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## Identification of genomic regions associated with caecal microbiota composition in a broiler line

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**WPSA France**

### Identification of genomic regions associated with caecal microbiota composition in a broiler line.

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Recent studies in Human as well as in animal livestock species have shown that intestinal microbiota composition is related to variations of many traits of interest, including health and production traits. Variations in intestinal microbiota composition probably contribute, together with host genetics, to the expression of chicken phenotypes of interest.

We report the study of 200 F8 animals derived from an advanced intercross between two lines genetically divergent for their digestive efficiency, namely D+ and D-. Previous studies have demonstrated that in addition to digestive efficiency, gut microbiota composition in these lines is partly under genetic control, with the detection of several QTL controlling the abundance of specific bacterial species, major bacterial groups or ratios of major bacterial groups measured using a targeted, specific Q-PCR approach. Here we used a more exhaustive approach by sequencing the V3-V4 region of the 16S rRNA bacterial gene to characterize the caecal microbiota composition. The composition in OTU (operational taxonomic units) was determined by using a QIIME pipeline. In parallel, animals were genotyped using a 580k SNP chip (Affymetrix) and a genome wide association analyses (GWAS) was performed using the GenABEL package of R, with OTU relative abundances as phenotypic traits.

We identified several genomic regions controlling the variations of specific OTU abundances, such as that of *Butyrivibrio pullicaecorum*, at the species level and higher taxonomic ranks. Some of these regions co-localised with previous QTL controlling either digestive efficiency (on chromosomes 2, 8 and 11) or abundance of bacterial groups previously identified. These results confirm that gut microbiota composition in the D+/D- line is partly under genetic control. Co-localisations with loci controlling other traits allow us to formulate some hypotheses on the putative candidate genes being involved in digestive efficiency or immunity. This study improved our understanding of the genetic relations between digestibility, immunity and microbiota composition.

Keywords: Gallus gallus; gut microbiota; GWAS; 16S approach; digestibility

### Benefits of testing biometric genomic selection

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A breeding program carried out in Denmark due to genotype by environment interactions in different environments, since only gain in P using pedigree-based BLUP prediction based on dense genotyping was used to explore the benefits of genomic selection in B and P. Given a limited test population allocated to be selection candidates, we investigated the benefits of genomic selection in P. We investigated genomic correlations ( $r_g$ ) between B and P was 0.28 while it was 0.15 in P. Genotyped and GBLUP was used to assign trait expressions in P. Testing in P significantly increased the improvement was largest in scenarios with 0, 15 and 30% gains by transferring birds to P if there is a strong GxE, a genotype to be tested in P has larger genomic

Keywords: GxE; bio-secure e