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Genomics and adaptation of chickens to suboptimal diets

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Modern genotypes of meat-type chicken have a very high genetic potential for production traits, but they need a high quality diet to express it. This implies using highly digestible cereals such as corn, concentrated and well balanced protein sources such as soybean. Under the increasing demand for human and animal consumption, the availability and prices of those feedstuffs could hamper the sustainability of broiler production schemes in countries relying on their importation. Adapting birds to alternative diets by genetic selection would allow increasing the percentage of suboptimal but locally produced feedstuffs in their diets.

Very few information is available on the genetics of adaptation of birds to alternative feedstuffs. The possibility of selecting birds on their growth under low protein diet has yet been demonstrated [1-3]. However, a higher selection pressure was required to achieve similar progress than under normal protein diet as the heritability of growth was lower under low protein diet. This selection strategy also led to fatter birds when they were fed a normal protein diet [1-3]. By contrast, digestive efficiency was more heritable when birds were fed a poorly digestible diet (wheat-based) instead of a classical and highly digestible corn-soy diet [4-5]. A divergent selection experiment on AMEn led to a 30-40% difference in digestive efficiency between the good (D+) and poor (D-) digesters when fed a low digestible diet. When fed an easily digestible diet, the difference was still present but reduced to 5-10%. In addition, birds from the D+ line presented more homogeneous digestive efficiency performances than those from the D- line [4].

The differences of digestive efficiency between D+ and D- lines were found to be associated to strong differences in anatomy of the gastro-intestinal tract, D+ birds having heavier gizzard and proventriculus and shorter intestines than D- birds [6-7]. The transit time was also much shorter in D- than in D+, due to a shorter retention time of the bolus in the gizzard [8]. Composition of the microbiota also differed between the two lines, e.g. *E. coli* were more frequent in D- than in D+ [9]. Finally, as a consequence of the difference in EMAn, the two lines presented strong differences in excretion, both for quantity and for the composition of excreta [10]. A multifactorial analysis of performances of these two lines showed that selection for an improved digestive efficiency improved the economic performances (lower feed intake and feed conversion), the environmental performances (lower quantity of excreta, less excretion of nitrogen and phosphorus), and did not modify social performances (behavior and welfare indicators), leading to a global improvement of sustainability of poultry production [11].

A QTL detection experiment has been done on a F2 cross between these two lines and revealed a large number of QTLs for digestive efficiency, anatomy of the digestive tract, microbiota composition and excretion traits [12-14]. Some of these QTLs co-localize with QTLs of feed conversion ratio, illustrating the importance of the digestive component in the global feed efficiency of the birds. Co-localization between QTL controlling efficiency and development of the gastro-intestinal tract, suggesting that mechanic processes are probably involved.

Finally, the presence of QTL of microbiota, the presence of many QTL on chromosome 16 and the difference of resistance to colibacillosis between the two lines set the need for further analysis of the relationships between digestive efficiency, microbiota composition and immune system (see Calenge et al. in these proceedings).

The analysis of transcriptomic data on tissues of the gastro-intestinal tract is also underway to look for functional and positional candidate genes controlling the activity of the gastro-intestinal tract.

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