Feed-a-Gene

Adapting the feed, the animal and the feeding techniques to improve the efficiency and sustainability of monogastric livestock production systems

INRA SCIENCE & IMPACT

# GWAS of digestive efficiency in chicken

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## Objectives

Feedstuffs used in poultry diets are more and more varied to cope with the increased cost of usual high quality feedstuffs and to limit environmental impact of animal productions. As these new feedstuffs are not as optimal as corn or soybean, animals are more challenged and have to be able to adapt to these new feeding conditions. Digestive efficiency is an essential component of chicken adaptability to feed. Heritability estimates of digestive efficiency indicated that this trait is partly under genetic control (Mignon-Grasteau et al., 2004). The purpose of this work was to improve our knowledge on the genetic basis of digestive efficiency through a genome-wide association study on chickens selected for their digestive efficiency.

## Materials and methods

### Animals

We used 192 animals from the 8th generation of an advanced intercross line between two divergent lines of broilers selected for their high or low digestive efficiency (criterion of selection: AMEn at 3 weeks, using a wheat-based diet). Before the start of cross, the difference in AMEn between the two divergent lines was around 30-40%.

Birds were reared on floor from hatch to 11 days and then transferred to individual cages for digestive efficiency measurement. Animals were fed with a wheat-based diet containing 55% of Rialto wheat, a viscous and hard variety.

### Balance trial

At 3 weeks, a balance trial was performed, using the method of total collection of feces of Bourdillon et al. (1990). After freeze-drying, feces were analyzed by NIRS to obtain AMEn, and coefficients of digestive use of dry matter, starch and nitrogen and lipids (Bastianelli et al., 2010).

### Genetic analyses

At the end of balance trial, animals were blood sampled and genotyped with the 540K SNP Affymetrix® Axiom® chip. After quality control (MAF, Hardy-Weinberg, Call rate), 353888 SNP were retained for the analysis. These SNP were located on chromosomes 1 to 28 and 33. Phenotypic data were pre-corrected for significant fixed effects. GEMMA software was used for GWAS analyses, with an univariate linear mixed model (polygenic effect, SNP effect). A Bonferroni correction was applied at genome level to take into account multiple testing.

## GWAS results

A total of 12 SNPs were genome-wide significant (Bonferroni adjusted *P*-value<0.05) for AMEn, coefficients of digestive use of dry matter, starch and nitrogen. None was significant for coefficient of digestive use of lipids.

