Genetic and maternal effects on growth and feed efficiency in rabbits

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Molecular indicators of feed efficiency as proposed by a meta-analysis of transcriptomics data

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Improving feed efficiency is an import challenge for pig production. This study aimed at proposing molecular traits able to predict feed conversion ratio (FCR) in growing pigs. A total of 71 pigs from two divergent lines selected for residual feed intake (RFI) and fed under different conditions (*ad libitum* or restricted) and different diets (low fat high starch or high fat high fiber) were considered, so that a broad range of FCR data was obtained. Transcriptomics data from the loin muscle and blood were obtained using porcine microarrays. The dataset (22,288 molecular probes per tissue and pig) was split into 70% for machine learning methods and 30% for cross-validation. Random forests were used to propose a reasonable set of 359 genes identified as very important predictors (VIP) of FCR. The FCR was well predicted (RMSE=0.16; R^2=0.63) by a model combining the expression levels of 50 genes in muscle (out of the 359 VIP). These genes were involved in various biological pathways, including the response to insulin, homeostatic processes, signal transduction, regulation of cell proliferation, apoptosis, protein metabolism, and inflammatory responses. About 82% of the muscle VIP were also expressed in the blood. The FCR was also predicted correctly (RMSE=0.21; R^2=0.52) by using the same model of genes expressed in blood. Technical validation is in progress to evaluate the predictive potential of the model when expression levels of these genes are measured by target methodology (qPCR) in blood of the same pigs. Further tests will be performed on blood samples taken at earlier growth stages to obtain early predictors and by using different pig populations to obtain generic predictors. In conclusion, identifying molecular traits related to feed efficiency could be helpful to identify important genomic regions and new biomarkers for genetic selection. This study is part of the Feed-a-Gene project and received funding from the European Union's H2020 program under grant agreement no. 633531.

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The aim of this study was to evaluate the significance of neonatal environment (ultimately including the microbiota composition) on feed efficiency. For that purpose, half of the rabbits of the G10 line, selected for 10 generations on residual feed intake (RFI), were fostered by does of a non-selected control line G0, and vice versa. In parallel, collaterals were adopted by mothers from their original line. Around 900 animals were produced in 3 successive batches and raised in individual or collective cages. Traits analyzed in this preliminary study were weights at weaning (32 days) and at the end of the test (63 days), average daily gain (ADG), feed intake between weaning and 63 days (FI), feed conversion ratio (FCR) and RFI. Line of the rabbit, type of housing (collective or individual cages: 2 levels) and batch (3 successive mating:3 levels) were significant effects for all traits. G10 does had a negative effect on FCR (+0.06, P=0.04), irrespective of the line of young rabbits. G10 animals were lighter than G0 at 32 days (-83 g) and at 63 days (-161 g). They also had a lower ADG (-2.36 g/day), FCR (-0.36), RFI (-548 g/day) and a lower FI (-839 g), confirming a better feed efficiency. Our results demonstrate that selection on feed efficiency was successful for direct effect but maternal effects were degraded by the selection. This study is part of the Feed-a-Gene Project, funded from the European Union's H2020 Programme under grant agreement no. 633531.