



**HAL**  
open science

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

Fanny Calenge, Jordi Estellé, Bertrand Bed'Hom, Ceren Simsek, Christelle Hennequet-Antier, Irène Gabriel, Sandrine Grasteau

### ► To cite this version:

Fanny Calenge, Jordi Estellé, Bertrand Bed'Hom, Ceren Simsek, Christelle Hennequet-Antier, et al.. Identification of genomic regions associated with caecal microbiota composition in a broiler line. 10th European Symposium on Poultry Genetics, Jun 2017, Saint-Malo, France. 2017, Proceedings of the 10th European Symposium on Poultry Genetics. hal-01607406

**HAL Id: hal-01607406**

**<https://hal.science/hal-01607406v1>**

Submitted on 2 Jun 2020

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution - ShareAlike 4.0 International License

Proceedings  
Of the  
Xth European Symposium  
on Poultry Genetics



26 - 28, June 2017  
Saint-Malo, France



WPSA France

---

**Proceedings of the  
10<sup>th</sup> European Symposium on Poultry Genetics**

---

26-28, JUNE 2017  
SAINT-MALO, FRANCE

Edited by  
Christophe BOSTVIRONNOIS (ELANCO)  
Christine LESSIRE (WPSA)  
Michèle TIXIER-BOICHARD (INRA)

for the French Branch of WPSA

<http://wpsa.fr/congres/EuropeanPoultryGenetics/Index%20ESPG.html>



**WPSA France**



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

Calenge Fanny, Estellé Jordi, Bed'hom Bertrand, Şimşek Ceren,  
 Hennequet-Antier Christelle, Gabriel Irène, Mignon-Grasteau Sandrine  
 INRA fanny.calenge@inra.fr, France  
 INRA jordi.estelle@inra.fr, France  
 INRA bertrand.bedhom@inra.fr, France  
 INRA ceren.simsek@inra.fr, France  
 INRA christelle.hennequet-antier@inra.fr, France  
 INRA irene.gabriel@inra.fr, France  
 INRA sandrine.grasteau@inra.fr, France

Corresponding author : fanny.calenge@inra.fr

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 selection

Chu Thinh T, Alemu Set

Center for Quantitative Genetics, Aarhus University  
 Blichers Allé  
 Center for Quantitative Genetics, Aarhus University

Center for Quantitative Genetics, Aarhus University  
 Blichers Allé  
 Cobb-Vantress Inc., United States  
 72761-1030

Cobb-Vantress Inc., United States  
 72761-1030  
 Center for Quantitative Genetics, Aarhus University  
 Blichers Allé  
 Center for Quantitative Genetics, Aarhus University  
 Blichers Allé

Corresponding author : chu.thinh@ Aarhus University

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, we allocated to be selection candidates. We investigated genomic correlations ( $r_g$ ) between B and P. It 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