**Figure 1. Manhattan plot for AMEn**

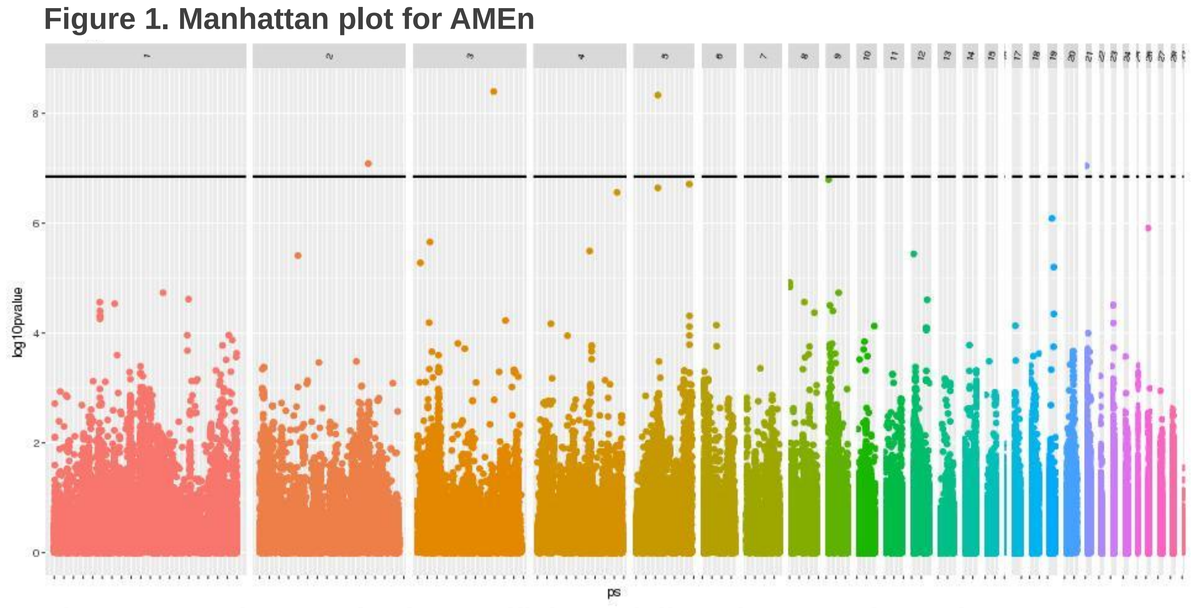
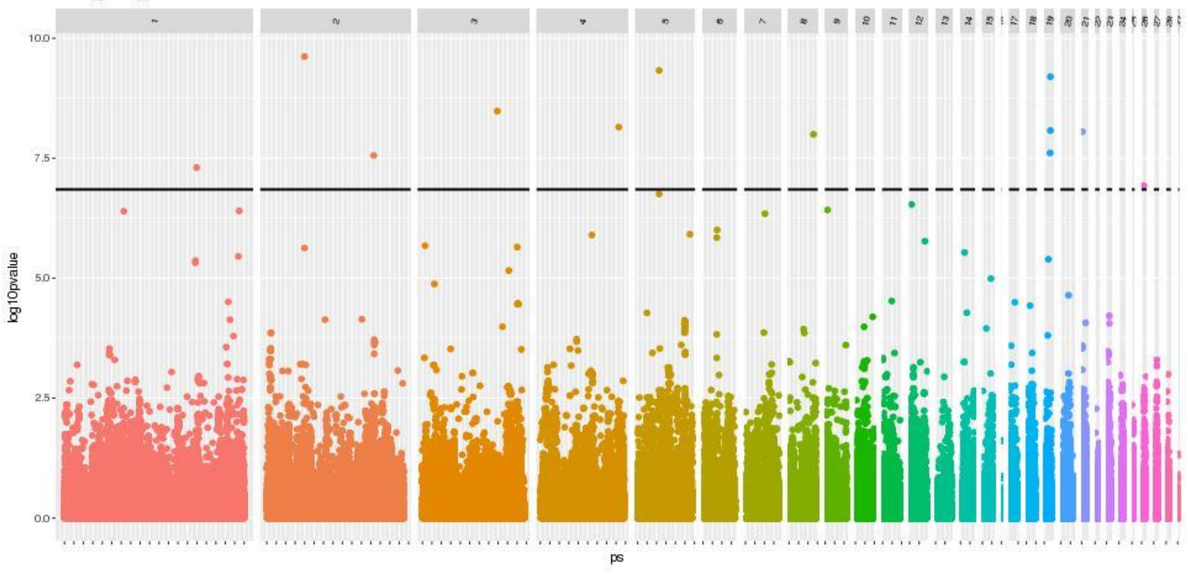



**Figure 2. Manhattan plot for coefficient of digestive use of starch**




Among the 12 genome-wide significant SNPs, 7 were located in intronic regions of known genes and 1 was in the regulatory region of C1ORF174. These genes were involved in intestinal morphology and development (ZIC2, ANO10, F2), immune system (SULF1, CUD109, F2), and regulation of energetic balance (FGGY, PM20D1).

**Table 1. Genes associated with 5% genome-wide significant SNPs.**

| Chr | SNP | Trait | Within Gene/ Intergenic |
|---|---|---|---|
| 1 | 144 284 848 | CDU (DM, Starch, Nitrogen) | ZIC2 |
| 2 | 41 039 328 | CDU (DM, Starch, Nitrogen) | ANO10 |
| 2 | 116 692 708 | AMEn, CDU (DM, Starch, Nitrogen) | SULF1 |
| 3 | 81 690 202 | AMEn, CDU (DM, Starch, Nitrogen) | CD109 |
| 4 | 85 583 360 | CDU (DM, Starch, Nitrogen) | Intergenic |
| 5 | 23 444 968 | AMEn, CDU (DM, Starch, Nitrogen) | F2 |
| 8 | 26 671 543 | CDU (Starch, Nitrogen) | FGGY |
| 19 | 6 390 258 | CDU (Starch, Nitrogen) | Intergenic |
| 19 | 6 677 286 | CDU (Starch, Nitrogen) | Intergenic |
| 19 | 6 764 624 | CDU (Starch, Nitrogen) | Intergenic |
| 21 | 897 100 | AMEn, CDU (Starch, Nitrogen) | 1000 bp before C1ORF174 |
| 26 | 2 317 884 | CDU (Starch, Nitrogen) | PM20D1 |

## Conclusions

These results suggest a list of potential candidate genes involved in digestive efficiency. This list will be enlarged by GWAS analyses on related phenotypes measured on the same birds (feed intake, feed conversion ratio, anatomy of digestive tract) and with transcriptomic data (gizzard, jejunum) obtained on a sample of birds from the F2 generation.

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## References

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