La sélection divergente pour la consommation alimentaire journalière résiduelle chez le porc modifie l'expression des gènes dans les tissus adipeux, hépatique et musculaire

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Changes in the expression of genes in adipose tissue, liver and skeletal muscle in response to divergent selection forresidual feed intake in growing pigs

Residual feed intake (RFI) is a selection criterion alternative to feed:gain ratio to improve feed efficiency, and thus to reduce production costs and the negative environmental impacts of pig production. Several studies based on RFI selection experiments have indicated that low RFI is associated with lower body fat content and decreased meat quality; these differences might arise from tissue metabolic reorientations for the storage and use of nutrients. To gain insights intothe molecular mechanisms underlying these differences, gene expression profiles in liver, skeletal muscle and subcutaneous adipose tissue were examined in16pigs(115 kg) from lines divergently selected for RFI. Transcriptomics analyses using a commercial microarray (Agilent-026440 *Sus scrofa* Oligo Microarray v2, 44K) revealed large differences between high and low RFI pigs in the three tissues examined. The number of oligonucleotides found to be differentially expressed ($P< 0.01$) between lines was much higher in muscle (1013) than in liver (809) and adipose tissue (657). Gene functional classification indicated that pigs selected for low RFI generally exhibited a higher expression level of genes known to be involved in mRNA translation in liver and muscle, and of genes associated with mitochondrial energy metabolism in adipose tissue. In contrast, the expression of genes linked to aminoacid catabolism in liver was lower in low RFI than in high RFI pigs. These suggested differences in amino acid synthesis and protein catabolism may be involved in the differences in body composition observed between the two RFI lines.