for the gastrointestinal microbiota but may also affect physicochemical conditions (pH, redox potential, and mucin composition) within the gut, which could influence microbial gut populations.

In the present study, the intestinal bacteria of two divergent lines of chickens (D+ and D-) selected for apparent metabolizable energy (AMEn) were compared. The microbiota was studied in two digestive segments: the small intestine (ileum), the region of digestion, and the ceca, main location of bacteria within the digestive tract. The bacterial community was studied in both the digestive contents and mucosa. The methods used to study these communities were two cultivation independent methods: a qualitative method, temporal temperature gradient gel electrophoresis (TTGE) with analysis of similarity between profiles (Proximity matrix of similarity with Pearson's coefficient), and a quantitative method, real-time PCR for the analysis of the major bacterial groups.

The results show that animals of these two divergent lines differing in both growth performance and digestive organ development also differed in gut microbial composition. Differences of similarities between bacterial TTGE profiles within animals from the same line appeared in the digestive contents of both the ileum (D+: 50% and D-: 74%) and ceca (D+: 60% and D-: 45%). In addition to this, bacterial profiles differed between the lines, markedly in both the contents and mucosa of the ceca ( $R=0.61$  and  $0.54$  respectively), and somewhat in the contents of the ileum ( $R=0.30$ ). Quantification of the major bacterial groups also revealed differences between strains. Thus, genetic selection based on AMEn leads to a marked change in digestive microbiota. These differences in bacterial composition could be due to changes in digestive biotope related to the selection criterion, and could help explain the energy metabolism differences between the two lines. This shows that genetic selection may be a way to control the digestive microbiota during rearing and therefore reduce the preventative use of veterinarian antimicrobial drugs.

### References

- [1] Gabriel, I., Lessire, M., Mallet, S., Guillot, J.F. *World Poultry Sci J.* 62 (2006) 499-511.
- [2] Williams, J., Mallet, S., Leconte, M., Lessire, M., Gabriel, I. *Br Poultry Sci.* 49 (2008) 329-339.
- [3] Gabriel, I., Mallet, S., Leconte, M., Travel, A., Lalles, J.P. *Anim. Feed Sci. Technol.* 142 (2008) 144-162.
- [4] Guardia, S., Recoquillay F., Juin, H., Lessire, M., Leconte M., Rideaud M., Moreau-Vauzelle, P., Dupont, C., Guillot, J.F., Gabriel, I. 7th Joint Symposium Rowett-INRA on Gut Microbiology (2010)
- [5] Guardia, S., Konsak B., Juin, H., Lessire, M., Rideaud, P., Moreau-Vauzelle, C., Dupont, C., Guillot, J.F., Gabriel, I. *Poultry Sci.* (2011) In press.