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Divergent selection for residual feed intake influences whole blood transcriptomic profile in growing pigs

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With the aim to improve livestock production efficiency, there is a need to gain insights into the molecular mechanisms underlying feed efficiency. There is increasing evidence that whole blood may provide valuable insight into whole-body energy homeostasis. The current study was undertaken to determine whether pig blood transcriptome was affected by genetic selection for feed efficiency and (or) by nutrition. Large White castrated male pigs from two lines divergently selected for residual feed intake (RFI) were fed diets with the same metabolizable energy level and the same protein content, but either rich in cereals (LF) or in crude fiber and lipids (HF) during 10 weeks in the growing period (n=12 by diet and by line). At the same slaughter age (132 d), pigs selected for low RFI had an improved gain to feed and were leaner than pigs selected for high RFI. Irrespective of selection line, pigs fed the LF diet were heavier and fatter at slaughter than pigs fed the HF diet. Analysis of the blood transcriptome using a porcine microarray (Agilent, GPL16524, 8 x 60K) reveals larger differences between RFI lines than between diets (2154 versus 92 probes differentially expressed (DE), $P < 0.01$). An interaction ($P < 0.01$) between line and diet was also detected for 106 probes corresponding to 57 unique genes. Among the 2154 probes DE according to the line, 1216 exhibited a ratio of expression above 1.2 or below 0.8. This corresponds to 260 unique over-expressed genes and 310 unique down-expressed genes in low RFI pigs compared with high RFI pigs. Genes over-expressed in the low RFI pigs compared with high RFI pigs were associated to the immune response (29 unique genes, cytokine binding, chemokine binding and receptor activity), protein catabolism (24 unique genes, protein ubiquitination, proteolysis) and cell signal (12 unique genes, regulation of signal transduction). Conversely, genes under-expressed in low RFI pigs compared with high RFI pigs were involved in the immune response (64 unique genes; inflammatory response, regulation of immune system process), nucleotide transport (49 unique genes), response to stimulus (25 unique genes), protein transport (22 unique genes), cell adhesion (21 unique genes), carbohydrate metabolism (19 unique genes), and cell organization (15 unique genes). These findings suggest differences in the immune status between pigs divergently selected for RFI. Altogether, this study demonstrates the usefulness of the blood transcriptome investigation to identify molecular differences between genotypes.